

Submission
Type
ID
Abstract Type
Abstract Title

Abstract

Submission
Complete?
Committee
Topic
Keywords
Consider for
Different
Presentation?
Presenting
Author Email
Address(es)
Presenting
Author(s)
Institution
Affiliation

Submission Type	Breakout/Quick/Lightning/Poster
ID	11603
Abstract Type	Breakout
Abstract Title	Automating NHSN Antimicrobial Usage Reporting

Abstract

BACKGROUND: Antimicrobial stewardship is crucial to the viability of existing therapies. To facilitate stewardship, the National Healthcare Safety Network (NHSN) receives antimicrobial usage data from hospitals and provides comparisons to national usage patterns. Hospital personnel can then assess whether their antimicrobial policies are consistent with current best practices. Participation in this program is limited. Barriers to participation include the challenge of mapping local medication information to the NHSN list of antimicrobials, the burden of tabulating the necessary statistics, and the technical requirements of generating CDA documents for submission. An automated solution based on existing HL7 interfaces and producing valid CDA documents could significantly lower some of these barriers.

METHODS: Medication administration and patient volume data from a multi-hospital health system were obtained via continuous HL7 message feed. Medication administration data elements included administration time, patient location, and a facility-specific medication identifier. Patient data included admission, transfer and discharge times and locations. Facility medication codes were reconciled to NHSN antimicrobial identifiers via a semi-automated process. The health system formulary included National Drug Code (NDC) identifiers. An RxNorm API mapped NDC identifiers to formulation-specific RxNorm identifiers, and then to parent identifiers for antimicrobials provided by NHSN. Duplicates were removed and missing associations were added manually by comparing names. Antimicrobial route was mainly indicated in the formulary; in rare cases when this was not sufficiently specific, site of administration was used. Antimicrobial therapy days, days present and facility-wide inpatient admissions were calculated per NHSN specifications. Results were compiled via CDA and submitted to NHSN via the web portal.

RESULTS: The RxNorm API yielded mapping between 15,472 NDC identifiers and 847 RxNorm codes, covering 86 (96%) NHSN antimicrobials. After automated and manual reconciliation and excluding formulations administered via nonreportable routes, 216 reportable antimicrobial formulations were identified, covering 67 (74%) NHSN antimicrobials. For July 2018, 206,921 medication administration messages were received, including 11,637 administrations of 48 NHSN antimicrobials at 14 NHSN inpatient locations. Antimicrobials represented 7% of completed administrations and 6,909 days of therapy. An additional 189,717 ADT messages for 5,420 distinct visits were received. These yielded 13,885 facility-wide days present and a 14,797 location-specific days present summed across all inpatient locations and facilities, from 4,054 facility-wide admissions.

CONCLUSIONS: Reconciling local facility formularies with a national standardized list of antimicrobials can be a complicated task requiring human intervention. Once completed, HL7 messages from existing interface engines can supply sufficient information for calculating antimicrobial usage statistics to report to NHSN.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Informatics; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	andy.walsh@hmsinc.com
Presenting Author(s)	Andy Walsh
Institution Affiliation	Health Monitoring Corporate Settings

Submission Type	Breakout/Quick/Lightning/Poster
ID	11754
Abstract Type	Breakout
Abstract Title	Descriptive Analysis of Carbapenemase Gene Distribution Among Enterobacteriaceae, <i>Pseudomonas Aeruginosa</i> , and <i>Acinetobacter baumannii</i> —Antibiotic Resistance Laboratory Network, 2017–2018

Abstract

BACKGROUND: In 2016, CDC began funding regional, state, and local public health laboratories (PHLs) across the United States to identify and characterize clinical isolates of carbapenem-resistant Enterobacteriaceae (CRE), *Pseudomonas aeruginosa* (CRPA), and *Acinetobacter baumannii* (CRAB) as part of the Antibiotic Resistance Laboratory Network (AR Lab Network). We summarize and describe data collected from the AR Lab Network from January 2017 through October 2018.

METHODS: AR Lab Network PHLs performed testing for organism identification, antimicrobial susceptibility (AST), carbapenemase production, and detection of KPC, NDM, VIM, IMP, and OXA-type carbapenemase genes. Network PHLs submitted monthly testing reports to CDC. On a small subset of isolates, CDC conducted AST for additional drugs, PCR, and whole genome sequencing for detection of carbapenemase genes not targeted by existing assays and identification of variants. ARLN regional laboratories also conducted colonization screening for carbapenemase-producing organisms (CPO) related to the CDC AR Containment Strategy.

RESULTS: Through October 2018, AR Lab Network tested 28,466 isolates. Isolates were considered carbapenemase-producing (CP) if positive by either the modified carbapenemase inactivation method or Carba-NP test or PCR-positive for at least one carbapenemase gene. The percentage of CP isolates and the distribution of carbapenemase genes varied by organism and geographic region. Among CP-CRE, KPC was the most common carbapenemase identified, but the distribution of carbapenemase genes varied by genera. NDM- and OXA-48-like-positive isolates were most common among *E.coli*; VIM was most common among *Enterobacter*, and IMP was most common among other genera. There were 86 CP-CRE isolates reported as having more than one carbapenemase gene. Among CRPA tested, 2.8% were CP and VIM was the most common carbapenemase gene detected. Among CRAB, 5.3% were CP and OXA-23-like carbapenemase genes were the most common. Of 10,925 swabs obtained through colonization screenings, 11% were positive for at least one carbapenemase gene.

CONCLUSIONS: The AR Lab Network now provides increased local testing capacity to detect and prevent the spread of emerging resistance threats. With almost 40,000 specimens tested in the first 22 months of the program, the data generated by AR Lab Network is helping identify targets for rapid public health responses and furthering our understanding of the biology and epidemiology of carbapenemase genes.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	uzo0@cdc.gov
Presenting Author(s)	Jennifer Y. Huang
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10764
Abstract Type	Breakout
Abstract Title	Inappropriate Intravenous Antimicrobial Starts: A New Antimicrobial Stewardship Metric for Hemodialysis Facilities

Abstract

BACKGROUND: Antimicrobial use is the most important modifiable risk factor for antimicrobial resistance. Roughly 50% of all antibiotics prescribed in the outpatient setting are inappropriate. This estimate excludes hemodialysis facilities (HDFs), where little is known about prescribing patterns. We measured the incidence of intravenous antimicrobial starts (IVASs) in Philadelphia HDFs and estimated the burden of inappropriate prescribing using a newly devised metric.

METHODS: All HDFs in Philadelphia report dialysis-related clinical events [IVASs, positive blood cultures (PBCs), and/or suspect infections (pus, redness, or increased swelling at the vascular access site)] into the National Healthcare Safety Network (NHSN). All prescribing data were from NHSN. An inappropriate IVAS was defined as one that was initiated in the HDF and reported without all of the following: a PBC, a blood sample collected for culture, and a suspect infection. Rates were calculated from January 2018-June 2018 and were stratified by access type. Pooled mean rates (PMRs) were calculated as the total count of an event over the number of patient-months reported.

RESULTS: Over the six-month study period, 483 IVASs (PMR=2.30 per 100 patient-months) occurred in Philadelphia HDFs (n=54). Of these, 303 (62.73%) were categorized as outpatient starts, as opposed to a continued inpatient course. Of the new outpatient starts, 171 (56.44%) were categorized as inappropriate (PMR=0.82 per 100 patient-months). Of the inappropriate starts, 71.35% involved vancomycin and 70.76% occurred without at least one reported symptom (cellulitis, chills/rigors, drop in blood pressure, and/or fever). The PMRs of inappropriate IVASs started in HDFs in patients with a central line compared to those with a fistula or graft were 2.04 and 0.57 per 100 patient-months, respectively ($p<0.0001$).

CONCLUSIONS: We estimate that more than half of all IVASs in Philadelphia HDFs occurred without an apparent indication; these likely represent opportunities to reduce inappropriate antimicrobial use. These findings show a need for promoting antimicrobial stewardship among HDFs. This new metric can allow HDFs and public health agencies to track and understand inappropriate prescribing, which can lead to targeted prevention efforts in high burden facilities or jurisdictions. This metric can also serve as a measure for longitudinally assessing the effectiveness of stewardship interventions. Secondary results showed a significantly higher rate of inappropriate IVASs in central line patients. In addition to reducing bloodstream infection rates, limiting the use of central lines may also reduce the rate of inappropriate antimicrobial prescribing in the hemodialysis setting.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Outcome Measures; Epidemiology; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	phillip.hahn@phila.gov
Presenting Author(s)	Phillip D. Hahn
Institution Affiliation	Philadelphia Department of Public Health CDC/CSTE Fellow

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Surveillance of Hospital Antimicrobial Use and Antimicrobial Stewardship Programs Via the National Healthcare Safety Network (NHSN): A State and National Progress Report

Abstract

BACKGROUND: The Centers for Disease Control and Prevention's (CDC's) National Healthcare Safety Network (NHSN) launched antimicrobial use (AU) surveillance in 2012 and added questions about antimicrobial stewardship program (ASP) status to the NHSN annual healthcare facility survey in 2014. State health departments, including Tennessee's and Oregon's, are spurring hospital participation in AU surveillance and are using AU data submitted to NHSN for analysis and action. The presenters in this session will provide a progress report on programmatic efforts underway at the state and national levels to expand and enhance AU surveillance and measure and motivate ASP activities.

METHODS: Descriptive statistical analyses of NHSN data provide up-to-date snapshots of AU surveillance coverage at the state and national levels, the extent of hospital variation in AU rates, and recent growth of hospital ASPs. The Tennessee Department of Health's (DOH's) use of AU data reported from hospitals throughout the State enable analysis of geographic variation. The Oregon Health Authority (OHA) has garnered practical insights into expanding AU surveillance coverage through its efforts to spur AU participation in hospitals. NHSN's newly updated AU summary measure—the Standardized Antimicrobial Administration Ratio (SAAR) —is reviewed and AU analytic features available to NHSN users in state, territorial, and local health departments are highlighted.

RESULTS: As of December 1, 2018, 1155 hospitals have submitted at least one month of AU data to NHSN, and in 2017 the percentage of hospitals reporting ASPs that include all core programmatic elements reached a new high of 76.4%. The Tennessee DOH's statewide analysis for all antimicrobials showed significant regional rate variation, with the highest rate in northeast Tennessee hospitals: 710 days of therapy/1,000 days present in 2017. Through AU onboarding efforts, OHA strengthened partnerships with ASPs and academic stakeholders and developed an antimicrobial stewardship collaborative. In late 2018, NHSN introduced a second iteration of the SAAR, enabling targeted analysis of an expanded set of antimicrobial categories across additional patient care locations and providing a new resource for public health and clinical professionals who seek to curb antimicrobial overuse.

CONCLUSIONS: New methods for measuring AU, substantial growth in AU surveillance coverage, and innovative analyses of AU data are important steps. Additional advances by public health programs at all geographic levels, accompanied by cross-jurisdictional knowledge transfers and extension of ASPs, including to healthcare settings beyond hospitals, can enable more rapid progress against the dual threats of indiscriminant AU and the spread of resistant pathogens.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	dap1@cdc.gov
Presenting Author(s)	Daniel Pollock
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Lightning
Abstract Title	An Epidemiologic Response to an Area of High Carbapenemase-Producing Carbapenem-Resistant Enterobacteriaceae Prevalence in Indiana

Abstract

BACKGROUND: Carbapenem-resistant *Enterobacteriaceae* (CRE) are an emerging antibiotic resistant threat, largely due to the emergence of carbapenemase-producing CRE (CP-CRE). In December 2015, the Indiana State Department of Health (ISDH) mandated CP-CRE reporting for both isolates and condition, allowing the ISDH to identify CP-CRE statewide. Through this surveillance, the ISDH identified a high prevalence of CP-CRE in northwest Indiana, with 43% (N=152/355) in 2016 and 46% (N=135/294) in 2017.

METHODS: In response to the CP-CRE burden, the ISDH refocused efforts to prioritize northwest Indiana long-term care facilities (LTCFs) for intervention. At the time of initial response, 51 LTCFs were located in the area. Response activities included site visits to promote education and identification of best practices and opportunities for improvement in all northwest LTCFs regarding infection prevention and CP-CRE transmission. All site visits utilized the Centers for Disease Control and Prevention (CDC) Infection Control Assessment and Response (ICAR) tool. Site visits were followed up with a written report outlining identified best practices and opportunities for improvement.

RESULTS: Site visits were conducted at 43 of the 51 (84%) LTCFs in northwest Indiana. Eight LTCFs declined a site visit. Most facilities reported having policies for implementing transmission-based precautions and having a written surveillance plan for tracking infections occurring within the facility. Improvement opportunities identified included the need for formal infection prevention and annual personal protective equipment (PPE) training, performing bundle measure audits, and increased staff retention.

CONCLUSIONS: Historically, healthcare facilities have viewed the ISDH as only a regulatory agency. This proved challenging for the ISDH team to collaborate with LTCFs. However, through careful communication and explanation of the non-punitive site visit, the ISDH was able to successfully reach nearly all northwestern LTCFs. This response effort allowed the ISDH to provide informational resources such as infection prevention guidance, communicable disease reporting requirements, and health department contact information. Furthermore, this response greatly improved communication channels between the ISDH and LTCFs in northwest Indiana. This communication has proved invaluable for collaboration to decrease healthcare-associated infections in Indiana healthcare facilities.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Infectious Diseases; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	cfeaster@isdh.in.gov
Presenting Author(s)	Christine A Feaster
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11378
Abstract Type	Lightning
Abstract Title	Infection Control Assessment of Long-Term Acute Care Facilities (LTACs)/Skilled Rehabilitation Facilities (SRFs) in Massachusetts: Building Capacity to Contain Antibiotic Resistant Pathogens

Abstract

BACKGROUND: Emergence of carbapenem-resistant *Enterobacteriaceae* as well as *Candida auris* represents substantial infection threats. Transmission of these and other multi-drug resistant organisms (MDROs) in healthcare settings is of concern as an increasing number of facility-based outbreaks are identified. Many outbreaks occur in LTACs where advanced, post-acute care is provided to patients with extensive prior exposure to healthcare and antibiotics, known risk factors for MDRO acquisition. To assess and support infrastructure to contain MDROs in LTACs, the Massachusetts Department of Public Health (MDPH) received funding from CSTE to partner with JSI Research and Training Institute, Inc. (JSI) in conducting infection control assessments at LTACs/SRFs. Previous MDPH assessments have targeted dialysis and long-term care facilities.

METHODS: MDPH recruited nine licensed LTACs/SRFs to participate in Infection Control and Response (ICAR) assessments. The standard CDC acute care hospital ICAR tool was utilized for these settings to conduct day-long, on-site assessments, including direct observation of practices. This tool assessed three domains: Infection Control Program and Infrastructure; Infection Control Training, Competency, and Implementation of Policies and Practices; and Systems to Detect, Prevent, and Respond to Healthcare-Associated Infections and MDROs. A debriefing was held with facility leadership to review findings and an infection control resource toolkit was provided. A facility-specific report summarized findings, highlighting areas for improvement and providing resources specific to the gaps identified. Findings from all ICAR assessments were analyzed and synthesized into a single comprehensive report and needs assessment to share with stakeholders and facilities.

RESULTS: ICAR assessments indicated that 100% of facilities achieved best practices in several key activities including: providing infection prevention information to families/visitors; performing hand hygiene audits with feedback; preferential promotion of alcohol-based hand rub; and having systems for inter- and intra-facility communication of patient infectious disease status. Activities for which *fewer than* 50% of facilities achieved best practices included: performing audits and feedback on urinary and central venous catheter insertion; competency-based trainings for proper use of PPE, ventilator adverse event prevention, injection safety and environmental cleaning; having policies for cleaning non-critical equipment; and having systems to detect infectious patients at the point of entry.

CONCLUSIONS: LTAC/SRF ICAR assessments identified key infection control gaps and provided opportunities for immediate feedback and corrective recommendations. A comprehensive needs assessment has also provided clear objectives for ongoing support from MDPH and other stakeholders for infection control to contain MDROs.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Infection Control; Prevention
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	melissa.cumming@state.ma.us
Presenting Author(s)	Melissa Cumming
Institution Affiliation	Massachusetts Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11732
Abstract Type	Poster
Abstract Title	Carbapenem-Resistant <i>Enterobacteriaceae</i> Surveillance, Wisconsin, 2010–2018

Abstract

BACKGROUND: Carbapenemase-producing carbapenem-resistant *Enterobacteriaceae* (CP-CRE) are emerging in the United States as important healthcare-associated pathogens. Carbapenemases, which include KPC, NDM, OXA, VIM, and IMP, are plasmid-encoded enzymes that can mediate resistance to penicillins, cephalosporins, monobactams, and carbapenems. Infections with these organisms are associated with high morbidity and mortality and represent both a clinical and public health challenge. To better characterize and prevent transmission of CP-CRE, during August 1, 2010 the Wisconsin State Laboratory of Hygiene (WSLH) began to request and conduct molecular testing on isolate submission of carbapenem non-susceptible *Enterobacteriaceae*.

METHODS: Demographic data is included for clinical isolates submitted to WSLH. PCR for KPC carbapenemase has been performed on carbapenem non-susceptible *Enterobacteriaceae* isolates since 2010. PCR tests for NDM (2013), OXA (2014), VIM (2017) and IMP (2018) have been added to the testing algorithm. Beginning in July 2017 all isolates were screened for the presence of any carbapenemases using the modified carbapenemase inactivation method (mCIM). mCIM-positive isolates were then tested by PCR. Speciation was confirmed by MALDI-TOF, antimicrobial susceptibility testing (AST) was performed using broth microdilution, and pulsed-field gel electrophoresis (PFGE) was performed on CP-CRE isolates.

RESULTS: From August 1, 2010 to November 30, 2018, clinical laboratories in Wisconsin submitted a total of 2912 isolates from 2309 unique patients. Patients ranged in age from 0 to 103, with a median age of 69; 59% of patients were female. Patients were residents of 62 of 72 counties (86%) with a plurality of the patients (36%) residing in the southeastern region of the state. Among the 2912 isolates, 432 (15%) tested positive for a carbapenemase (393 for KPC, 18 for NDM, 12 for OXA, and 9 for IMP); 253 were *Klebsiella* spp., 62 were *Enterobacter* spp., 59 were *Escherichia coli*, and 48 were other *Enterobacteriaceae* species; 406 (94%) were tested using PFGE. Among the 1033 isolates with AST performed, 466 (45%) were found to be resistant to at least one carbapenem. A total of 22 potential clusters were identified by PFGE, with resultant epidemiologic investigations by the Wisconsin Division of Public Health, and infection prevention education to staff members at the involved hospitals.

CONCLUSIONS: Enhanced CRE surveillance in Wisconsin has provided comprehensive data on CRE and CP-CRE in the state. Future analysis includes review of differences between patient characteristics among the different carbapenemases, in particular IMP, which has largely been found in patients from more rural counties.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Surveillance; Antimicrobial Resistance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	megan.lasure@wi.gov
Presenting Author(s)	Megan Lasure
Institution Affiliation	Wisconsin State Laboratory of Hygiene State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11347
Abstract Type	Poster
Abstract Title	Clinician Perceptions and Experiences with Antibiotic Prescribing for Acute Respiratory Infections before and after an Outpatient Antimicrobial Stewardship Campaign

Abstract

BACKGROUND: More than 50% of antibiotic prescriptions for acute respiratory infections (ARI) in primary care clinics (PCC) are inappropriate which contributes to the development of antimicrobial resistance. Factors influencing inappropriate prescribing include patient pressure, clinician perceptions of decreased patient satisfaction, and visit time constraints. Nebraska Medicine partnered with Nebraska Antimicrobial Stewardship Assessment and Promotion Program (NE ASAP), an initiative funded by Nebraska DHHS through a CDC grant, in an antimicrobial stewardship campaign (ASC) to reduce antibiotic prescribing for ARI in PCC. Clinician perceptions on antibiotic prescribing were evaluated pre- and post-ASC.

METHODS: The ASC was implemented in 10 PCC in Winter 2018. Five clinics received clinician-directed interventions (ARI educational videos, management pocket cards and posters) with the remaining 5 received both clinician- and patient-directed (empowerment posters, Be Antibiotic Aware pledge card) interventions. Clinicians (N=164) in all 10 PCC received anonymous web-based surveys before and after ASC. Self-reported responses were captured using Likert scale. The survey was opened for 3 weeks, with reminders sent weekly. Statistical analyses used Fisher's exact test.

RESULTS: Survey response rate was higher pre- vs. post-ASC periods (54.3% vs. 31.1%, $p < 0.01$). Most respondents cared for both children and adults (69.2%) with 50% in practice >5 years. One-third of clinicians in both periods (32.6% pre- and 31.4% post-ASC) reported experiencing frequent patient requests for antibiotics. Many clinicians (44.9% pre- and 47.1% post-ASC) felt moderate to extreme pressure from patients to prescribe antibiotics. Some (11.8%) clinicians perceived a change in prescribing pressure post-ASC. When patients requested antibiotics for ARI, 39.3% of clinicians reported prescribing antibiotics occasionally or often before, decreasing to 23.5% after ASC ($p = 0.06$). Majority of clinicians reported success in both periods in convincing patients that antibiotics were unnecessary (78.7% pre- and 80.4% post-ASC). When asked whether they will prescribe antibiotics for ARI upon patient request in the next 6 months, over two-thirds in both periods reported they would not (77.5% vs 66.7%, $p = 0.17$). While 45.1% of clinicians thought ASC materials facilitated meaningful discussion with patients, only 15.7% changed prescribing practices. More than half of survey responders (54.9%) agreed or strongly agreed ASC was useful and should continue.

CONCLUSIONS: Clinicians in PCC frequently experience patient pressure to prescribe antibiotics for ARI. Implementation of ASC was associated with a reduction in self-reported antibiotic prescribing. State health departments can play a vital role in supporting outpatient antimicrobial stewardship efforts by educating the public never to pressure clinicians to prescribe antibiotics.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Health Care
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	salman.ashraf@unmc.edu
Presenting Author(s)	Muhammad Salman Ashraf
Institution Affiliation	University of Nebraska Medical Center Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	10823
Abstract Type	Poster
Abstract Title	Resistance to Antifungals in <i>Candida Glabrata</i> Isolates in the Southeast Region

Abstract

BACKGROUND: *Candida* spp. are the leading cause of central line-associated bloodstream infections (CLABSI) in adult and pediatric wards and ICUs in Tennessee. *C. glabrata* causes approximately one-third of all candidemia, and this proportion has increased over time. This species is commonly resistant to antifungal medications, leading to treatment challenges and increased morbidity and mortality. Primarily due to high rates of fluconazole resistance in *C. glabrata* (10% in recent Emerging Infections Program [EIP] surveillance), recommended initial therapy for candidemia recently changed from fluconazole to echinocandins. However, the proportion of *C. glabrata* isolates nonsusceptible (NS) to echinocandins is increasing, with 6.0% of isolates NS (4.6% resistant and 1.4% intermediate) in EIP surveillance. In 2016, the Antibiotic Resistance Laboratory Network (ARLN) was created to monitor for resistance threats, including in *Candida*. The Tennessee State Public Health Laboratory serves as the Southeast ARLN laboratory for six states and Puerto Rico and performs confirmatory identification and susceptibility testing of *Candida* isolates from sentinel laboratories. We describe the proportion of resistance in *C. glabrata* isolates sent to the Southeast ARLN since 2017.

METHODS: *C. glabrata* isolates submitted to the Southeast ARLN from Alabama (n=6), Florida (n=1), Georgia (n=4), Mississippi (n=4), and Tennessee (n=53) sentinel laboratories were included for analysis. Species identification was confirmed by Bruker Biotyper matrix assisted laser desorption-ionization time of flight (MALDI-TOF). Antimicrobial susceptibility testing (AST) was performed using TREK frozen broth microdilution panels. Data were extracted from the laboratory information management system. Analyses were conducted using SAS v9.4.

RESULTS: During April 2017–November 2018, the Southeast ARLN performed AST on 68 *C. glabrata* isolates, all from U.S. residents. Of the 68 isolates, 12 (18%) were resistant to fluconazole and 5 (7%) were NS (2% [n=1] intermediate, 6% [n=4] resistant) to at least one echinocandin. One isolate was echinocandin NS and resistant to fluconazole. The predominant specimen source was blood (n=41, 60%), followed by urine at 13% (n=9). When restricted to bloodstream isolates, 9 of 41 (22%) were resistant to fluconazole, 1 of 41 (2%) was intermediate to echinocandins, and 1 of 41 (2%) was both echinocandin and fluconazole resistant.

CONCLUSIONS: Although the sample size was small and not necessarily representative, the proportion of isolates resistant to fluconazole was higher than expected, particularly in bloodstream isolates. Characterizing *C. glabrata* isolates submitted to the Southeast ARLN informs both regional resistance patterns and clinical decision-making, and should allow for monitoring of dynamic resistance profiles.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Surveillance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Carolyn.Stover@tn.gov
Presenting Author(s)	Carolyn A. Stover
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10891
Abstract Type	Poster
Abstract Title	Understanding the Needs of Antibiotic Stewardship Program Leaders: A Survey of Statewide Antibiotic Stewardship Summit Attendees

Abstract

BACKGROUND: Antibiotic resistance (AR) is a serious threat to public health and antibiotic stewardship (AS) is the most important action to combat AR. We studied the needs of AS program leaders to inform public health AS efforts.

METHODS: Nebraska Antimicrobial Stewardship Subcommittee and Nebraska Antimicrobial Stewardship Assessment and Promotion Program (ASAP), funded by the Nebraska Department of Health and Human Services Healthcare-Associated Infections Program through a CDC grant, developed a 13-question survey. The anonymous survey was conducted with all attendees during the inaugural statewide AS summit held in June 2018. The survey instrument included questions on demographics, identified areas of antibiotic misuse, barriers to AS implementation, and expectations for infrastructure and educational assistance from the health department. Results were summarized using descriptive statistics.

RESULTS: Of 264 attendees, 153 (58%) responded to the survey. Most respondents (54%) worked primarily in long-term care, followed by acute care hospitals (42%) and outpatient (11%) settings. Respondents included pharmacists (37%), infection preventionists (20%), nursing leaders (15%), nurses actively involved in patient care (15%) and prescribers (11%). An overwhelming majority (85%) have been in healthcare for >5 years with 43% having >20-year tenure. Top areas of antibiotic misuse identified by the respondents included asymptomatic bacteriuria (63%), inappropriate diagnostic testing (54%), unnecessary broad spectrum antibiotic use (43%), guideline-discordant antibiotic use for upper respiratory tract infections or chronic obstructive pulmonary disease (42%), and excessive duration of antibiotics (41%). The top three reported barriers of AS program implementation included lack of prescriber buy-in (41%), limited resources or competing priorities (40%), and deficiencies in knowledge (30%). The most requested support from the state health department included educational webinars for healthcare workers (51%), public education (47%), provision of local antibiotic use and resistance (AUR) data (37%) and benchmarking of statewide AUR (36%). The top three educational topics requested were infection management (48%), AS implementation (19%) and AS related laboratory and microbiology concepts (15%). Although most (87%) respondents reported having at least one social media account, the more preferred methods of receiving AS related updates included emails (81%), in-person conferences (60%) and webinars (59%). Social media and/or online videos were chosen as a preferred method by 30% of respondents.

CONCLUSIONS: Healthcare professionals expect state health departments to support development of AS programs in healthcare facilities by providing AS resources and disseminating AS education. Educational efforts should be multimodal, targeting both healthcare workers and the public.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	salman.ashraf@unmc.edu
Presenting Author(s)	Muhammad Salman Ashraf
Institution Affiliation	University of Nebraska Medical Center Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11684
Abstract Type	Quick
Abstract Title	An Outbreak of Oxa-23 Carbapenem-Resistant <i>Acinetobacter Baumannii</i> (CRAB) in a Connecticut Acute Care Hospital

Abstract

BACKGROUND: *Acinetobacter baumannii* is known to efficiently contaminate the healthcare environment and lead to outbreaks of healthcare-associated infections. Carbapenem-resistant *Acinetobacter baumannii* (CRAB) is reportable in Connecticut (CT); characterization of these isolates is conducted by the CT State Public Health Laboratory (SPHL) and the Antibiotic Resistance Laboratory Network (ARLN) regional laboratory.

METHODS: In July 2018, the Connecticut Healthcare Associated Infections/ Antimicrobial Resistance (HAI/AR) Program of the CT Department of Public Health (DPH) received notification from the Northeast ARLN regional laboratory at Wadsworth Center that a patient in Connecticut had tested positive for the carbapenemase gene, Oxa-23, in an *Acinetobacter baumannii* blood isolate collected from a patient at an acute care hospital. The HAI/AR Program reached out to the infection prevention team at the acute care hospital to provide technical assistance in the interpretation of test results and the implementation of an investigation and control strategy. The hospital infection control team worked to identify potential sources of the infections and to implement recommendations for outbreak control. Staff from the HAI/AR Program travelled to the facility to provide CRAB education to staff and to provide on-site technical assistance regarding the implementation of infection control guidance.

RESULTS: Working closely with DPH, the acute care hospital identified 9 patients with CRAB isolates carrying the Oxa-23 gene collected over an eight-week period, representing an outbreak of CRAB at the facility. The majority (6/9, 67%) of cases were identified with isolation of the organism from a respiratory site. Unreported construction within an area used for the cleaning and storage of ventilator equipment for affected units was identified.

CONCLUSIONS: This outbreak investigation illustrates the complex nature of outbreaks of emerging antimicrobial-resistant organisms, including the need for targeted education of medical, infection control, laboratory, and pharmacy staff. The ability to identify clusters of antimicrobial-resistant organisms may be impacted by the specimen sources included in routine surveillance. Investigations of antimicrobial-resistant organisms should also account for both potential points of organism acquisition and onset of infection. Outbreaks of Oxa-23 CRAB present specific challenges, as this carbapenemase gene is not identified by commercial systems typically used for the characterization of clinical isolates and/or colonization screening.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Infection Control; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	meghan.maloney@ct.gov
Presenting Author(s)	Meghan Maloney
Institution Affiliation	Connecticut Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11759
Abstract Type	Quick
Abstract Title	Carbapenem Resistant Enterobacteriaceae Infections in New Hampshire

Abstract

BACKGROUND: Carbapenem-Resistant *Enterobacteriaceae* (CRE) are a family of bacteria that are difficult to treat due to high levels of antibiotic resistance. The New Hampshire (NH) communicable disease rules require facilities, laboratories, and providers to identify, and report CRE to the NH Division of Public Health Services (DPHS) within 72 hours of diagnosis or suspicion of diagnosis.

METHODS: A confirmed CRE case was defined as a NH resident or patient with an *Enterobacteriaceae* isolate recovered from a culture that tested resistant to one of the following carbapenems: imipenem, meropenem, doripenem or ertapenem and/or demonstrated production of a carbapenem inactivation enzyme (2012 CDC CRE definition). However, organisms intrinsically resistant to imipenem, were required to be resistant to a carbapenem other than imipenem to be considered a case. Twelve months are required to elapse between positive culture results with the same organism from the same person for an individual to be considered a new case. DPHS requested that all CRE isolates be sent to the Public Health Lab (PHL) for further cascade testing which included identification confirmation, select antibiotic susceptibility testing, phenotypic as well as carbapenemase genetic testing for common CP-CRE mechanisms of resistance.

RESULTS: In 2017, the NH Healthcare-Associated Infections Program identified 52 confirmed CRE cases. The majority of isolates were resistant to ertapenem only (54%), isolated from urine specimens (75%), and obtained from an outpatient setting (54%). Additionally, 42% had documented inpatient and 43% had outpatient healthcare exposure in the six months prior to the isolation of a CRE organism. The PHL identified 3 carbapenemase producing CRE (CP-CRE) among 50 tested by the Public Health. All 3 harbored the KPC plasmid; 2 were *Klebsiella oxytoca* while 1 was *Enterobacter cloacae*.

CONCLUSIONS: While the relatively high percentage of patients identified as having CRE isolated from a culture had healthcare exposure aligns with the results of recent research indicating the main risk factor for CRE acquisition is healthcare exposure, further exploration of this correlation is needed overall[1]. However, these data have implications for important infection prevention activities for the state of NH as well as for surrounding states. NH is one of the few states collecting data on CP-CRE and Non-CP-CRE cases. The low incidence of CRE, especially CP-CRE, has allowed NH a more aggressive containment approach to prevent the further emergence of CRE.
[1] <https://www.cdc.gov/hai/organisms/cre/cre-clinicianfaq.html>

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Surveillance; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	yvette.perron@dhhs.nh.gov
Presenting Author(s)	Yvette Perron
Institution Affiliation	New Hampshire Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11302
Abstract Type	Quick
Abstract Title	Cumulative Regional and Statewide Antibigram Using Whonet and National Healthcare Safety Network (NHSN) Antimicrobial Resistance (AR) Module Data

Abstract

BACKGROUND: Cumulative antibiograms inform empiric antibiotic therapy. They report proportions of specific organism isolates that are susceptible to antimicrobials tested. The National Healthcare Safety Network (NHSN) Antibiotic Resistance (AR) Option allows facilities to voluntarily report AR data for certain bug-drug combinations. The Tennessee Department of Health (TDH) extracted NHSN data and developed a statewide antibiogram and for Tennessee's eight emergency medical services (EMS) regions.

METHODS: Acute care hospitals across Tennessee submitted data to the NHSN AR Option and conferred rights to TDH. NHSN data was transposed in SAS 9.4 with each row representing all susceptibility results for a single isolate. The final antibiotic interpretation (susceptible, intermediate, or resistant) entered in NHSN was used as the variable to create susceptibility profiles. Isolates without a clear interpretation were excluded. A data library, created using BacLink, was analyzed using WHONET 5.6. Antibiogram specimens were stratified by type and location of collection (wards, critical care units, and emergency departments [ED]).

RESULTS: During February 2017–November 2018, twenty-one hospitals from four EMS regions submitted data to NHSN for a total of 48,917 isolates. Of submitting hospitals, eleven were from the Northeast region, four from the Middle region, and three from the Southeast and South Central regions. Thirty organisms were reported: 22 gram-negative rods, six gram-positive cocci, and two candida species. Forty antibiotics were tested in urine, blood, and respiratory samples. 70% of isolates were collected from the ED, 14% from inpatient wards, 9% from critical care units and the remaining 6% from various units. Urinary *E. coli* isolates from EDs were more likely to be ciprofloxacin susceptible (73.8%) than those from inpatient units (63.4%). 83.9% of Northeast TN *E. coli* isolates were ciprofloxacin susceptible vs. 70.5% in Middle TN. Northeast TN had the highest percentage imipenem susceptible *Enterobacter* spp. (95.2%) vs. Middle TN (90.8%). For *Klebsiella* spp., Middle TN had the most imipenem susceptible isolates (99.4%) vs. Northeast TN (98%).

CONCLUSIONS: Regional cumulative antibiograms vary significantly. This suggests that in Tennessee, regional antibiograms may provide better data than statewide antibiograms to guide empiric therapy. At present, antibiotic resistance data submitted voluntarily to NHSN allows TDH to develop regional antibiograms that represent half of the EMS regions in Tennessee. Additional outreach and recruitment from facilities in non-reporting EMS regions is needed.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Surveillance; Healthcare Associated Infections (HAI); Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Matthew.Estes@tn.gov
Presenting Author(s)	Matthew D. Estes
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11030
Abstract Type	Quick
Abstract Title	Epidemiology of Methicillin Resistant Staphylococcus Aureus (MRSA) Blood Stream Infections (BSI) in Acute Care Hospitals in Tennessee, 2011–2017

Abstract

BACKGROUND: Acute care hospitals in Tennessee have reported MRSA BSIs from inpatient areas and emergency departments (ED) to CDC’s National Healthcare Safety Network (NHSN) since July 2010. We describe trends in community onset (CO) and health-care onset (HO) MRSA BSI across the state.

METHODS: We assessed the burden of MRSA BSIs at 117 acute care hospitals between 2011 and 2017. NHSN definitions were used to classify events as HO or CO based on specimen collection day. CO BSIs were further stratified by location on specimen collection date (ED and inpatient [IP]). Accounting for 2015 NHSN protocol changes, individuals with same day cultures in ED and IP locations were classified as a single CO-ED event. BSI counts and proportions were calculated per year by each onset group for all emergency medical service regions as well as the state. Prevalence and incidence rates were defined as follows. HO incidence: number of HO BSIs per 10,000 patient-days, CO-IP prevalence: number of CO-IP BSIs per 10,000 admissions, and CO-ED prevalence: number of CO-ED BSIs per 10,000 encounters.

RESULTS: Between 2011 and 2017, all MRSA BSIs increased 33% from 2,271 to 3,031 cases per year. In 2011, the HO, CO-IP, and CO-ED groups accounted for 19.4%, 41.7%, and 38.9% of events, respectively. In 2017, HO, CO-IP, and CO-ED groups represented 9.6%, 27.4%, and 63.0% of MRSA BSIs, respectively. HO incidence decreased from 1.2 to 0.8 BSIs/10,000 patient-days from 2011 to 2015 and remained stable until 2017. In contrast, the CO-ED prevalence maintained an average of 3.2 BSIs/10,000 encounters until 2015, after which it increased by 69% to 5.4 BSIs/10,000 encounters in 2017. All regions except West Tennessee saw increases in CO-ED prevalence. East Tennessee had the highest prevalence of 8.9 BSIs/10,000 encounters in 2017, a 186% rise from 4.9 BSIs/10,000 encounters in 2011. CO-ED BSIs increased in all adult age and gender groups from 2011–2017. The proportion of all CO-ED BSIs attributable to women aged 18 to 34 increased from 4.5% in 2011 to 9.5% in 2017, making it the demographic with the largest increase.

CONCLUSIONS: HO MRSA BSIs in Tennessee have decreased since 2011. Despite this success, this analysis highlights the alarming rise of CO-ED MRSA BSIs. The regional and demographic differences observed, as well as results of data not described here, lead us to hypothesize that the increases in CO-ED MRSA BSIs may be associated with increasing injection drug use in Tennessee.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Surveillance; Antimicrobial Resistance; Substance Abuse
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	meghana.parikh@tn.gov
Presenting Author(s)	Meghana Pendurthi Parikh
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11546
Abstract Type	Quick
Abstract Title	Outbreak of <i>Acinetobacter Baumannii</i> with Rare Carbapenemase OXA-72 in an Intensive Care Unit and Associated Long-Term Care Facilities, Wisconsin 2018

Abstract

BACKGROUND: During October 2018, the Wisconsin Division of Public Health (WDPH) was notified of a cluster of carbapenem-resistant *Acinetobacter baumannii* (CRAB) with identical resistance patterns on antimicrobial susceptibility testing (AST) in three patients admitted to intensive care units in one facility (facility A) in southeastern Wisconsin. In the United States, approximately half of *Acinetobacter* organisms are nonsusceptible to carbapenems. Carbapenem resistance mediated through plasmid-encoded carbapenemases contributes to transmissibility and spread of clinically important resistance. However, detecting plasmid-encoded resistance can be challenging.

METHODS: Additional cases were identified through the Wisconsin Clinical Laboratory Network. The three major clinical laboratories in southeastern Wisconsin were asked to provide information, including AST, on all CRAB isolate submissions from January 1 to October 31, 2018. For patients with available CRAB isolates, information on healthcare exposures was collected. Available isolates were submitted to Wisconsin State Laboratory of Hygiene (WSLH). AST was performed using broth microdilution. Isolates resistant to amikacin, aztreonam, ceftriaxone, gentamicin, levofloxacin, meropenem, piperacillin-tazobactam, tobramycin, and susceptible to polymyxin-B underwent Illumina whole-genome sequencing (WGS) at WSLH to determine their relatedness. Isolates that were closely related were analyzed using the MinION to obtain long read sequences for more comprehensive sequencing data, including plasmid identification.

RESULTS: During 2018, the three clinical laboratories reported 34 CRAB out of 73 *Acinetobacter baumannii* isolates. Twelve CRAB isolates were available for further analysis at WSLH. Seven isolates with characteristic AST pattern underwent WGS, with five found to be closely related. All five had plasmids that contained OXA-72 and were considered to be part of the same cluster. Among those five, three were further characterized using the MinION. The plasmids were subsequently found to be identical, suggesting that transmission occurred between these patients. Among the five patients with identical plasmids, two of the patients from facility A had been admitted from long-term care facility B, and one patient from an unrelated acute care facility had also been admitted from long-term care facility B. The remaining two patients from facility A had been admitted from home and an unrelated long-term care facility.

CONCLUSIONS: Clinical laboratory networks provide timely data in the investigation of clusters and outbreaks. In CRAB and other organisms with demonstrated resistance to multiple classes of antimicrobials, AST might prioritize resources such as WGS in the detection of plasmid-encoded carbapenemases and investigation of outbreaks. Furthermore, long read WGS might identify plasmids containing carbapenemases when PCR assays do not detect rare carbapenemases.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Outbreaks; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email	uxt2@cdc.gov
Address(es)	
Presenting Author(s)	Lina I Elbadawi
Institution Affiliation	Wisconsin Department of Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10860
Abstract Type	Quick
Abstract Title	Under the Radar: Detecting and Responding to IMP-13 Producing <i>Pseudomonas Aeruginosa</i> in Colorado, 2018

Abstract

BACKGROUND: In 2018, the Colorado Department of Public Health and Environment (CDPHE) identified the first isolate of carbapenemase-producing carbapenem-resistant *Pseudomonas aeruginosa* (CP-CRPA) in Colorado from a patient hospitalized in an intensive care unit (ICU) at an acute care facility. CP-CRPA is uncommon in the U.S.; a rapid response to contain emerging carbapenemases is crucial to halt their spread. We aimed to characterize the extent of transmission through culture-based point prevalence surveys (PPSs) in the ICU and to use whole genome sequencing (WGS) to contextualize the epidemiology of known cases.

METHODS: A six-month retrospective laboratory audit of clinical *P. aeruginosa* isolates non-susceptible to at least one carbapenem (excluding ertapenem) from ICU patients was reviewed to ascertain possible epidemiologically-linked patients. CDPHE and the hospital performed an infection prevention (IP) assessment among current ICU patients with a modified culture-based screening protocol using sputum specimens. Isolates were forwarded to the CDC's regional Antibiotic Resistance Laboratory Network (ARLN) for phenotypic and genotypic mechanism testing; isolates positive by modified carbapenem inactivation method (mCIM) at the ARLN were sequenced with Illumina MiSeq at the CDPHE laboratory. A CDC polymerase chain reaction (PCR) assay was used to identify the Imipenemase metallo-beta-lactamase (IMP) variants not detected by commercial PCR. High quality single nucleotide polymorphism (hqSNP) analysis was performed to determine relatedness.

RESULTS: Four patient isolates were identified from the laboratory review, and one of nineteen patients screened had CRPA identified as part of the PPS. In sum, six isolates were available for mechanism testing including the index patient. The index case and one additional isolate were found to harbor the IMP-13 variant by PCR. These two isolates had one hqSNP difference (1 hqSNP out of 83.1% shared core genome). Both patients resided in the same ICU room, six weeks apart. The remaining isolates were not genetically related (>1600 SNP difference) and did not harbor carbapenemases. The IP assessment identified gaps in hand hygiene, environmental cleaning practices, and equipment storage around room sinks.

CONCLUSIONS: The temporal lag between the two IMP-13 CRPA isolates suggests the presence of undetected colonized intermediates among patients and/or environmental contamination, although the specific mechanism of transmission was not identified. WGS augmented the molecular epidemiology when phenotypic and genotypic tests were unable to determine relatedness based on mechanism alone. Ongoing surveillance of CRPA, isolate testing for carbapenemase identification, and epidemiologic investigation and implementation of containment strategies are critical to preventing the transmission of these emerging organisms.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Epidemiologic Methods; Emerging Infections; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kyle.schutz@state.co.us
Presenting Author(s)	Kyle Schutz
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11796
Abstract Type	Quick
Abstract Title	Use of a Real-Time Regional Antibigram to Direct Stewardship and Infection Prevention Improvement Efforts in a Remote Community in Nebraska

Abstract

BACKGROUND: A higher number of CP-CRE (carbapenemase producing carbapenem resistant Enterobacteriaceae) infections were reported from a hospital and a long-term care facility (LTCF) in a remote part of Nebraska (small city/ region B). Since 2017 all isolates of gram negative species that can carry resistance to carbapenems are reportable by laboratories that report via ELR (electronic laboratory reporting.) From these data a statewide and some regional antibigrams were developed. Review of Region B antibigram revealed concerning resistance patterns. All positive *Clostridioides difficile* lab tests are reportable in NE and Region B had a high rate of *C. difficile* infection. For all of these reasons, a community-wide effort to address antimicrobial resistance and infection prevention (IP) was warranted.

METHODS: Region B antibigram was examined for resistance of *E.coli* to the fluoroquinolones and of *Klebsiella pneumoniae* to ceftriaxone to assess resistance of gram negative pathogens. For *E.coli* the percentage of isolates statewide in 2017 resistant to levofloxacin was 20%, for region B, 28%. For *K.pneumoniae*, resistance to ceftriaxone was 4% overall, 7% in Region B. The hospital and one LTCF had begun participation in ICAP (Nebraska Infection Control Assessment and Promotion Program) and ASAP (Nebraska Antimicrobial Stewardship Assessment and Promotion Program). A combined effort by the HAI/AR (Healthcare Associated Infection/Antimicrobial Resistance) program at NDHHS, ICAP and ASAP was made to recruit the hospital's outpatient clinics and the other 3 LTCFs in city B via educational presentations including the antibigram resistance data, discussions with CEOs, Medical Directors, Directors of Nursing, Administrators and IPs.

RESULTS: The additional 3 LTCFs and 5 outpatient specialty clinics agreed to ICAP assessments and 3 out of the 4 LTCFs to the ASAP remote coaching program. Over 4 days, the HAI/AR team, ICAP and ASAP met with each facilities' leaders and relevant staff to assess and recommend solutions to challenges in IP and antimicrobial stewardship. Among gaps noted were some that might lead to transmission of resistant pathogens in LTCFs and gaps in disinfection and sterilization in one outpatient clinic. Most LTCFs had not begun antimicrobial stewardship. Many strengths and a community dedication to patient safety were noted.

CONCLUSIONS: Regional antibigrams provide epidemiologic data to direct public health efforts to contain the spread of resistance and promote stewardship to stem further development of resistance. Having data facilitated the establishment of relationships with facility leadership, prescribers, and frontline staff, and increased receptivity to infection-control tools and recommendations for improvement.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Surveillance; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	maureen.tierney@nebraska.gov
Presenting Author(s)	Maureen Tierney
Institution Affiliation	Nebraska Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11198
Abstract Type	Quick
Abstract Title	Using Automated Code for Early Identification of Carbapenem-Resistant Enterobacteriaceae (CRE) Clusters

Abstract

BACKGROUND: Carbapenem-resistant Enterobacteriaceae (CRE) are reportable in Tennessee (TN); isolate submission is required. The State Public Health Laboratory (SPHL) performs additional characterization, including carbapenemase-production (CP) and resistance mechanism testing. CRE case investigation and laboratory data are entered into the National Electronic Disease Surveillance System Base System (NBS). Since 2017, additional CP-CRE epidemiological data (*e.g.* , healthcare facility of origin) was collected using REDCap. Containment is time-sensitive and ideally requires real-time and resource-efficient monitoring of surveillance data. We developed an automated code for early identification of clusters.

METHODS: We transformed NBS laboratory and case investigation data so that each line represents a single isolate. This was merged with the CP-CRE REDCap data. Patient addresses from NBS were matched with nursing home addresses to identify nursing home residents. Healthcare facility of origin was identified by prioritization of variables in the following order: healthcare facility of origin (REDCap), ordering facility (NBS), reporting facility (NBS), and nursing home. In addition, we analyzed for potential clusters among nursing home residents, even if the healthcare facility of origin was not a nursing home. Case counts within the last four weeks were aggregated by facility. Alerts were generated if the case(s) met the Council for Outbreak Response: Healthcare-Associated Infections and Antibiotic-Resistant Pathogens (CORHA) threshold for reporting of CRE and CP-CRE cases from facilities to public health. REDCap application programming interface (API) code, SAS macros, and task scheduler were used to automatically capture potential clusters and deliver daily alerts. We applied this automated code to historical CRE surveillance data to gain insights into how frequently alerts were generated.

RESULTS: Between July 1, 2018, and December 31, 2018, the code generated 18 alerts (21 cases). There were six alerts from single cases of non-KPC CP-CRE, two alerts from clusters of KPC- CP-CRE cases in a high prevalence county (2 cases each), one alert from a cluster of 2 CP-CRE from a hospital in a low prevalence county, two alerts from single CRE cases in critical access hospitals (CAH), and seven alerts from nursing home residents (all single cases of CRE). Three CRE cases from nursing home residents were also hospitalized in acute care hospitals. None of the nursing home cases had their isolates submitted to SPHL for characterization. **CONCLUSIONS:** An automated code allows for earlier detection of potential clusters. We will continue to evaluate this method by running this automated cluster detection in real time.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Outbreaks; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rany.octaria@vanderbilt.edu
Presenting Author(s)	Rany Octaria
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	AR Laboratory Network Experience Exchange: How HAI Programs Are Using the Antibiotic Resistance Laboratory Network to Detect and Protect

Abstract

Key Objectives:

Roundtable participants will discuss the impact the Antibiotic Resistance Laboratory Network (AR Laboratory Network) has had on state and local health departments and share strategies and challenges for using isolate-level antibiotic resistance data to guide public health actions.

Brief Summary:

The AR Laboratory Network consists of 56 state and local public health laboratories, including 7 regional labs. Begun in 2016, this ELC-funded program has increased public health capacities for AR threat detection and response. For state and local labs, testing has focused on detection and characterization of carbapenemase-producing Enterobacteriaceae (CP-CRE) and *Pseudomonas aeruginosa* (CP-CRPA). The isolate testing data has been used to inform rapid containment and prevention activities to halt the spread of these antibiotic resistance threats. As a fairly young program, feedback from stakeholders will help strengthen the program by identifying challenges, solutions, and emerging needs. This roundtable will provide participants with the opportunity to discuss how their jurisdictions have used the AR Laboratory Network and share stories or successes, hurdles, and novel solutions. Topics to be discussed include jurisdiction implementation and utilization of the AR Laboratory Network, protocols for epidemiologic response, procedural tools developed to aid local and state health departments in responding to antibiotic resistant threats, and communication strategies for crucial stakeholders and partners (i.e., hospital administration staff, medical staff, and clinical and commercial laboratories). The goal of this roundtable is to facilitate dialogue among state and local health departments and encourage participants to share their experiences in order to improve epidemiologic responses and strategies across the nation.

Submission Complete?	Yes
Committee Topic	Infectious Disease Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Antimicrobial Resistance; Evaluation
Consider for Different Presentation?	No
Presenting Author Email Address(es)	uzo0@cdc.gov
Presenting Author(s)	Jennifer Y. Huang
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Future Proofing Antibiotic Resistance Surveillance

Abstract

Key Objectives:

Roundtable participants will discuss strategies to share and incorporate emerging knowledge and new methods as well as public health actions regarding emerging antibiotic resistant pathogens testing and surveillance at the state and local levels.

Brief Summary:

Antibiotic resistance is one of today's most serious public health threats. To combat this threat, state and local public health departments must conduct surveillance to generate data for action. The Centers for Disease Control and Prevention (CDC) has dedicated funding to establish and maintain the Antibiotic Resistance Laboratory Network (AR Lab Network), which aims to provide stronger detection, faster results to support containment and prevention activities, a more robust antibiotic resistance (AR) Isolate Bank, and more isolate-level data to inform epidemiologic investigations. The enhanced capacities provided by the AR Lab Network have supported more efficient and rapid responses to AR new and emerging threats at the state and local level. Despite these capacities for enhanced detection and response, many public health systems are not built to respond well to emerging threats. Many public health jurisdictions must work with outdated systems when updating communicable disease reporting regulations, sometimes waiting years for reporting rule updates. Given this, healthcare-associated infections and antibiotic resistance (HAI/AR) public health programs must work creatively to "future proof" reporting requirements in an attempt to catch the next big AR threat. This roundtable will provide participants the opportunity to discuss strategies for public health to keep AR surveillance relevant. Topics to be discussed include efforts to transition to a modernized communicable disease reporting rule structure (e.g., "Commissioner's List") and expanding AR surveillance to include antibiotic susceptibility testing for a list of pathogens, rather than for specific drug-bug resistance combinations. The goal of this roundtable is to provide a forum for jurisdictions to discuss successes and challenges in conducting surveillance in an ever-emerging field.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Antimicrobial Resistance
Consider for Different Presentation?	Antimicrobial Resistance; Surveillance
Presenting Author Email Address(es)	No
Presenting Author(s)	dshannon1@isdh.in.gov
Institution Affiliation	DJ Shannon
	Indiana State Department of Health
	State Public Health Agency

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Local Health Department Experiences in AR Containment in Healthcare and Community Settings

Abstract

Key Objectives:

- Share lessons learned and promising practices from local health departments who are or have recently been engaged in activities to contain the spread of new or emerging drug resistant pathogens;
- Identify strategies for provider and public outreach and education, inter-facility coordination, or healthcare facility assessments that have been successful in advancing local public health's prevention, preparedness, and response efforts for outbreaks of multidrug resistant organisms, as well as related healthcare-associated infection prevention and response activities; and
- Increase participants' understanding of how local health departments are involved in prevention, preparedness, and response efforts for infections that spread across healthcare and community settings.

Brief Summary:

Each year, antimicrobial resistance (AR) causes at least 23,000 deaths across the United States and novel and unusual resistance microbes continue to emerge. Rapid response to these emerging threats is vital to stop their spread and prevent costly, dangerous infections. Local health departments are on the front lines of public health, uniquely positioned to respond to AR. With proper support, local health departments can collect and analyze data to establish trends, target prevention, and identify outbreaks; investigate reportable diseases and unusual resistance; and promote containment strategies. Moreover, coordinated efforts across multiple healthcare facilities has a greater impact on preventing AR than independent, individual facility efforts alone and local health departments are in an ideal position to facilitate this coordination to reduce resistance community-wide. The National Association of County and City Health Officials (NACCHO) is working with local health departments to support response to unusual resistance and improve infection control, preparedness, and response through strengthening local public health organizational and administrative capacity, expertise, and partnerships with key stakeholders. This roundtable session will feature local health departments' experiences and lessons learned while implementing a response to novel drug resistant pathogens, such as Verona Integron Encoded Metallo-Beta-Lactamase producing *Pseudomonas aeruginosa* (VIM CRPA). During the session, participants will share strategies implemented and tools developed, and explore challenges that still remain. This conversation will provide an opportunity for health department representatives and other stakeholders to share useful approaches to strengthen capacity and partnerships for infection prevention, control, preparedness, and response.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Antimicrobial Resistance
Consider for Different Presentation?	Healthcare Associated Infections (HAI); Infection Control; Antimicrobial Resistance
Presenting Author Email Address(es)	No
Presenting Author(s)	cbaum@naccho.org
Institution Affiliation	Christina Baum
	National Association of County and City Health Officials
	Non-profit

Submission Type	Breakout/Quick/Lightning/Poster
ID	11277
Abstract Type	Breakout
Abstract Title	<i>Chlamydia Psittaci</i> Outbreak Among Poultry Processing Plant Employees — Georgia, 2018

Abstract

BACKGROUND: In September 2018, the Georgia Department of Public Health (GDPH) was notified of 3 poultry slaughter plant employees hospitalized with laboratory-confirmed *Chlamydia psittaci* infection (psittacosis). During the next 6 weeks, 27 more employees developed illness consistent with psittacosis. *C. psittaci* can be found in respiratory and fecal secretions of birds and can be inhaled through aerosolization. The last psittacosis outbreak among U.S. poultry plant workers occurred in 1986. We investigated to evaluate risk factors for illness and guide worker safety practices.

METHODS: Cases were identified through screening surveys and GDPH notification. Cases were defined as respiratory illness in a poultry plant employee who worked after August 13 with either *C. psittaci* infection laboratory-confirmed by PCR (confirmed), physician-diagnosed pneumonia (probable), or fever (>101°F) or chills plus ≥2 of the following symptoms: headache, cough, or myalgia (suspected). A case-control study was conducted. Control subjects were randomly selected from all 662 hourly workers across all 3 shifts. Case-patients and control subjects were administered a survey in person or by telephone to assess work environment, live bird exposure, symptoms, and personal protective equipment usage. All cases were included in the analysis.

RESULTS: We identified 30 case-patients (8 confirmed, 12 probable, and 10 suspected) and 141 control subjects. Case-patients reported symptom onset during August 17–October 22; mean age was 44 years (range: 22–58 years). Frequently reported symptoms included cough (83%), fever (80%), and chills (67%). Pneumonia was diagnosed among 67% of case-patients; 47% were hospitalized (1 ICU patient). Significant risk factors for illness included working second shift (odds ratio [OR]: 5.68; 95% CI: 2.35, 13.73), handling live and recently slaughtered chickens before the acid wash or chill step (OR: 6.84; 95% CI: 1.98, 23.60), working in the evisceration area (OR: 2.60; 95% CI: 1.17, 5.81), and eviscerating chickens (OR: 3.09; 95% CI: 1.34, 7.09). Always wearing dust masks was reported by 40% of case-patients and 35% of control subjects, but was not associated with illness (OR: 1.21, 95% CI: 0.54, 2.72).

CONCLUSIONS: Second shift workers who handled live or recently slaughtered birds and eviscerated birds were at greater risk for illness. Employees infrequently used dust masks, but it was not associated with illness. Employee training on mask usage and use of N95 respirators might increase protection. Psittacosis is rarely reported among poultry workers, but can cause severe illness. Study findings will be shared with state and federal animal health partners to increase industry awareness.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Occupational Exposure; Zoonotic Diseases; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Christine.Szablewski@dph.ga.gov
Presenting Author(s)	Christine M. Szablewski
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	10986
Abstract Type	Breakout
Abstract Title	Coccidioidomycosis in U.S. Residents Returning from House-Building Trips in Baja California, Mexico, June–July, 2018

Abstract

BACKGROUND: On August 8, 2018, New York City health authorities notified CDC of two high school students hospitalized following house-building trips to Baja California, Mexico. By October 15, 2018, both students and six additional travelers were diagnosed with coccidioidomycosis, a disease caused by inhalation of a soil-borne fungus found in parts of the U.S. and Mexico. A seroepidemiologic survey was conducted to identify potential sources and inform prevention measures.

METHODS: We identified 209 people who traveled to the area during June–July 2018, performed serum *Coccidioides* antibody enzyme immunoassays, and conducted interviews in person or by online questionnaire. Interviews included questions on activities, exposures, symptoms, and prior knowledge of coccidioidomycosis.

RESULTS: We interviewed 109 (52%) travelers, of whom 48 (44%) reported coccidioidomycosis symptoms. Among 75 with antibody testing, 13 (17%) were seropositive, of whom 12 (92%) were symptomatic. Fourteen (29%) with symptoms sought healthcare, and four were hospitalized, including one in intensive care, for a median of seven days (range 3–12). Travelers who worked on a particular house (odds ratio [OR] 5.7, 95% confidence interval [CI] 1.2–54.9), performed backfilling of the foundation (OR 2.8, 95% CI 1.1–7.4), or took no precautions against dust generation (OR 9.4, 95% CI 1.3–424.1) had higher odds of developing symptoms compared with those who did not perform such functions. Only six (6%) travelers had ever heard of coccidioidomycosis.

CONCLUSIONS: Almost one in five travelers Baja California, Mexico showed serological evidence of coccidioidomycosis infection, and over one-third exhibited symptoms compatible with coccidioidomycosis, likely from foundation work at a particular house. Further investigation is needed to determine reasons this site posed elevated risk. Despite engaging in dust-generating activities in a coccidioidomycosis-endemic area, nearly all travelers were unaware of the risk. Service organizations performing soil-disturbing activities in endemic areas should educate travelers and implement prevention measures.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nrk7@cdc.gov
Presenting Author(s)	Mitsuru Toda
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	10990
Abstract Type	Breakout
Abstract Title	Five Years of Acute Flaccid Myelitis Surveillance- Colorado, 2014-2018

Abstract

BACKGROUND: Acute flaccid myelitis (AFM) is a rare neurological condition that affects the gray matter of the spinal cord resulting in limb weakness and/or cranial nerve dysfunction. First described in California in 2012, Colorado and other states experienced a surge of AFM cases in the late summer and early fall of 2014 during a nationwide outbreak of enterovirus D68 (EV-D68). In Colorado, AFM has been explicitly reportable since 2015. During 2018, Colorado experienced an outbreak of enterovirus A71 (EV-A71) that included multiple AFM cases.

METHODS: We describe five years of AFM surveillance in Colorado, including demographic and clinical features. We also discuss efforts to increase and challenges surrounding provider awareness and reporting of AFM.

RESULTS: A total of 31 confirmed and probable AFM cases have been reported in Colorado since 2014, with notable peaks during 2014 (N=11) and 2018 (N=17). Only one case of AFM was reported each year from 2015 through 2017. The median age of case patients during 2014 was 13 years compared to a median age of 2 years in 2018. Most case patients were male (77%). No deaths were reported. A respiratory prodrome was typical in 2014; during 2018, gastrointestinal illness or hand foot and mouth lesions were more common. Testing practices changed over time, but in 2014, 3 patients (27%) tested EV-D68 positive while in 2018, 12 patients (80%) tested EV-A71 positive and 2 (12%) tested EV-D68 positive. Since 2014, Colorado performed outreach to improve surveillance and encourage reporting of AFM. Activities included Health Alert Network bulletins, “Dear Provider” letters and emails to a small number of specialist providers (infectious disease, neurology, radiology), presentations, and publications. In 2018, an innovative provider contact database was used to send “Dear Provider” letters to more than 1,100 specialist physicians. At least one case was reported as a result of this expanded outreach.

CONCLUSIONS: AFM is an emerging illness of public health concern due to its severity, lack of well-defined risk factors, and absence of effective treatment. Differences in age, clinical presentation, and outcomes were observed between seasons and highlight the need for continued surveillance. Early patient outcomes were poorer when associated with EV-D68; long-term follow-up is not standard. Surveillance for AFM is particularly challenging without an AFM-specific ICD-10 code or confirmatory lab test. Efficient and rapid reporting largely relies on provider awareness and close working relationships between providers, medical facilities, and the health department.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Children and Adolescents; Surveillance; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	emily.spencedavizon@state.co.us
Presenting Author(s)	Emily E Spence Davizon
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Increase in Invasive Group A Streptococcus Infections Among High-Risk Populations—Denver, 2013-2017

Abstract

BACKGROUND: Group A *Streptococcus* (GAS) causes illnesses from pharyngitis to severe invasive disease, including bacteremia, sepsis, and necrotizing fasciitis (NF). As part of CDC's Emerging Infections Program (EIP), Colorado conducts active surveillance on invasive GAS (iGAS), a reportable condition in the metropolitan Denver area. Rates of iGAS increased in the metropolitan Denver area from 4.3/100,000 in 2013 (n = 110) to 13.7/100,000 in 2017 (n = 379). People experiencing homelessness (PEH), people who inject drugs (PWID), and residents of long-term care facilities (LTCFs) are at a higher risk for infections with GAS. We sought to describe the role of these risk factors in the overall increase in iGAS. **METHODS:** We defined an iGAS case as illness with isolation of GAS from either a normally sterile site, or a wound accompanied by NF or streptococcal toxic shock syndrome. Case data during 2013—2017 were collected in the Colorado Electronic Disease Reporting System and through medical chart abstraction, and data were queried to identify people belonging to any of three risk groups (LTCF residents, PEH or PWID). CDC's *Streptococcus* laboratory determined *emm* types for available isolates, and determined genomic relatedness using whole-genome sequencing where applicable. **RESULTS:** During 2013—2017, of 1152 iGAS cases identified, 92(8%) were in LTCF residents, 169 (15%) in PEH and 83 (7%) in PWID. Forty-five cases were in people identified as both PEH and PWID. The proportion of iGAS cases in people in at least one risk group increased from 17/110 (15%) in 2013 to 164/379 (43%) in 2017. This increase was associated with emergence of three previously rare *emm* types in Colorado - 11.10, 49 and 82. Among 152 cases in PWID or PEH with isolates available, 50 (33%) were due to *emm*49 and 30 (20%) due to *emm*82. Isolates from a multi-LTCF outbreak were identified as *emm*11.10 and were genomically highly related (average pairwise single nucleotide polymorphism distance: 2.8). **CONCLUSIONS:** The increased incidence of iGAS in the Colorado EIP catchment area since 2013 has been disproportionately in three high-risk populations: LTCF residents, PWID and PEH. Emergence of previously rare *emm* types in these populations could have contributed to this increase. Response has included visits to affected LTCFs to provide infection control guidance and interviews with hospitalized PWID or PEH with iGAS infection to understand risk factors for infection.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Outbreaks; Underserved Populations
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nisha.alden@state.co.us
Presenting Author(s)	Nisha B. Alden
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11148
Abstract Type	Breakout
Abstract Title	Number of Poultry Processing Plant Employees and Psittacosis Reporting in Counties—United States, 1992–2017

Abstract

BACKGROUND: In 2018, the first outbreak of *Chlamydia psittaci* infection (psittacosis) among poultry processing plant employees in 30 years was reported. Humans can present with flu-like symptoms and sometimes pneumonia. *C. psittaci* poultry-to-human transmission is considered rare in the United States. However, the outbreak highlighted diagnostic challenges of psittacosis and under-recognized *C. psittaci* exposure risks among poultry processing plant employees, especially in smaller poultry processing plants. We assessed if presence of poultry processing plant employees increased the likelihood of reporting psittacosis to the National Notifiable Diseases Surveillance System (NNDSS).

METHODS: We used a zero-inflated Poisson model consisting of a logistic model (any cases) and a Poisson count model (case count) to predict NNDSS psittacosis case reporting (confirmed and probable; 1992–2017 total) by county-level exposures: 1990–2010 population mean (decennial U.S. Censuses), 1998–2016 poultry processing plant employee mean and its square (Wholedata Establishment and Employment database), and imported poultry/psittacine bird port presence (proxy for bird exposure outside poultry processing plants; Code of Federal Regulations).

RESULTS: During 1992–2017, 468 psittacosis cases were reported from 263 of 3,144 (8.4%) U.S. counties (84.4% [222/263] had ≤ 2 cases; range: 1–14). Poultry processing plant employees were reported in 681 counties; 62.0% of these counties had 1–150 employees (median: 39; range: 1–6628). County population (odds ratio: 5.8; $P < .001$) predicted reporting any cases. County population (count ratio [CR]: 3.3; $P = .001$), bird ports (CR: 1.6; $P = .006$), and having up to 150 compared to no poultry processing plant employees (CR: 1.5–1.7; $P < .050$) predicted higher reported case counts; having >150 poultry processing plant employees did not predict higher reported case counts.

CONCLUSIONS: Our model suggests counties with 1–150 poultry processing plant employees or a bird port reported more psittacosis cases. Failure to detect this association with >150 employees may be related to differences in poultry processing plant work environment. Better understanding of psittacosis burden and occupational exposure risks can inform and prioritize prevention strategies.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	NNDSS; Zoonotic Diseases; Occupational Exposure
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	okp3@cdc.gov
Presenting Author(s)	Olivia L. McGovern
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Outbreak of Enterovirus A71 Among Colorado Children, 2018

Abstract

BACKGROUND: In May 2018, the Colorado Department of Public Health and Environment (CDPHE) was notified by Children’s Hospital Colorado (CHCO) of an increase in enterovirus (EV) infections with neurologic complications. Early testing at CDC identified enterovirus A71 (EV-A71) in 6 of 8 specimens. Like other EVs, EV-A71 infections are typically mild, but EV-A71 may cause meningitis, encephalitis, or acute flaccid myelitis (AFM). EV-A71 has caused large-scale outbreaks in the Asian Pacific region, but is uncommon in U.S.

METHODS: We responded to an outbreak of EV-A71 associated neurologic illness in children from the spring through the fall of 2018. A case was defined as a person ≤18 years of age with a specimen PCR positive for EV-A71 and central nervous system disease including meningitis, encephalitis, AFM, ataxia, or myoclonus on or after March 1, 2018. Specimens from patients with an acute febrile illness and neurological symptoms that tested positive for enterovirus were sent to CDC lab for EV typing. Outreach was conducted to urge coroners, physicians, and hospital infection preventionists to report patients with a febrile neurological illness and collect specimens for EV testing.

RESULTS: Forty-four Colorado residents met the outbreak case definition. Cases ranged in age from 2 weeks to 15 years with a median age of 21 months. Twenty nine (66%) cases were white, non-Hispanic. Thirty-three cases (79%) were male. Thirty-one children who tested positive for EV-A71 met criteria for encephalitis, 39 had meningitis, 23 had vomiting or diarrhea, 18 had abnormal MRIs, 16 had lesions consistent with hand, foot and mouth disease, and 10 had acute flaccid myelitis (AFM). Forty-two cases occurred in the Denver Metro area, with 3 cases occurring in one child care facility. No other social, environmental, or geographic similarities were noted among cases.

CONCLUSIONS: While outbreaks of EV-A71 are well described in the Asian-Pacific region, this is the largest reported outbreak of EV-A71 associated neurologic illness in the United States. EV infections are not routinely reportable to public health and limited information is available about circulating strains of EV, burden and spectrum of disease, and risk factors for infection and severe outcomes. Routine surveillance of enterovirus infections would improve our understanding of the burden of neurologic illness, including AFM, meningitis, and encephalitis, that may be associated with these infections.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Surveillance; Infectious Diseases; Children and Adolescents
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	emily.spencedavizon@state.co.us
Presenting Author(s)	Emily E Spence Davizon
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11304
Abstract Type	Breakout
Abstract Title	Psittacosis Outbreak at a Chicken Slaughter Plant — Virginia, 2018

Abstract

BACKGROUND: On August 31, 2018, a hospital notified the Virginia Department of Health (VDH) that 2 people who worked at a chicken slaughter plant were hospitalized with fever, cough, and pneumonia. Polymerase chain reaction (PCR) detected *Chlamydia psittaci*, a zoonotic pathogen which can cause psittacosis, a respiratory illness in humans. Sixty psittacosis cases were reported in the United States during 2008–2017. VDH and CDC investigated to determine outbreak source and prevent additional illnesses. **METHODS:** VDH collected environmental samples, observed work practices, and conducted a cohort study, surveying workers about illness and exposures. Clinical specimens from ill workers were sent to CDC for PCR testing. Among anyone who worked at the plant during August 1–September 7, 2018, a case was defined as illness with any of the following: a clinical specimen PCR-positive for *C. psittaci*; physician-diagnosed pneumonia; or fever or chills with ≥ 2 symptoms of headache, cough, and muscle aches. **RESULTS:** VDH identified 50 cases among 141 workers. Overall, 23/50 (46%) ill workers had pneumonia. Of clinical specimens from 13 workers, 5 were PCR-positive for *C. psittaci*. Workers ever in the evisceration area were more likely to be ill compared with unexposed workers (Relative Risk: 2.1; 95% CI: 1.1–3.8). *C. psittaci* was not detected in any of 62 environmental samples, including 10 from the evisceration area. Repositioning cooling fans, misting birds on entry, and inspecting evisceration equipment were recommended to reduce aerosol formation and exposure. No cases were identified with onset later than September 8. **CONCLUSIONS:** This is the largest psittacosis outbreak associated with a chicken slaughter plant in the US. Exposure to the evisceration area increased illness risk among workers. Environmental sampling results did not suggest ongoing contamination with *C. psittaci*. Recommendations to prevent future illnesses focused on reducing worker exposure to contaminated aerosols at the plant.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Zoonotic Diseases; Occupational Health; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kelly.shaw@vdh.virginia.gov
Presenting Author(s)	Kelly A Shaw
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	11077
Abstract Type	Quick
Abstract Title	Acute Flaccid Myelitis in Minnesota Children

Abstract

BACKGROUND: Acute flaccid myelitis is rare but serious cause of sudden onset limb weakness, especially in children, and should be considered in the differential diagnosis. From September 2018 to November 2018, the Minnesota Department of Health (MDH) was notified of 6 children hospitalized in the Minneapolis-St. Paul region with symptoms consistent with acute flaccid myelitis (AFM). All six patients were confirmed as AFM cases by the Centers for Disease Control and Prevention (CDC).

METHODS: Cases of acute flaccid myelitis were identified and evaluated clinically. An epidemiological investigation was completed by the Minnesota Department of Health in conjunction with the Center for Disease Control and Prevention.

RESULTS: The median patient age was 6.0 years (range 1.3–9.2). All experienced fever and upper respiratory signs and symptoms (e.g., rhinorrhea, cough) beginning a median of eight days (range 5–11) prior to weakness onset. Four patients presented with marked weakness of proximal muscle groups in one arm, while distal motor function was largely preserved. Two patients presented with single leg weakness that became bilateral with rapid ascending paralysis requiring mechanical ventilation. In all patients, limb weakness was first noted in the morning after waking. Magnetic resonance imaging (MRI) showed spinal cord grey matter involvement in all nine patients, largely in the anterior horns. The extent of grey matter involvement did not always correlate with deficits seen on physical exam. Cerebrospinal fluid (CSF) pleocytosis was present in three of five patients. One nasal wash specimen from Case 2 was positive for EV-D68 and a second specimen for EV-D68 and parechovirus A6 by RT-qPCR; CSF from this patient was also positive for EV-D68.

CONCLUSIONS: Despite all patients reporting upper respiratory signs and symptoms, testing for viruses that commonly cause upper respiratory infections was positive from non-sterile specimens in only two cases. Identification of EV-D68 in the CSF of Case 2 is considered the cause of AFM in this patient, and does provide further support for the neurotropic potential of this virus. Detection of a pathogen in the CSF may be related to the severity and prolonged nature of illness in this patient; however, host or other factors contributing to the severity are unknown. Public health classification of AFM cases involves expert review of clinical and imaging findings; however, it is important that clinical care not be delayed pending case classification.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Children and Adolescents; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	hmoline@umn.edu
Presenting Author(s)	Heidi Moline
Institution Affiliation	University of Minnesota Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11388
Abstract Type	Quick
Abstract Title	Acute Flaccid Myelitis Surveillance in the United States, 2018

Abstract

BACKGROUND: Acute flaccid myelitis (AFM) is a rare but serious neurologic condition that results in paralysis of one or more limbs over the course of several hours to days. Standardized surveillance for AFM began nationally in 2015. After limited AFM activity in 2017, CDC started receiving increased reports of AFM beginning in August 2018.

METHODS: Health departments report cases meeting the clinical criteria for AFM, defined as acute onset of flaccid limb weakness, to CDC using a standardized form. Confirmed cases of AFM are patients who met the clinical criteria and have magnetic resonance imaging (MRI) showing spinal cord lesions largely restricted to gray matter and spanning one or more vertebral segments. Cerebrospinal fluid (CSF), respiratory, and stool specimens were tested for enteroviruses (EV), rhinoviruses (RV), and parechoviruses at CDC.

RESULTS: From January 1, 2018 through January 4, 2019, 193 cases of AFM from 39 states were classified as confirmed; 88% had limb weakness onset between August and November with a peak in September. The median age was 5.0 years (range, 6 months–81 years), 94% were <18 years, 116 (60%) were male, and 187 (97%) were hospitalized. A preceding respiratory or febrile illness in the four weeks before weakness onset was reported in 183 (95%) patients. Only upper limbs were affected in 89 (46%), while 48 (25%) reported all four extremities affected; 152 (79%) cases had CSF pleocytosis (white blood cell count >5 cells/mm³). No fatalities were reported among cases with onset in 2018. CSF specimens were submitted from 60 cases; one was positive for EV-A71 and one for EV-D68. Respiratory specimens were tested from 111 cases and 28 (25%) were positive for EV-D68, 10 (9%) for EV-A71, 7 (63%) for non-specified RV, and 6 (5%) for non-specified EV/RV. Of 87 cases with stool specimens tested, 1 (1%) was positive for EV-D68, 2 (2%) for EV-A71, 3 (4%) for coxsackieviruses, 1 (1%) for echovirus 11, 4 (5%) for parechoviruses, 2 (4%) for non-specified EV/RV, and none for poliovirus.

CONCLUSIONS: Similar to 2014 and 2016, AFM activity was high in 2018, with cases peaking in September. Most cases were pediatric and had a preceding respiratory or febrile illness. The clinical presentation and laboratory results suggest an association with a viral infection, including enteroviruses. Additional research is needed to further explore this association and better characterize the pathogenesis of AFM.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Surveillance; Emerging Infections
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	alopez@cdc.gov
Presenting Author(s)	Adriana Lopez
Institution Affiliation	Centers for Disease Control and Prevention Federal Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10554
Abstract Type	Quick
Abstract Title	Barriers to TB Evaluation and Treatment Among Immigrants and Refugees-Arizona, 2015—2017

Abstract

BACKGROUND: Approximately, one third of the world’s population has latent tuberculosis infection (LTBI), the non-contagious infection of *Mycobacterium tuberculosis* without clinical symptoms or radiologic or bacteriologic evidence of active TB disease. The estimated lifetime risk of TB reactivation among persons with LTBI is 10%, with the majority of cases developing within the first five years of infection. Most TB disease is due to reactivation of LTBI. Most TB disease in the United States is among refugees and immigrants from TB prevalent countries, due to such factors as low socioeconomic status, forced displacement, and poor living conditions. To provide proper care for persons immigrating into the United States, CDC developed the Electronic Disease Notification System(EDN) to notify health departments and screening clinics of the arrival of refugees and immigrants with health conditions requiring medical follow-up including Tuberculosis. Conditions requiring follow-up after arrival into the United States are called Class B conditions

METHODS: Using EDN data from 2015–2017, the Arizona Department of Health Services (ADHS) assessed the main barriers to TB evaluation and treatment among refugees and immigrants who came into Arizona with a TB Class B condition.

RESULTS: During 2015–2017, 1,413 Class B individuals came to Arizona and were included in the EDN database. Of those, 60% (852) had an evaluation initiated by the local health department, 839 (59%) persons completed an evaluation; 37% (314/839) of whom were diagnosed with LTBI and referred for treatment. Of those diagnosed with LTBI and referred for treatment, 58% (182/314) did not initiate treatment; 56% (102/182) of whom declined treatment against provider advice.

CONCLUSIONS: Due to the inability to evaluate and treat individuals at risk for LTBI, there were substantial missed opportunities to prevent TB reactivation. Barriers to TB evaluation and treatment among immigrants and refugees calls for improved efforts among all public health partners.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Disease Prevention; Barriers to Care; Special/Vulnerable Populations
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	amswanson2492@gmail.com
Presenting Author(s)	Amanda Swanson
Institution Affiliation	Arizona Department of Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10775
Abstract Type	Quick
Abstract Title	Enhanced Surveillance for Histoplasmosis in 10 States: Preliminary Results

Abstract

BACKGROUND: Histoplasmosis is often described as the most common endemic mycosis in the United States. However, much remains unknown about its epidemiology in the general population because most information comes from studies of high-risk patients or outbreak investigations. Histoplasmosis is not nationally notifiable, and no multistate data exists about cases identified using the 2016 CSTE standardized case definition. We are conducting enhanced surveillance to improve understanding of its epidemiology and effects on patients and to improve surveillance practices and educational efforts.

METHODS: State and local health department professionals in 10 states (Arkansas, Delaware, Indiana, Kentucky, Louisiana, Michigan, Minnesota, Nebraska, Pennsylvania, and Wisconsin) where histoplasmosis is reportable interviewed consenting histoplasmosis patients identified through routine surveillance beginning July 1, 2018, using CSTE probable and confirmed case definitions. Interviewers asked about exposures, symptoms, underlying conditions, healthcare use, treatment, and outcomes using a standardized questionnaire. Histoplasmosis diagnostic test information was extracted from health departments' surveillance systems or patients' medical records. Data were aggregated at CDC.

RESULTS: As of November 9, 2018, 45 patients (29 [64%] probable and 16 [36%] confirmed) were interviewed. Thirty-one (70%) were male, 40 (89%) were white, median age was 54 years (range, 11–83), and 14 (31%) were immunosuppressed. Fatigue, (n=32, 71%), cough (n=25, 56%), and fever (n=24, 53%) were the most commonly reported symptoms. Median time from seeking healthcare to diagnosis was 21 days (range, 1–113). Positive histoplasmosis laboratory test results included antibody tests (n=27 patients, 60%), antigen tests (n=13, 29%), and culture (n=8, 18%). Abnormal chest imaging was the most common reason for testing (n=21 patients, 47%). Before being tested, 64% saw a healthcare provider ≥ 3 times, and 52% received antibacterial medication. Forty-nine percent were hospitalized, 44% received antifungals, and 72% said that histoplasmosis interfered with their daily activities (for a median of 30 days [range, 2–300]). Possible exposures in the month before onset included gardening or other handling of plants (58%), digging in soil (38%), contact with bird or bat guano (31%), and construction or demolition (29%). Five patients (11%) had heard of histoplasmosis before their illness.

CONCLUSIONS: Histoplasmosis can cause severe and prolonged illness that is often initially misdiagnosed. Based on the high rates of hospitalization and culture positivity, milder cases likely go undiagnosed and unreported. Diagnostic delays and antibacterial use (ineffective for histoplasmosis), were common, and general awareness was low, indicating the need for improved messaging to healthcare providers and the public.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Epidemiology; Surveillance; Emerging Infections
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jsy8@cdc.gov
Presenting Author(s)	Kaitlin Benedict
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11455
Abstract Type	Quick
Abstract Title	Extrapulmonary Nontuberculous Mycobacteria Infections — Minnesota, 2013–2017

Abstract

BACKGROUND: Approximately 80 species of nontuberculous mycobacteria (NTM) causing disease are found environmentally and in animal reservoirs. Typically, pulmonary NTM infections are sporadic; extrapulmonary infections are commonly outbreak-associated. Recent sources of extrapulmonary NTM (ENTM) outbreaks in Minnesota include contaminated heater-cooler units used during cardiac surgery and contaminated hormone injections. We examined patient demographics and characteristics of laboratory-confirmed ENTM isolates to assess potential value of systematic laboratory-based ENTM surveillance in Minnesota.

METHODS: The Minnesota Department of Health requested laboratory data from *Mycobacterium* testing during 2013–2017 from 3 Minnesota reference laboratories that characterize *Mycobacterium* isolates. Using the CSTE case definition, we excluded *M. tuberculosis* complex, *M. bovis* and *M. leprae* isolates, and isolates from feces, lung, bronchoalveolar lavage, tracheal secretion, and sputum.

RESULTS: Of 4,017 NTM isolates, 415 (10.3%) were ENTM, representing an estimated burden of 15/1,000,000 people/year in Minnesota. Thirty-one species or complexes were identified; most common were *M. avium* or *M. avium* complex (30.6%), *M. chelonae* (21.7%), *M. fortuitum* or *M. fortuitum* complex (9.2%), and *M. abscessus* or *M. abscessus* complex (8.0%). Most common specimen collection sites included skin and soft tissue (41.2%), neck lymph node or tissue (14.5%), blood (13.5%), sinus (8.9%), and joint fluid (2.2%). The patient's median age was 55 years (range: 3–98 years); 19.1% were from patients aged <18 years, 19.3% aged 18–44 years, 26.1% aged 45–64 years and 35.5% aged ≥65 years. Sex was documented for 244 (58.8%) patients; 126 (51.6%) were males. County information was available for 315 isolates (75.9%); approximately half (48.5%) of patients resided in metropolitan Minneapolis-Saint Paul.

CONCLUSIONS: Laboratory data can be used for ENTM surveillance in Minnesota. Implementing laboratory-based surveillance could detect ENTM cases, provide a mechanism for obtaining clinical and epidemiological information, and enable earlier identification of potential healthcare transmission or community clusters.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Surveillance; Infectious Diseases; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	okp2@cdc.gov
Presenting Author(s)	Joanne K Taylor
Institution Affiliation	Minnesota Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10689
Abstract Type	Quick
Abstract Title	Invasive Group a Streptococcus in Arizona, 2014-2017

Abstract

BACKGROUND: In Arizona, invasive group A *Streptococcus* (iGAS) has been reportable since 1990. The number of cases of iGAS has been consistently increasing in Arizona, with a 143% increase between 2014 and 2017. The Arizona Department of Health Services assessed iGAS reports to characterize the cases and potential economic impact of disease increase.

METHODS: iGAS cases reported by laboratories and providers between 2014-2017 were analyzed. Facilities with at least three-fold increases in iGAS case reports were contacted to assess any changes in reporting practices or testing protocols. Case-patients were cross-matched to the Arizona Hospital Discharge Database (AHDD) and the Arizona Death Database (DD). The AHDD was used to calculate the total hospital charges for each matched iGAS case and assess outcomes of disease, such as hospital and emergency room utilization and severe disease presentation. Mortality rates were assessed using the DD.

RESULTS: The number of iGAS cases reported in 2014, 2015, 2016 and 2017 was 250, 344, 555 and 608, respectively. None of the six contacted facilities reported any changes in iGAS reporting practices, diagnostic tests performed or testing protocols. High rates of iGAS were observed in infants under 1 year and individuals aged 45 years and older. Males were more affected by the increase in iGAS cases, comprising 57% of cases as compared to 50% of the overall population. The Native American population was also disproportionately affected, comprising 10-14% of cases as compared to 4% of the overall Arizona population. Of the 1770 cases reported, 1496 (84.5%) matched to the AHDD, indicating utilization of hospital or emergency room services. Approximately 10% of the cases were diagnosed with necrotizing fasciitis or toxic shock syndrome in 2017, compared to 8% during 2014. The total hospital charges for iGAS cases increased by 170% between 2014 and 2017, total charges exceeding \$55 million in 2017. Approximately 12% of iGAS cases died within one month of sample collection.

CONCLUSIONS: Arizona is experiencing annual increases in reported iGAS cases. This increase in cases represents significant economic burden and causes severe presentations and mortality in a notable proportion of cases. Reasons for the increase in reported iGAS cases are unknown, and no changes in reporting practices or diagnostics were identified. Preliminary genomic analyses suggest the introduction of a new virulent emm type, such as emm59, may be contributing to the increase, and further studies to investigate circulating serotypes and potential clusters are warranted.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rachana.bhattarai@azdhs.gov
Presenting Author(s)	Rachana Bhattarai
Institution Affiliation	Arizona Department of Health Services State Public Health Agency

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Adapting Fungal Disease Surveillance to a Changing Environment: Tracking Coccidioidomycosis, Histoplasmosis, and Blastomycosis

Abstract

Key Objectives:

- Outline changes underway in fungal disease surveillance, including proposed case definitions
- Discuss recent epidemiological trends in endemic mycoses
- Describe efforts to improve and update understanding of the geographical ranges of these diseases
- Identify opportunities for enhanced standardized surveillance to inform awareness and prevention efforts
- Strategize about ways to address key knowledge gaps in endemic mycoses

Brief Summary:

Over half of states require reporting of at least one of the so-called endemic mycoses, specifically the fungal diseases coccidioidomycosis, histoplasmosis, and blastomycosis. The endemic regions of these diseases have been incompletely defined and may be changing in the face of shifting environmental conditions. Public health surveillance is a key way to identify populations at risk, allowing targeted clinician and public outreach, which is important because these diseases are widely underdiagnosed, often mistaken as a bacterial or viral respiratory illnesses. Standardized surveillance is actively being revamped. The nearly decade-old case definition for coccidioidomycosis, already a nationally notifiable disease, is under revision, and the first consensus case definition for blastomycosis is being debated. The first histoplasmosis consensus case definition was approved by CSTE in 2016, and feedback is needed on its implementation. Incidence of coccidioidomycosis has varied dramatically (>2-fold) over the past decade, with a substantial increase in the past few years. Several jurisdictions have been investigating possible locally-acquired disease in regions previously thought to be non-endemic. For histoplasmosis, state-based surveillance has identified a substantial number of cases in states not thought to be endemic (e.g., Minnesota, Wisconsin, and Michigan) based on decades old maps and skin testing. Blastomycosis is perhaps the least understood of these diseases, and a new epidemic focus was recently identified in central New York. Environmental conditions are a key driver of the incidence of these diseases, but a far better understanding of these links is needed. Single-jurisdiction enhanced surveillance efforts, including patient interviews about exposures and clinical features, have yielded important insights into these diseases. Harmonized, systematic cross-jurisdiction enhanced surveillance could help address many unanswered questions and prevent illness and death. A discussion among states, territories, and CDC about surveillance for these diseases could lead to improved data collection and new opportunities for collaboration.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Climate and Health; Surveillance; Emerging Infections
Consider for Different Presentation?	No
Presenting Author Email Address(es)	ilyn0@cdc.gov
Presenting Author(s)	Brendan R. Jackson
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Bacterial and Fungal Infections As a Complication of Injection Drug Use (IDU)

Abstract

Key Objectives:

1) Review current knowledge regarding burden and epidemiology of bacterial and fungal infections among people who inject drugs (PWID), and limitations of current surveillance efforts 2) Share states' and other jurisdictions' efforts to address this public health problem 3) Discuss best practices for accessing and analyzing data on non-reportable IDU-associated infections 4) Discuss the role that health departments can play in investigating and preventing bacterial and fungal infections among PWID, and collaboration between public health and healthcare

Brief Summary:

Bacterial and fungal infections associated with drug use are increasing. A 2018 article showed that the percentage of invasive methicillin-resistant *Staphylococcus aureus* (MRSA) cases associated with IDU increased from 4.1% in 2011 to 9.2% in 2016. New York's Emerging Infections Program showed that 10% of investigated invasive *S. aureus* (ISA) infections were identified as being in PWID and that among young adults, rates of ISA infections associated with IDU have doubled. North Carolina's Division of Public Health found a more than twelvefold increase in the incidence of hospital discharge diagnoses for drug dependence combined with endocarditis between 2010 and 2015. These infections are likely also a significant problem for other jurisdictions experiencing increases in IDU in association with the opioid crisis. The opioid crisis is a priority topic for both the Department of Health and Human Services (HHS) and the Office of the Surgeon General, and was declared a Public Health Emergency under Federal law in October 2017. A comprehensive response to the crisis includes addressing the injection of drugs such as heroin and synthetic opioids. Improved treatment services and better data are two components of HHS's 5-point Strategy to Combat the Opioid Crisis; however many barriers exist to providing services to and conducting surveillance among PWID. Some challenges unique to preventing bacterial and fungal infections include education about appropriate skin cleansing, particularly among the homeless; understanding the importance of sterile injection equipment in preventing bacterial and fungal infections; access to resources for promoting hygiene and proper wound care; and management of substance use disorder during and after healthcare encounters for infection, especially during long treatment courses for infections such as endocarditis. This round table session offers an important opportunity to share practices currently utilized by state and jurisdictional health departments to identify, track, treat and prevent bacterial and fungal infections associated with IDU, explore the feasibility of developing best practices, and discuss next steps towards developing and implementing successful strategies.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Emerging & Miscellaneous Infectious Diseases
Keywords	Substance Use; Infectious Diseases; Substance Abuse
Consider for Different Presentation?	No
Presenting Author Email Address(es)	rgokhale@cdc.gov
Presenting Author(s)	Runa Hatti Gokhale
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Roundtable
ID	11889
Abstract Type	Roundtable
Abstract Title	Infectious Disease Position Statements Roundtable I

Abstract

Key Objectives:

To review infectious disease-related position statements that were submitted for consideration at the 2019 Annual Conference.

Brief Summary:

To review infectious disease-related position statements that were submitted for consideration at the 2019 Annual Conference.

Submission Complete?	Yes
Committee Topic	Infectious Disease Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	richard.danila@state.mn.us
Presenting Author(s)	Richard N Danila
Institution Affiliation	Minnesota Department of Health State Public Health Agency

Submission Type	Roundtable
ID	11890
Abstract Type	Roundtable
Abstract Title	Infectious Disease Position Statements Roundtable II

Abstract

Key Objectives:

To review infectious disease-related position statements that were submitted for consideration at the 2019 Annual Conference.

Brief Summary:

To review infectious disease-related position statements that were submitted for consideration at the 2019 Annual Conference.

Submission Complete?	Yes
Committee Topic	Infectious Disease Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	richard.danila@state.mn.us
Presenting Author(s)	Richard N Danila
Institution Affiliation	Minnesota Department of Health State Public Health Agency

Submission Type	Roundtable
ID	11891
Abstract Type	Roundtable
Abstract Title	Infectious Disease Position Statements Roundtable III

Abstract

Key Objectives:

To review infectious disease-related position statements that were submitted for consideration at the 2018 Annual Conference.

Brief Summary:

To review infectious disease-related position statements that were submitted for consideration at the 2018 Annual Conference.

Submission Complete?	Yes
Committee Topic	Infectious Disease Emerging & Miscellaneous Infectious Diseases
Keywords	Infectious Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	richard.danila@state.mn.us
Presenting Author(s)	Richard N Danila
Institution Affiliation	Minnesota Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10855
Abstract Type	Breakout
Abstract Title	A Decision Tree Algorithm for Categorizing Foodborne Disease Outbreaks Based on the Regulatory Jurisdiction Under Which Pathogen Contamination Likely Occurred

Abstract

BACKGROUND: The Interagency Food Safety Analytics Collaboration (IFSAC), established in 2011 by the Centers for Disease Control and Prevention (CDC), Food and Drug Administration (FDA), and the United States Department of Agriculture's Food Safety and Inspection Service (FSIS), works to improve U.S. foodborne illness source attribution. As a first step in understanding where along the farm-to-table continuum the contamination of foods implicated in foodborne disease outbreaks happens, IFSAC developed a decision tree algorithm for categorizing outbreaks based on the regulatory jurisdiction under which pathogen contamination likely occurred.

METHODS: We analyzed outbreaks from CDC's Foodborne Disease Outbreak Surveillance System (FDOSS) for outbreaks from 1998 to 2013 with one of IFSAC's four priority pathogens (*Salmonella*, *Escherichia coli* O157, *Listeria monocytogenes*, and *Campylobacter*) as the confirmed or suspected etiology and an implicated food assignable to one of the 17 food categories of the IFSAC Food Categorization Scheme (<https://www.cdc.gov/foodsafety/ifsac/projects/food-categorization-scheme.html>). Existing FDOSS variables were used to develop a decision tree algorithm to automatically assign outbreaks to one of 4 categories of regulatory jurisdiction based on FDA/FSIS regulatory authority, food type, and other factors. For outbreaks unassignable to one of these 4 categories, the protocol required ≥2 subject matter experts (SME) to conduct manual review to determine assignment into jurisdictional categories with majority rule for any differences identified in the experts' assignment.

RESULTS: Of the 1,043 outbreaks included in this analysis, the algorithm assigned 80% to one of 4 jurisdictional categories, and 20% required manual review by SMEs. Of the 834 algorithm-assigned outbreaks, 281 (34%) were determined to have an implicated food suspected to be contaminated in a setting within federal jurisdiction, 124 (15%) were within state or local jurisdiction and involved raw milk products, 296 (35%) were within state or local jurisdiction and did not involve raw milk products, and 133 (16%) were in unregulated food preparation settings such as private homes, camps, or religious facilities not within federal, state, or local jurisdiction.

CONCLUSIONS: These preliminary results contribute to a better understanding of source attribution, provide information about where intervention may be most effective, help regulatory agencies at both the federal and state/local level better understand how to distribute finite resources, and support evidence-based food safety decision-making. Additionally, these analyses further emphasize how the data collected by state/local health departments and CDC is critical in federal agencies' efforts to understand where food safety prevention measures are working.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Food Safety; Foodborne Disease; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	cary.parker@fda.hhs.gov
Presenting Author(s)	Cary Chen Parker
Institution Affiliation	Food and Drug Administration Federal Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10847
Abstract Type	Breakout
Abstract Title	A Shared Effort to Better Attribute Illnesses to Foods – 9 Years of the Interagency Food Safety Analytics Collaboration (IFSAC)

Abstract

BACKGROUND: In 2011, three of the federal agencies that protect U.S. food safety—the Centers for Disease Control and Prevention (CDC), U.S. Food and Drug Administration (FDA) and the United States Department of Agriculture’s Food Safety Inspection Service (USDA-FSIS)—created the Interagency Food Safety Analytics Collaboration (IFSAC) to improve coordination of food safety analytic efforts and address cross-cutting priorities for data collection, analysis, and use. In the past 9 years, IFSAC has dramatically improved agency coordination of analytical efforts, particularly focusing on what foods cause the most illnesses, also known as foodborne illness source attribution. State, local, and territorial agencies are critical partners in IFSAC’s efforts to understand foodborne illness attribution through surveillance and outbreak data.

METHODS: IFSAC has undertaken several projects aimed at improving foodborne illness source attribution. These include the creation of a harmonized food categorization scheme that is in line with regulatory oversight of food. This scheme has been adopted across all three partner agencies, as well as by external food safety partners. IFSAC also developed a new method to attribute illnesses to these food categories based on statistical modeling of foodborne disease outbreaks, which gives more weight to recent outbreaks than older ones to develop estimates.

RESULTS: . Using this method, IFSAC has produced annual reports with estimates of the proportion of illnesses attributed to food categories for IFSAC’s priority pathogens (*Salmonella* , *E. coli* O157, *Listeria monocytogenes* , and *Campylobacter*). IFSAC is currently refining a tool to evaluate temporal trends in changes of foodborne outbreak attribution using Bayesian thin plate spline models, as well as developing methods to proportionally attribute outbreaks linked to foods containing multiple ingredients to single food categories. Additional work has focused on determining the location along the farm-to-fork continuum where food contamination occurred and exploring whole genome sequencing to attribute *Salmonella* Enteritidis illnesses to food sources.

CONCLUSIONS: Future research may focus on assessing the impact of multi-year outbreaks on annual attribution estimates and trend modeling, evaluating geographical biases in foodborne illness reporting, assessing attribution to more specific food categories, and further refining the attribution model used for annual estimates. IFSAC intends to share its past findings, current research projects, and future work and solicit feedback from our state, local and territorial partners. IFSAC invites engagement from state and local partners to develop methods, tools, and outreach to most effectively use the data that they collect and help us make the US food supply even safer.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Enteric Infectious Diseases; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	michael.bazaco@fda.hhs.gov
Presenting Author(s)	Michael C. Bazaco
Institution Affiliation	Food and Drug Administration Federal Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11636
Abstract Type	Breakout
Abstract Title	Association between Communities of Color, Poverty, Unemployment and Salmonella and E. coli Rates in 20 Large American Cities

Abstract

BACKGROUND: Social determinants of health may influence risk for foodborne disease, as they determine where one lives, is able to shop or eat, and what food items one can buy. Nationally, non-White populations have higher incidence of *Salmonella*, but the highest incidence of *E. coli* infections is among people who are White. Since other social determinant measures are not routinely collected during foodborne public health investigations, they have not been widely characterized with respect to infection risk. The objective of this study was to determine if any social determinant is associated with *Salmonella* or *E. coli* infection rates in a sample of 20 large American cities.

METHODS: The Big Cities Health Inventory is an online data platform that provides a “snapshot of health” in large American cities. Twenty cities with no missing data for any disease/social determinant during 2012-2014 were included in analyses (SAS v9.4, ArcGIS v10.4). Social determinants included city-level demographics, (total population; %>65 years; %<18 years, %Non-white; %foreign born) measures of poverty/income, (%living below 200% of the Federal Poverty Level; %children living in poverty; household income; %unemployed) education, (%with ≥high school diploma) and health insurance (%uninsured). Negative binomial regression was used to determine if any social determinant was associated with either *Salmonella* or *E. coli* rates (stratified by pathogen).

RESULTS: On average, 15.6 cases/100,000 of *Salmonella* and 2.2 cases/100,000 of *E. coli* were reported. The mean population size was ~2million(SD=1.8M), percent non-White was 63%(SD=14%), percent living in poverty was 44%(SD=10%), percent unemployed was 11%(SD=4%). A 10% increase in the percent of non-White city residents was associated with 17% lower *Salmonella* (95%CI:4-28%) and 41% lower *E. coli* (95%CI:16-59%) rates. A 10% increase in percent of people living in poverty was associated with 47% lower *E. coli* rates (95%CI:4-70%). A 10% increase in the percent unemployed was associated with 55% lower *Salmonella* (95%CI:21-74%) and 96% lower *E. coli* (95%CI:68-100%) rates.

CONCLUSIONS: These results suggest that among 20 large American cities, cities with larger communities of color, more people living in poverty and higher unemployment may have lower rates of *Salmonella* and *E. coli* infections. Because enteric bacteria are killed during cooking/food processing, highly processed/heat-treated foods may cause less enteric illness than fresh, uncooked, or raw foods. People who have limited access or economic means to purchase fresh meats, poultry and produce items at may be at lower risk of contracting enteric disease from these items if they are instead purchasing processed or shelf-stable items.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Health Disparities; Foodborne Disease; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ees73@drexel.edu
Presenting Author(s)	Erica Smith
Institution Affiliation	Drexel University School of Public Health Student

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Comparing Shiga Toxin-Producing <i>Escherichia coli</i> O157 and Non-O157 Outbreaks, National Outbreak Reporting System — 2010–2017

Abstract

BACKGROUND: An estimated 265,000 Shiga toxin-producing *E. coli* (STEC) infections occur in the United States each year, ranging in severity from mild diarrhea to hemolytic uremic syndrome. The most common serogroup is O157, but the number of reported non-O157 STEC infections is increasing as more laboratories have acquired culture-independent tests that detect the presence of Shiga toxin or its genes. We describe the epidemiology of O157 and non-O157 STEC outbreaks during 2010–2017.

METHODS: We reviewed National Outbreak Reporting System data, including number of cases, route of transmission, and source. We defined an outbreak as an event with STEC detected by culture in ≥ 2 persons due to a common exposure.

RESULTS: During 2010–2017, health departments reported 466 STEC outbreaks. Among the 460 with serogroup identified, 330 were O157, 125 non-O157, and five included both. Compared with 2010–2013, the median annual number of STEC outbreaks decreased during 2014–2017 (68 vs. 55, $p=0.03$). The median number of illnesses per outbreak was five for both O157 (range 2–105) and non-O157 (range 2–56). The transmission route was reported for 330 (77%) O157 and 99 (79%) non-O157 outbreaks. The majority (55%) were foodborne (O157 57%; non-O157 52%). Among these, 104 (52%) were attributed to a single food category. The most commonly implicated food categories for O157 and non-O157 respectively were vegetable row crops (such as leafy greens) (29%, 40%), beef (29%, 10%), dairy (18%, 15%), and fruits (7%, 10%). Other transmission routes for O157 and non-O157, respectively, were person-to-person (22%, 30%), animal contact (14%, 11%), water (5%, 7%), and environmental contamination (2%, 0%). Among person-to-person-associated outbreaks, 62 (71%) occurred in a childcare setting (O157 67%; non-O157 80%). A festival or fair was the most common setting for animal contact-associated outbreaks (18, 38%); the 17 with a serogroup determined were O157. Most (10, 48%) waterborne transmission was associated with lakes (O157 31%; non-O157 85%).

CONCLUSIONS: STEC O157 caused >2 -fold more reported outbreaks than non-O157. Most outbreaks were associated with food, most commonly vegetable row crops and beef for O157, vegetable row crops and dairy for non-O157. Although the proportion of outbreaks associated with animal contact was similar for O157 and non-O157, visiting a fair or festival was only associated with O157 outbreaks. Continued surveillance of STEC by serogroup will enable scientists to identify changes in epidemiology to inform regulatory and public health actions.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	Outbreaks; Enteric Infectious Diseases; NORS (National Outbreak Reporting System)
Presenting Author Email Address(es)	Yes
Presenting Author(s)	dot7@cdc.gov
Institution Affiliation	Danielle M. Tack
	Centers for Disease Control and Prevention
	CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11613
Abstract Type	Breakout
Abstract Title	Cyclosporiasis Outbreak Associated with Vegetable Tray Consumption

Abstract

BACKGROUND: Cyclosporiasis is an intestinal illness caused by the parasite *Cyclospora cayetanensis* that is endemic in many tropical countries. Individuals in the U.S. typically become infected by traveling to or eating fresh produce imported from endemic countries. The incubation period is approximately one week. Cyclosporiasis is a reportable condition in Wisconsin with a median of 12 confirmed cases reported annually during 2013–2017 (range: 1–24). During the 6-day period of May 29–June 4, 2018, 16 cases were reported in 11 Wisconsin public health jurisdictions. Wisconsin local and state public health agencies initiated an investigation and notified partners.

METHODS: Case-patient interviews were completed using both the CDC’s Cyclosporiasis National Hypothesis Generating Questionnaire and a supplemental outbreak questionnaire which collected detailed product descriptions and purchase locations to aid in product traceback.

RESULTS: Patient interviews quickly identified a common food item (vegetable trays containing broccoli, cauliflower, carrots, and dill dip) purchased at multiple locations of convenience store A (Store A) across Wisconsin. On June 8, 2018, following notification of the investigation findings, Store A voluntarily removed the vegetable trays from sale at all Store A locations, and a press release was issued by Wisconsin Department of Health Services informing the public of the outbreak and advising people to discard any previously-purchased trays. The vegetable trays were formally recalled from all retail locations by the vegetable tray manufacturer on June 15, 2018. This investigation identified 176 laboratory-confirmed cyclosporiasis cases occurring in Wisconsin residents who consumed vegetable trays. Onset dates ranged from May 14–June 13, 2018. Case-patients had a median age of 44 years and were 52% female, with 4% hospitalized overnight. Case-patients resided in 49 of 72 Wisconsin counties. Less than 25% of case-patients reported consuming vegetable trays on a single day. All but two case-patients reported having consumed and discarded the product when interviewed. Nationwide, 250 cases associated with this outbreak were reported from Iowa, Michigan, Minnesota, and Wisconsin. The Food and Drug Administration investigation did not identify a source or point of contamination.

CONCLUSIONS: Rapid and thorough interviews allowed for identification of a novel food vehicle for cyclosporiasis and prompt removal of the suspected product from sale. The lack of available lot numbers or leftover product, and the high proportion of patients with multiple exposure dates were challenges during traceback. Additionally, the lack of real-time genotyping methods available for *Cyclospora cayetanensis* decreased the ability to distinguish between sporadic and outbreak cases.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Emerging Infections; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jordan.mason@dhs.wisconsin.gov
Presenting Author(s)	Jordan L Mason
Institution Affiliation	Wisconsin Department of Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10952
Abstract Type	Breakout
Abstract Title	Epidemiology of Campylobacteriosis, Salmonellosis, and Shigellosis—Miami-Dade County 2012-2017

Abstract

BACKGROUND: It is estimated that there are 48 million cases of foodborne illness in the United States annually and 9 million of these illnesses are caused by major known pathogens. Despite being highly preventable, campylobacteriosis, salmonellosis, and shigellosis are the most commonly reported bacterial causes of foodborne illnesses in the United States. Understanding the epidemiology of these foodborne illnesses can help improve food safety measures and targeted interventions. This report examines trends in campylobacteriosis, salmonellosis, and shigellosis in Miami-Dade County with regards to demographics and geographic location of cases.

METHODS: Data regarding confirmed cases of campylobacteriosis, shigellosis, and salmonellosis between 2012-2017 were extracted from Merlin, the Florida Department of Health Epidemiology Surveillance System. Poverty level population measures by census tract were retrieved from the U.S. Census Bureau, 2012-2016 American Community Survey 5-Year Estimates and linked to geocoded cases. Population data was retrieved from FLHealthCHARTS.com. The data was analyzed using SAS 9.4 and ArcGIS 10.3.1.

RESULTS: Between 2012-2017 there were 4,126 cases of salmonellosis, 1,943 cases of campylobacteriosis, and 1,143 cases of shigellosis. The majority of salmonellosis and campylobacteriosis cases were between the ages of 0 to 4, 44% and 28% respectively. Most shigellosis cases were between 5 to 17 years old (38%), followed by those 0 to 4 years old (31%). Hispanics had the highest rates of salmonellosis (27.66 per 100,000) and campylobacteriosis (14.29 per 100,000), followed by non-Hispanic White (21.85 per 100,000) and (10.06 per 100,000) respectively. Non-Hispanic Blacks had the highest rates of shigellosis (14.02 per 100,000) followed by Hispanics (6.18 per 100,000). Salmonellosis and campylobacteriosis had overlapping geographic hotspots that were not shared with shigellosis. Forty-one percent of shigellosis cases were from an area where 25% of the population live below the poverty level. Annual rates for all three diseases have remained steady, excluding the spike in shigellosis that occurred in 2014 from 4.9 per 100,000 in 2013 to 24.71 per 100,000 in 2014.

CONCLUSIONS: Campylobacteriosis and salmonellosis are geographically clustered in overlapping residential areas of Miami-Dade County and have similar demographics. Most cases occurred among the Hispanic population and in children aged 0 to 4. Shigellosis cases were clustered in a separate geographic area and had differing demographics. The highest rates were in non-Hispanic Blacks and most cases occurred in children 5 to 17. Shigellosis was significantly associated with areas with higher poverty than campylobacteriosis and salmonellosis.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Local Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Vanessa.Villamil@flhealth.gov
Presenting Author(s)	Vanessa Villamil
Institution Affiliation	Florida Department of Health in Miami-Dade County Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Epidemiology of <i>Listeria Monocytogenes</i> , Miami-Dade County, 2001—2018

Abstract

BACKGROUND: Listeriosis is an infectious disease that causes meningitis, septicemia, and spontaneous abortions. Infections typically affect pregnant women, newborn children, adults over 65 years old, and individuals with compromised immune systems. Pregnant women are 10 times more likely to get *Listeria* infection and Hispanic pregnant women are 24 times more likely to get *Listeria* infection. The purpose of this study was to examine the burden of *Listeria* infections in Miami-Dade County—a predominantly Hispanic community.

METHODS: *Listeria* cases between January 1, 2001 and December 1, 2018 were obtained from Merlin, the Florida Department of Health surveillance system. Variables of interest included age, gender, race/ethnicity, pregnancy status, vertical transmission, hospitalization, origin of infection, outbreak association, and mortality. All statistical analyses were performed in SAS 9.4.

RESULTS: A total of 116 individuals met the inclusion criteria for this report, all of which (100%) met the confirmed case definition for *Listeria*. The mean age of cases were 54 years (range 0 to 95). Fifty-eight (50%) were male. Fifty (51.7%) were Hispanic, 19 (16.3%) Non-Hispanic White, and 11 (9.4%) were Non-Hispanic Black. Race/ethnicity and reporting confusion as a symptom was statistically associated with death. Four (6.8%) of the female cases were pregnant, among which two (50%) were Hispanic, 1 (25%) Other/Asian, and 1 (25%) was unknown. Among non-pregnant *Listeria* cases, 87 (77%) had evidence of septicemia (*Listeria* identified in Blood) and 12 (10%) had evidence of CNS infections (*Listeria* identified in CSF). Among pregnant cases, 1 (27%) had evidence of septicemia, none had evidence of CNS infections, but 3 (75%) had placental evidence of infection. Location of where *Listeria* was isolated (Blood, Placenta, CSF, etc.) was not associated with death. An increase in the number of cases among those 19 to 64 and over the age of 65 was observed after 2010 (Figure 1). Three (75%) of the four pregnant cases occurred in 2014.

CONCLUSIONS: The findings of this report indicate that pregnant women do not appear to be disproportionately affected by *Listeria* in Miami-Dade County. This report did identify that almost half ($n=52$, 48.6%) of the reported *Listeria* cases were over the age of 65 and 47 (92.1%) of these elderly cases had acquired their *Listeria* infections in Florida. However, most fatal *Listeria* cases were among individuals in the 19 to 64 age group. This report highlights the need for additional education on the avoidance of high-risk foods for the elderly, not just pregnant women.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	Epidemiology; Foodborne Disease; Maternal and Child Health
Presenting Author Email Address(es)	Yes
Presenting Author(s)	Isabel.Griffin@flhealth.gov
Institution Affiliation	Isabel Griffin
	Florida Department of Health in Miami-Dade County
	Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Evidence-Based Practices to Inform the Conduct of Enteric Disease Interview and Questionnaire Design

Abstract

BACKGROUND: Detection and investigation of enteric disease outbreaks depends on detailed data collected during routine and hypothesis-generating case interviews. The completeness and accuracy of individual responses are influenced by a number of factors, including the phrasing, ordering, and delivery of questions, and the interviewer's ability to obtain a thorough food history. Our objective was to identify evidence-based practices for interview conduct and questionnaire design, in order to provide resources that will yield more data-rich enteric disease interviews.

METHODS: The Arizona Department of Health Services Outbreak Net Enhanced Site (ADHS), in collaboration with the Colorado Integrated Food Safety Center of Excellence (CoE), conducted a cross-disciplinary literature review. Online databases were searched for articles regarding development of interviewing skills, building rapport, questionnaire design, asking sensitive questions, and special considerations, such as interviewing children and cross-cultural interviews. Articles most relevant to enteric disease investigation were selected by the authors. In addition, key informant interviews were conducted with expert enteric disease interviewers to describe their perspectives of techniques used during enteric disease case interviews.

RESULTS: Seventy-three articles relevant to enteric disease were selected from the disciplines of public health, clinical medicine, survey design, marketing theory, psychology, nutrition, sociology, and anthropology. Published literature specific to enteric disease was limited. Key areas for evidence-based practices were identified based on common themes among the selected articles and consultation with subject matter experts; some are as follows. Interviews improved when interviewers were familiar with the questionnaire in advance. Interviewee rapport improved when interviewers explained laboratory results and answered the interviewee's questions. Important questions should be at the beginning of a questionnaire, followed by general then more specific questions. Demographic and sensitive questions were found to be ideally placed at the end of the questionnaire and phrased with appropriate terminology, which lessens the chance they negatively impact participation. Organization of food items in sequential order using a comprehensive food list improved food recall. Children's food history self-reporting has been found to be reliable as young as age six; additional techniques include using taste/smell/texture and visual questions for young children and interviewing teenagers in private. Cross-cultural variations in food habits and understanding of nutrition exist; special considerations should be taken when interviewing and designing questionnaires cross-culturally.

CONCLUSIONS: This review incorporates direct input from expert enteric disease investigators as well as literature findings from across disciplines; the information gathered has potential to improve questionnaires used for enteric disease investigations.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Surveillance; Data Collection
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rebecca.kruc@azdhs.gov
Presenting Author(s)	Rebecca Kruc
Institution Affiliation	Arizona Department of Health Services State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Food Security Versus Food Safety: <i>Salmonella</i> Enteritidis Outbreak Linked to a Pop-up Food Pantry

Abstract

BACKGROUND: On May 23, 2018, the Wisconsin Department of Health Services (DHS) was notified of three cases of *Salmonella* infections among patrons of the same pop-up food pantry. Case-patients reported obtaining food from the same pantry stop on April 28, 2018. The case-patients received many different food items from the pantry, including frozen breaded chicken products. The pantry has warehouses in Wisconsin and Minnesota and trucks food to at least 74 locations in those states, stopping at each location monthly. At each location, bulk food may be repackaged by community volunteers and provided to patrons for a monetary donation.

METHODS: The Wisconsin Department of Agriculture Trade and Consumer Protection (DATCP) and Minnesota Departments of Health (MDH) and Agriculture (MDA) were notified of the outbreak by DHS. The pantry was notified and provided DHS limited patron information for case finding and notification purposes. Patrons were interviewed with a standardized questionnaire for case finding and to gather exposure information. A confirmed case was defined as a food pantry patron with *Salmonella* cultured from a clinical specimen. Frozen breaded chicken products from patrons were cultured for *Salmonella*. Onsite inspections at the pantry warehouses and pop-up locations were conducted by DATCP and MDA.

RESULTS: Five confirmed Wisconsin case-patients with *Salmonella* Enteritidis infection with PulseNet pattern JEGX01.0004 were identified; all reported receiving and consuming frozen breaded chicken products with no labeling or cooking instructions from two different pantry locations in Wisconsin. Onset dates ranged from May 2–May 31, 2018 and four case-patients were hospitalized. MDH identified six additional case-patients who reported obtaining chicken from Minnesota pantry stops. Raw frozen breaded chicken from two Wisconsin and one Minnesota case-patients were culture positive for *Salmonella* Enteritidis. Clinical and food isolates were all highly related by whole genome sequencing single nucleotide polymorphism comparison. DATCP and MDA worked with the food pantry to halt the distribution of raw chicken products, ensure the warehouses were licensed, and confirm distribution methods met food safety standards.

CONCLUSIONS: This outbreak was linked to an unconventional food distribution method intended to improve access to food, but demonstrates the need to ensure food safety along with food security. Public health and regulatory agencies balanced these needs during their response ensuring on-going access to food while implementing food safety interventions. This outbreak reinforces the need for proper food labeling especially of raw breaded chicken products that can appear cooked to the consumer, and highlights issues with repackaging bulk products.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Food Safety; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jordan.mason@dhs.wisconsin.gov
Presenting Author(s)	Jordan L Mason
Institution Affiliation	Wisconsin Department of Health Services State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Hypothesis Generation during a Foodborne Illness Outbreak Investigation: Tools and Resources from the Integrated Food Safety Centers of Excellence

Abstract

BACKGROUND: Of the foodborne outbreaks reported to Centers for Disease Control and Prevention each year, only about 60% identify a confirmed or suspected etiology. Of those, only about 50% implicate a food vehicle. Implicating a food vehicle during an outbreak investigation is challenging; however, generating robust hypotheses about likely food sources can focus the investigation and improve to likelihood of success.

METHODS: The Integrated Food Safety Centers of Excellence (CoE) aim to improve foodborne illness outbreak investigations by providing public health professionals with effective trainings, tools, and other resources. The aim of this presentation is to highlight trainings, tools and resources that aid in hypothesis generation during a foodborne illness outbreak. We will review several CoE products, including the Outbreak Source Prediction Tool, the Binomial Probability calculator, and Key Points series.

RESULTS: The Outbreak Source Prediction Tool from the Colorado CoE provides data to help guide investigators as they hypothesize about the most likely (or unlikely) source of an STEC or *Salmonella* outbreak. Developed using historical outbreak data from CDC's National Outbreak Reporting System (NORS) and statistical prediction methods, the tool provides associated probabilities for potential common sources based on the most current outbreak information available (i.e., total cases, month of first illness onset, geography, agent, serotype, age, and gender). The Binomial Probability tool/worksheet from the Oregon CoE calculates cumulative binomial probabilities and can be used to estimate how likely it is that the observed number of cases reporting an exposure is due to chance alone given a background exposure rate; thereby, guiding subsequent epidemiological or environmental studies towards food items that are more likely the source of the outbreak. Two Key Points on "Interviewing" and "Cluster Prioritization" from the Minnesota CoE, highlight major questionnaires and interview skills used for hypothesis generation and how cluster prioritization and hypothesis generation are affected by whole genome sequencing. In addition to tools, the CoEs offer a bi-directional learning opportunity "Hypothesis Generation during a Foodborne Outbreak ECHO Series" for investigators to learn more about hypothesis generation and how to use these tools and others during an investigation.

CONCLUSIONS: Hypothesis generation during a foodborne outbreak investigation is an essential step in identifying likely food sources. In this presentation, we will introduce several resources for hypothesis generation and illustrate how to use them in conjunction with other methods of investigation.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Epidemiologic Methods; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	alice.white@ucdenver.edu
Presenting Author(s)	Alice E White
Institution Affiliation	Colorado Integrated Food Safety Center of Excellence, Colorado School of Public Health Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11092
Abstract Type	Breakout
Abstract Title	International Travel-Associated <i>Campylobacter</i> , <i>Salmonella</i> , and <i>Shigella</i> Infections — Foodborne Diseases Active Surveillance Network, 2008–2017

Abstract

BACKGROUND: Diarrhea is the most common travel-associated illness, affecting 40% of US travelers. A Foodborne Diseases Active Surveillance Network (FoodNet) study determined 13% of *Campylobacter*, *Cryptosporidium*, *Cyclospora*, *Listeria*, *Salmonella*, Shiga toxin-producing *E. coli*, *Shigella*, *Vibrio*, and *Yersinia* cases during 2004–2009 traveled internationally. *Campylobacter*, *Salmonella*, and *Shigella* accounted for >90% of those infections. We analyzed FoodNet data to better understand travel-associated infections and identify changes over time.

METHODS: *Campylobacter*, *Salmonella*, and *Shigella* infections reported to FoodNet during 2008–2017 were included. Patients who traveled internationally during their incubation period were considered to have travel-associated infections. Characteristics of travelers and non-travelers were compared during two five-year periods.

RESULTS: Among 52,390 *Campylobacter*, 59,908 *Salmonella*, and 18,054 *Shigella* infections reported to FoodNet with travel information during 2008–2017, 12% traveled internationally (*Campylobacter* =16%; *Salmonella* =10%; *Shigella* =12%). During 2013–2017 compared with 2008–2012, incidence of travel-associated infections increased significantly for *Campylobacter*, by 35% (1.94 vs. 1.44 infections per 100,000 persons; $p<0.01$); *Salmonella*, by 30% (1.39 vs. 1.07; $p<0.01$); and *Shigella*, by 47% (0.51 vs. 0.35; $p<0.01$). The most common destinations were Latin America/Caribbean (48% of *Campylobacter* infections; 63% of *Salmonella*; 64% of *Shigella*) and Asia (26% of *Campylobacter* infections; 25% of *Salmonella*; 23% of *Shigella*). Comparing 2013–2017 with 2008–2012, the percentage with travel to Latin America/Caribbean increased among *Salmonella* (+13%) and *Shigella* (+9%) cases but decreased for *Campylobacter* (-2%). Conversely, the percentage with travel to Asia increased among *Campylobacter* cases (+2%), but decreased for *Salmonella* (-7%) and *Shigella* (-7%). Compared with non-travelers, significantly fewer travelers were hospitalized (13% vs. 25%; $p<0.001$) or had bloody diarrhea (26% vs. 37%; $p<0.001$). Hospitalization was significantly higher for travelers to Asia (20% vs. 11%; $p<0.001$) and Africa (17% vs. 13%; $p<0.01$) compared with other destinations. The most common *Salmonella* serotype among travelers to Asia was Typhi (31%), a rare serotype among non-travelers (<1%). Concord (7%) and Virchow (4%) were among the five most common serotypes identified among travelers to Africa, but were rare among non-travelers (<1%).

CONCLUSIONS: Incidence of travel-associated infections is increasing. Travel-associated pathogens and serotypes vary by destination, and travel destinations by pathogen have changed over time. Severe infections were less common among travelers compared with non-travelers, and hospitalization varied by destination. These findings may be important to consider for prevention, treatment, and public health investigations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Food Safety; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	omx9@cdc.gov
Presenting Author(s)	Hazel J Shah
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10738
Abstract Type	Breakout
Abstract Title	Investigation of a Multistate Outbreak of <i>Salmonella</i> Enteritidis Associated with Shell Eggs Using Whole Genome Sequence Analysis

Abstract

BACKGROUND: In August 2018, the Tennessee (TN) Department of Health and the Alabama (AL) Department of Public Health, along with local counterparts, investigated separate restaurant-associated outbreaks of an indistinguishable *Salmonella* Enteritidis pulsed-field gel electrophoresis (PFGE) pattern. Human cases of this pattern are common, accounting for over 10% of *Salmonella* Enteritidis cases annually in the United States. Both outbreaks were linked to consumption of dishes containing under-cooked eggs. The eggs were traced back to Farm X in AL. A multistate outbreak investigation was initiated to identify additional cases in TN, AL, and other states and implement control measures.

METHODS: Due to the clonality of the PFGE pattern, PulseNet, the national molecular subtyping network for foodborne disease surveillance, used whole genome sequencing (WGS) to further characterize the relatedness of isolates of this PFGE pattern. A confirmed case was defined as illness in a person infected with the outbreak strain of *Salmonella* Enteritidis and a specimen isolation date on or after June 20, 2018. Patients were interviewed to identify common food exposures. The U.S. Food and Drug Administration (FDA) and AL Department of Agriculture conducted an environmental investigation at the farm. Environmental samples, samples from eggs, and prepared food were cultured for *Salmonella*.

RESULTS: Of 352 sequences analyzed, forty-four confirmed cases from eleven states within 0-10 alleles different by WGS were identified. Among 37 cases with food exposure information available, 29 (78.4%) reported consuming any eggs. Eggs from Farm X were distributed to three states: TN, AL, and Georgia (GA). Living in or traveling to TN, AL, or GA was reported by 39 (88.6%) of 42 cases. An additional 24 cases without laboratory testing were identified during the restaurant-associated outbreak investigations in TN and AL. Environmental swabs from Farm X, shell eggs from Farm X, and one prepared food sample yielded the outbreak strain. The investigation found that Farm X, which supplied local, free-range eggs to restaurants and retail locations, had recently increased its flock size above the 3,000 bird threshold for FDA regulation, but was not in compliance with the rule at the time of the outbreak.

CONCLUSIONS: Whole genome sequencing was critical in determining the magnitude of a multistate outbreak investigation of a common PFGE pattern of *Salmonella* Enteritidis. This outbreak suggests that as 'locally-sourced' and 'farm to table' products increase in popularity, efforts by small food producers to meet this demand may result in critical gaps in regulation and food safety knowledge and practices.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Foodborne Disease; Food Safety
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	mugdha.golwalkar@tn.gov
Presenting Author(s)	Mugdha Golwalkar
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Is a Positive Shiga Toxin Test a Shiga Toxin-Producing <i>E. coli</i> Infection? — Foodborne Diseases Active Surveillance Network (FoodNet) — 2012–2017

Abstract

BACKGROUND: FoodNet conducts active laboratory-based surveillance for Shiga toxin-producing *E. coli* (STEC) in 10 US sites. During 2007–2017, FoodNet reported increased culture-independent diagnostic test (CIDT) use and decreased isolation of STEC by culture. In the absence of an STEC isolate, FoodNet has excluded cases whose Shiga toxin (Stx) CIDT results were not confirmed by a public health laboratory (PHL). In 2018, the STEC national case definition was updated to include infections diagnosed by any CIDT.

METHODS: We examined STEC infections reported to FoodNet during 2012–2017 with a positive Stx immunoassay (IA) or polymerase chain reaction (PCR) test at a clinical laboratory, followed by testing of the same or another specimen at a PHL. Three test type combinations were assessed (IA/IA, PCR/PCR, and IA/PCR) by state, symptoms, test discordance, and culture result. A positive Stx CIDT at a clinical laboratory followed by a negative Stx CIDT at the PHL was considered discordant.

RESULTS: During 2012–2017, 8,260 (76% of all STEC reported) cases tested positive by IA or PCR at a clinical laboratory followed by an IA or PCR at a PHL. Among these, 1,736 (21%) were excluded from FoodNet case counts. Twenty-nine percent of cases had positive results by CIDT alone. Some cases had two CIDT tests performed, resulting in 8,989 total test combinations. The most frequent combination was IA/PCR (57%), followed by IA/IA (26%) and PCR/PCR (25%); most (98%) were also tested by culture. Of the test combinations performed, 1,911 (29%) were discordant (range by state, 10%–44%). Among the IA/PCR test results, 18% were discordant, and 14% of those cultured had STEC isolated. A higher proportion of IA/IA (27%) and PCR/PCR (23%) results were discordant, and 5% of those cultured had STEC isolated. Persons with discordant test results were less likely to have diarrhea (91% vs. 97%) or bloody diarrhea (28% vs. 57%). Test result discordance increased markedly from 2012 to 2017 in all sites for IA/PCR (11% to 21%), IA/IA (17% to 34%), and PCR/PCR (6% to 24%).

CONCLUSIONS: Accepting multiple test results with differing sensitivity and specificity complicates surveillance. Marked variation in frequency of discordant Stx results and identification of STEC isolates by state highlights how sensitivity and specificity of different test types, test targets, and specimen transport might affect STEC results and surveillance. Including all infections diagnosed by any CIDT could increase FoodNet STEC case counts and challenge interpretation of national trends.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Infectious Diseases; Surveillance; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	dot7@cdc.gov
Presenting Author(s)	Danielle M. Tack
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	It Must Have Been Something I Ate...Two Outbreaks at One Facility

Abstract

BACKGROUND: In the summer of 2018, the Cleveland Department of Public Health (CDPH) encountered a retail food establishment (RFE) that was found to have concurrent Salmonellosis and Cyclosporiasis outbreaks associated with one facility. These two outbreaks caused a chain reaction of environmental health inspections of the facility and several other control measures to mitigate the outbreaks. Eventually, the nature and severity of the outbreaks led to a suspension order on the facility.

METHODS: Key information was gathered from patients and the RFE to identify any food exposures and potential sources of contamination. Food and stool samples were collected from the RFE and employees/patients, respectively. Multiple site visits to the RFE that prepared and sold the food were conducted.

RESULTS: *Salmonella infantis* was confirmed in four (4) patients that had exposure to the RFE and met our case definition. Additionally, during the same time period, six (6) cases of *Cyclosporiasis* were identified in people that attended an event catered by the RFE and who consumed guacamole. Several foods were tested in the Salmonella outbreak, which led epidemiologists to a direct genotype match between meat served by the RFE and stool samples collected from all four (4) patients. During the registered sanitarians' inspections, they found the RFE was in violation of several offenses that could be related back to both outbreaks.

CONCLUSIONS: The Cleveland Department of Public Health collaborated with several departments internally and externally to identify the source of both outbreaks at the RFE. Once identified, prevention and control measures were put into place to limit the public health threat. These outbreaks helped identify gaps in communication systems and foodborne illness investigations. Lessons learned from this event have helped shed more light on the intersecting roles epidemiologists and sanitarians play in any foodborne investigation.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Epidemiology; Foodborne Disease; Collaboration
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kromig@city.cleveland.oh.us
Presenting Author(s)	Katherine A. Romig
Institution Affiliation	Cleveland Department of Public Health Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11680
Abstract Type	Breakout
Abstract Title	Multi-Serotype Outbreak of Salmonella Infections Linked to Kratom — United States, 2017–2018

Abstract

BACKGROUND: *Salmonella* is a leading etiology of bacterial gastroenteritis in the United States, causing an estimated 1 million foodborne illnesses annually. Many of these illnesses are linked by molecular subtyping and investigated as multistate outbreaks. These investigations can lead to the identification of novel foodborne illness vehicles. In January 2018, PulseNet, the national laboratory network for foodborne disease surveillance, detected a cluster of 14 *Salmonella* 14,[5],12:b:- infections with an indistinguishable pulsed-field gel electrophoresis (PFGE) pattern. We investigated to identify the source and prevent additional illnesses.

METHODS: Patient interviews were reviewed for commonly reported exposures. A focused questionnaire collected detailed information on the suspected vehicle. Product samples collected from patient homes and retail locations were cultured for *Salmonella*. Investigators conducted traceback to determine product distribution chains and identify suppliers. A case was defined as infection with one of eight PFGE patterns representing six *Salmonella* serotypes occurring between January 1, 2017, and May 24, 2018.

RESULTS: Early interviews indicated kratom was an exposure of interest. Kratom is a plant consumed for its stimulant effects and as an opioid substitute. During the investigation, several state officials and FDA identified strains of *Salmonella* from collected leftover and unopened kratom products that matched clinical isolates by PFGE. As additional strains were identified in kratom products, a search of the PulseNet database identified ill people infected with some of these strains, including *Salmonella* Heidelberg, Javiana, Okatie, Weltevreden, and Thompson. These ill people were added to the outbreak investigation. We identified 199 cases from 41 states; 54 hospitalizations and no deaths were reported. Seventy-six (74%) of 103 people interviewed reported consuming kratom in pills, powder, or tea. People who reported consuming kratom purchased it from in-person retail locations in several states and from various online retailers. Several companies issued recalls of kratom products. Eighty-five different PFGE patterns of *Salmonella* bacteria were identified in samples of kratom products.

CONCLUSIONS: This investigation is the first to establish kratom consumption as a vehicle for *Salmonella* transmission. Kratom and similar products with an indistinct regulatory status pose unique challenges to public health investigators, regulatory agencies, and the food safety community. Because these products are also not traditional outbreak vehicles, any outbreaks they cause may be under-identified. The diversity of *Salmonella* cultured from kratom suggests widespread microbial contamination, the ultimate sources of which have not been identified. These results underscore serious safety concerns regarding minimally-processed botanical substances intended for oral consumption.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Food Safety; Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	hvf44@cdc.gov
Presenting Author(s)	Colin Schwensohn
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10909
Abstract Type	Breakout
Abstract Title	Multiple Pathogen Gastroenteritis Outbreak Associated with an Outdoor Recreational Facility — Tennessee, 2018

Abstract

BACKGROUND: During June–July 2018, the Tennessee Department of Health received reports of acute gastroenteritis among visitors to a recreational facility featuring zip lines and mountain bike trails. We investigated to identify the source and stop transmission.

METHODS: On July 6, 2018 an internet-based survey was sent to 2,904 visitors who purchased tickets on-line to identify ill persons and conduct a case-control study. A case was defined as diarrhea (≥ 3 loose stools < 24 hours) or vomiting after the user visited the facility during June 15–July 6, 2018. Controls were non-ill survey respondents. We interviewed staff and conducted an environmental assessment. Case-patient stool specimens and environmental samples were tested for enteric pathogens by polymerase chain reaction.

RESULTS: We identified 693 (67%) case-patients and 338 (33%) controls among 1,031 survey respondents. Mountain biking (odds ratio [OR]: 2.5; 95% CI: 1.4–4.5) and drinking well water (OR: 4.4; 95% CI 3.1–6.3) were associated with illness. The facility had no ill-worker exclusion policy and staff reported working while ill. The well supplying water was untreated and unregulated. In nine (60%) of fifteen stool samples collected, norovirus was detected; two (22%) were co-infected with Enteropathogenic *Escherichia coli* (EPEC). *E. coli*, total coliforms, and EPEC were detected in well water. Pooled swabs from the lobby, break room, restroom, and mountain bike course were positive for EPEC, *Giardia*, and *Cryptosporidium*. Norovirus was detected on gloves in the gear room, lobby, staff area, and was identified among case-patients; 2 were co-infected with EPEC. Recommendations included using bottled drinking water and disinfection with diluted-bleach solution. No further cases were identified.

CONCLUSIONS: This large, multi-pathogen gastroenteritis outbreak involved multiple transmission modes and widespread facility contamination. Outdoor recreation facilities should be in compliance with public water system regulations, consider implementing ill-worker exclusion policies, and disinfect publicly used equipment.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Outbreaks; Waterborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	brittany.isabell@tn.gov
Presenting Author(s)	Brittany S. Isabell
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11157
Abstract Type	Breakout
Abstract Title	Multistate Outbreak of <i>Salmonella</i> Infections Linked to Raw Turkey Products — United States, 2017--2018

Abstract

BACKGROUND: Foodborne salmonellosis causes approximately 1 million illnesses annually in the United States. In January 2018, Minnesota investigators notified CDC of recent *Salmonella* Reading infections in their state potentially associated with raw turkey products. We queried PulseNet, the national laboratory network for foodborne disease surveillance, for additional *Salmonella* Reading infections with an indistinguishable pulsed-field gel electrophoresis (PFGE) pattern. We investigated to determine the outbreak source and prevent additional illnesses.

METHODS: A case was defined as an infection with the outbreak strain of *Salmonella* Reading occurring since November 20-, 2017. Case-patients were identified in PulseNet and interviewed to determine common exposures. Investigators conducted traceback to determine sources of reported foods and tested products for *Salmonella* .

RESULTS: As of November 5, 2018, we identified 164 cases from 35 states. The median case-patient age was 45 years (range <1–91), 56% were female. Of 135 case-patients with information, 63 (47%) were hospitalized, and one death was reported. Of 85 case-patients interviewed, 50 (59%) reported exposure to turkey. Among these, 44 reported preparing or eating turkey products that were purchased raw, including ground turkey, turkey parts, and whole turkey, three became sick after pets in their home ate raw turkey pet food, and three worked in a facility that raises or processes turkeys, or lived with someone who did. The outbreak strain was identified in raw turkey pet food in Minnesota, raw turkey products collected from case-patient homes in Arizona and Michigan, raw turkey products from 22 slaughter and 7 processing establishments, and live turkeys from five states. Raw turkey pet food associated with two illnesses was recalled in February 2018. No single, common, supplier of turkey products has been identified. Investigators shared outbreak information with representatives from the turkey industry and posted outbreak information publicly through web announcements to remind consumers that raw turkey may be contaminated with bacteria.

CONCLUSIONS: Results suggest that this strain of *Salmonella* Reading is present in live turkeys and raw turkey products. Therefore, interventions to reduce the prevalence of this strain should target both the live turkey industry and turkey slaughter/processing establishments. Accordingly, investigators presented epidemiologic, traceback, and food testing data to the entire turkey industry during this response, rather than to a single company, in order to better inform industry-wide prevention strategies to reduce *Salmonella* contamination. Consumers should also follow steps to prevent *Salmonella* infection when handling raw turkey products, including washing hands, cooking raw turkey to 165°F, and avoiding cross contamination.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Outbreaks; Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ykm6@cdc.gov
Presenting Author(s)	Rashida Hassan
Institution Affiliation	CAITTA, Inc CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10985
Abstract Type	Breakout
Abstract Title	Multistate Outbreak of Shiga Toxin-Producing <i>E. coli</i> Infections Associated with Romaine Lettuce

Abstract

BACKGROUND: Produce-associated outbreaks of Shiga toxin-producing *Escherichia coli* (STEC) were first identified in 1991. In 2006, spinach was identified as the vehicle for a multistate outbreak of *E. coli* O157:H7 (STEC O157) infections. This outbreak resulted in enhanced industry guidance in 2011 to improve the safety of leafy green vegetables. In April 2018, New Jersey reported a cluster of STEC O157 infections associated with multiple locations of a restaurant chain. CDC queried PulseNet, the national laboratory network for foodborne disease surveillance, for additional cases and began an investigation.

METHODS: A case was defined as an infection of STEC O157 occurring between March 16, 2018, and August 28, 2018, that was closely related by whole genome sequencing. Case-patients were interviewed using a questionnaire focused on leafy greens and restaurant exposures in the week before illness onset. Sub-clusters (two or more unrelated case-patients who reported eating or shopping at a common restaurant or store) were investigated. This information was shared with regulatory partners for traceback activities. An FDA-led environmental assessment was conducted to evaluate environmental routes of STEC contamination to food products. Water, soil, and scat samples were collected as part of this assessment.

RESULTS: 240 case-patients were identified from 37 states; 104 were hospitalized, 28 developed hemolytic uremic syndrome, and five died. Of 179 case-patients who were interviewed, 152 (85%) reported consuming romaine lettuce in the week before illness onset. Twenty sub-clusters were identified. Product traceback from sub-cluster restaurants identified numerous romaine lettuce distributors and growers; all lettuce originated from the Yuma growing region. Water samples collected from an irrigation canal in the region that was adjacent to multiple romaine lettuce farms and a concentrated animal feeding operation yielded the outbreak strain. Health officials warned the public to avoid eating or selling romaine lettuce from this region during the outbreak.

CONCLUSIONS: This outbreak was larger than previous leafy green outbreaks linked to a single contaminated field, and highlighted the complexities associated with investigating outbreaks linked to widespread environmental contamination. Creating clear public messaging was complicated because the outbreak was not linked to a single source of romaine lettuce, but rather to an entire growing region. Consumer advice focused on avoiding romaine lettuce from the Yuma growing region, but consumer packaging rarely includes that level of detail. New labeling on packages that debuted in December 2018 may improve future traceability and simplify public messaging. Continued research on produce irrigation water will help future outbreak prevention.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Environmental Health; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	xmm8@cdc.gov
Presenting Author(s)	Lyndsay Bottichio
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10982
Abstract Type	Breakout
Abstract Title	Outbreak of <i>Salmonella</i> Enteritidis Associated with Eggs – a Local Public Health Response, August 2018

Abstract

BACKGROUND: *Salmonella* causes about 1.2 million illnesses and 23,000 hospitalizations in the United States annually, with shell eggs being a common cause of outbreaks. Local public health officials identified an outbreak of *Salmonella* Enteritidis on August 4, 2018 upon receipt of multiple illness complaints following meals at Restaurant A in Nashville, TN. An outbreak investigation was initiated to determine the source and implement control measures.

METHODS: A comprehensive environmental assessment was conducted, including staff interviews, general observation, event reconstruction, and food flow evaluation. Seventeen eggs and twelve environmental samples were collected for testing. Trace back investigations were conducted by reviewing Restaurant A's product invoices. Cases and controls for a case-control study were identified through snowball sampling of ill patrons, well meal companions, and on-line restaurant reviews from patrons who dined at the restaurant between August 3rd and 5th. Cases and controls were interviewed by phone with a standardized questionnaire to gather clinical details and food history. Clinical specimens from individuals who reported illness were collected and isolates underwent pulse field gel electrophoresis (PFGE) and whole genome sequencing (WGS).

RESULTS: The environmental assessment found that gnocchi were made with raw eggs and were not adequately cooked to destroy pathogens. During reconstruction of events, portions of the raw gnocchi were cooked to 130°F, well below the required 165°F necessary to kill *Salmonella*. The eggs used in the implicated dish were traced back to Farm X in Alabama (AL). Officials identified 26 cases, with illness onset ranging from August 4-8, 2018. Nineteen cases (73.1%) sought medical attention and five (19.2%) were hospitalized. The case-control study suggested that illness was significantly associated with the short rib gnocchi dish containing eggs (OR=91.67, CI=8.56-982.24). While all egg and environmental samples collected were negative for *Salmonella*, clinical specimens were positive for *Salmonella* Enteritidis with an indistinguishable PFGE pattern and were closely related by WGS.

CONCLUSIONS: Appropriate and timely control measures were implemented at the restaurant that resulted in removal of the gnocchi dish. While eggs and environmental swabs collected during this investigation were negative, subsequent samples taken at the farm during the multistate outbreak investigation matched the local outbreak strain. A swift, local response contributed to the identification of a multi-state outbreak associated with Farm X shell eggs. Findings at the local level were imperative to provide evidence to state and federal agencies for a larger response, which led to a recall of eggs contaminated with *Salmonella* Enteritidis.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Local Epidemiology; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email	tyler.means@nashville.gov
Address(es)	
Presenting Author(s)	Tyler Means
Institution	Metro Public Health Department
Affiliation	Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10730
Abstract Type	Breakout
Abstract Title	What Does It Take to Go Pro: Considerations for a National Population Survey

Abstract

BACKGROUND: The Foodborne Diseases Active Surveillance Network (FoodNet) Population Survey is a population-based survey conducted in the 10 FoodNet sites, which comprise 15% of the US population, used to estimate the burden of foodborne illnesses and background rates of exposures. The sixth cycle began in December 2017 and will conclude in July 2019. To inform design of a national survey, we evaluated current methodology for quality and cost effectiveness.

METHODS: The survey has a target sample size of 40,000 and uses four administration modes: computer-assisted telephone interview (CATI) surveys of landline and cell phone respondents and address-based sample for web and paper surveys. Three reminders were sent every two weeks to web survey non-responders; the final reminder included a paper survey. Survey questions include exposures related to enteric disease, gastroenteritis, and health care. The web survey has additional questions and modules, including site-specific modules to assess important regional exposures.

RESULTS: By November 2018, among 39,103 households reached by phone, 8,121 (21%) completed CATI surveys; among 103,805 households mailed web survey invitations, 12,098 (12%) completed the survey. A paper survey was mailed to 17,958 households; 1,951 (11%) completed and returned it. The cost per complete survey for CATI cell and landline was 3.4 and 2.4 times, respectively, that of web. Among the first 5,000 surveys completed, mail surveys had a much higher proportion of missing answers among key questions compared with other modes (11% average for 15 questions; range by question 0–30% vs. 3%; range 0–5%) and were excluded from further analyses. Among completed interviews, 15% of CATI and 20% of web surveys were from children and approximately 50% of adult respondents for both modes were aged 55–74 years. Other demographics were similar to the general population.

CONCLUSIONS: Due to low response and high rates of missing information, the mail survey was discontinued in June 2018 and the target sample size for web was increased. Web was selected over CATI due to lower costs, fewer interview attempts required to reach the target number of complete surveys, and greater flexibility to include more questions such as site-specific modules. Although the proportion of older and children CATI and web respondents differed from the FoodNet population, this can be accounted for in analysis. Based on these results, a web survey could be implemented nationally as a cost-effective, flexible method to collect more nationally representative data on gastrointestinal illness and relevant exposures.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiologic Methods; Foodborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	uyk1@cdc.gov
Presenting Author(s)	Ellyn Marder
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11383
Abstract Type	Breakout
Abstract Title	"It Didn't Taste Right, but I Ate It Anyway"...an Investigation of Foodborne Botulism

Abstract

BACKGROUND: Foodborne botulism is a neuromuscular illness caused by contamination of foodstuffs with heat-stable toxin from germinating spores of *Clostridium botulinum* or related species. Environmentally hardy *Clostridium* spores are widespread in some soils. Since 2008, all U.S. outbreaks of foodborne botulism have been attributed to home-prepared or -canned foods. In April 2018, a hospital contacted the Pennsylvania Department of Health (PA DOH) to report 2 suspected cases of botulism. We investigated to confirm the clinical diagnosis, facilitate obtaining antitoxin from the Centers for Disease Control and Prevention, identify and test potentially contaminated food items, and determine whether other persons were at risk.

METHODS: The cases and their family members were interviewed to obtain their food histories, description of food preparation of several items, and information about other individuals who may have consumed contaminated food items. Clinical and environmental specimens were submitted to the PA DOH Laboratory for analysis.

RESULTS: Two ill people from one household reported simultaneous onset of gastroenteritis several hours after consumption of chung gook jang, a traditional Korean dish consisting of fermented soy beans (similar to natto beans) that was prepared at home by another family member. Neurological symptoms consistent with early botulism started about 48 hours after the dish was consumed and prompted the couple to seek medical care. Both patients received antitoxin roughly 48 hours after neurological symptoms started and were monitored until their discharge 5 days later; neither required mechanical ventilation. On discharge, ptosis continued in one patient and neurological symptoms were completely resolved for the second patient. Interviews revealed that another family member consumed chung gook jang. This individual was monitored for symptoms of botulism for 10 days from the last date of consumption but did not become ill. *Clostridium botulinum* toxin type B was detected by mouse bioassay in a sample of chung gook jang. Toxin was not detected in the clinical specimens submitted from both patients.

CONCLUSIONS: Foodborne botulism associated with consumption of a home-prepared fermented bean dish was confirmed in two cases in Pennsylvania, neither of whom developed severe disease; one other person was exposed but did not become ill. This investigation demonstrates that home-prepared and -canned items continue to pose an unexpected and significant risk of foodborne botulism. In addition, clinical findings of these case patients underscore that foodborne botulism may be mild, not necessarily progressing to whole-body paralysis. Finally, consumption of implicated foodstuff may not result in intoxication.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Infectious Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	elnegron@pa.gov
Presenting Author(s)	Elizabeth A. Negrón
Institution Affiliation	Pennsylvania Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11836
Abstract Type	Lightning
Abstract Title	Detecting a Multi-State Outbreak Using Environmental Sampling, Whole Genome Sequencing, and Data Sharing Platforms

Abstract

BACKGROUND: Oregon’s Health Authority (OHA) and Wisconsin’s Division of Public Health routinely investigate disease clusters detected by molecular methods, with epidemiologic associations to vehicles identified through administration of standardized questionnaires. Outbreaks associated with uncommon vehicles are typically difficult to detect and require epidemiologic evidence from a relatively larger number of cases, which can extend time to recall of a product.

METHODS: During a Salmonella cluster investigation in mid-August through early September 2018 with a strong raw cake mix signal, OHA collected 43 boxes of unopened cake mix and sent samples to IEH Labs in Washington for Salmonella testing. Salmonella Agbeni was isolated from an unopened box of white cake mix, and whole genome sequencing (WGS) data were uploaded to the U.S. National Library of Medicine’s National Center for Biotechnology Information (NCBI) web site. Using the NCBI isolate browser and CDC’s System for Enteric Disease Response, Investigation, and Coordination (SEDRIC), OHA cross-referenced the sequence data from the cake mix isolate with available clinical isolates in the NCBI database.

www.ncbi.nlm.nih.gov/Structure/tree/#!/tree/Salmonella/PDG000000002.1230/PDS000001865.145?key=xIplqULLh7_U9bRZtZXRRf-zlgxCL_VWzSi9QdwMh0bFCYtJ6wk

RESULTS: OHA determined that four clinical isolates from three states were genetically related within four single nucleotide polymorphisms (SNPs). OHA notified the states, inquiring about raw cake mix exposures among their cases. The Wisconsin case reported having consumed an entire box of raw white cake mix over several days within their exposure period; WGS analysis indicated that this clinical isolate was within one SNP of OHA’s Duncan Hines white cake mix isolate. OHA contacted CDC et al., and on 5 November 2018, Duncan Hines announced a voluntary recall (2.4 million boxes) of several cake-mix flavors because of possible contamination with Salmonella.

CONCLUSIONS: We used WGS data on the NCBI website to detect a multistate outbreak associated with a widely distributed consumer product, which subsequently resulted in a regulatory action. WGS of food and environmental isolates and subsequent sharing on the NCBI and SEDRIC platforms are emerging as useful tools in identifying outbreaks associated with widely distributed products with long shelf-lives and low background rates of consumption, such as raw cake mix. These efforts highlight the value of collaborations between public health epidemiologists and laboratorians as well as the use of new technological tools for outbreak detection. We recommend obtaining food and environmental samples whenever practical and implicated by highly significant epidemiologic associations during outbreak or cluster investigations; and employing WGS, in conjunction with the NCBI website and SEDRIC, to quickly identify genetically related case isolates.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Collaboration; Epidemiologic Methods; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Stephen.G.Ladd-Wilson@state.or.us
Presenting Author(s)	Stephen Ladd-Wilson
Institution Affiliation	Oregon Public Health Division State Public Health Agency

Submission Type ID Breakout/Quick/Lightning/Poster 10732

Abstract Type Lightning

Abstract Title Foodcore Centers Improve Isolate Testing Using Whole Genome Sequencing As Pulsed-Field Gel Electrophoresis Is Phased out for Enteric Disease Surveillance

Abstract

BACKGROUND: In 2009, CDC started the Foodborne Diseases Centers for Outbreak Response Enhancement (FoodCORE) program to provide targeted resources for enhanced laboratory, epidemiology, and environmental health capacity to detect, investigate, and respond to enteric disease outbreaks. To demonstrate the impact of their resources, centers developed and operationalized performance metrics to evaluate the burden, timeliness, and completeness of enteric disease surveillance and outbreak response activities. Laboratory subtyping of *Salmonella*, Shiga toxin-producing *Escherichia coli* (STEC), and *Listeria* (SSL) is one critical component of detecting and solving outbreaks. Public health laboratories (PHLs) in the United States are increasingly using whole genome sequencing (WGS) because it is more precise and more detailed than the current standard technique, pulsed-field gel electrophoresis (PFGE). Currently, PHLs use both PFGE and WGS to subtype isolates.

METHODS: FoodCORE centers submit isolate/specimen-based metrics biannually to evaluate the timeliness and completeness of surveillance and subtyping data for SSL. In Year 6 (Y6, 1/1/2016 – 12/31/2016), centers pilot-tested a set of expanded SSL metrics to evaluate the timeliness and completeness of WGS. Centers reported on the expanded metrics in Y6, Year 7 (Y7, 1/1/2017 – 12/31/2017), and Year 8 (Y8, 1/1/2018 – 12/31/2018).

RESULTS: From the beginning of Y6 through the end of Y7, centers reported a total of 21,141 primary SSL isolates/isolate-yielding specimens. In Y7, the proportion of SSL isolates with PFGE information increased to 98.4% (from 94.6% in Y6). Completion of WGS varied by pathogen. During Y7, WGS was performed on 81.3% of *Salmonella*, 82.1% of STEC, and 83.1% of *Listeria* isolates. Among all SSL isolates, the proportion with WGS information increased from 45.2% in Y6 to 98.9% during the first half of Y8. From Y6 through 6/30/2018, the average time to complete PFGE subtyping for SSL and upload to the national database increased from 2.4 days to 3.9 days; however, the average time to conduct sequencing and upload to the national database decreased from 12.0 days to 8.0 days.

CONCLUSIONS: Centers continue to improve enteric disease outbreak surveillance and response activities using WGS while performing PFGE simultaneously. PFGE will be phased out in 2019, and FoodCORE performance metrics are expected to demonstrate further improvements in the completeness and timeliness of WGS activities, leading to faster and more complete investigations to help stop the spread of enteric diseases.

Submission Complete? Yes

Committee Infectious Disease

Topic Enteric Diseases

Keywords Food Safety; Capacity / Capacity Building; Foodborne Disease

Consider for Different Presentation? Yes

Presenting Author Email Address(es) moi0@cdc.gov

Presenting Author(s) Frances P. Tilashalski

Institution Affiliation Centers for Disease Control and Prevention
CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11022
Abstract Type	Lightning
Abstract Title	Use of a Health Alert Network's (HAN) Mass Text Messaging Functionality to Investigate Foodborne Outbreaks – Tennessee, 2018

Abstract

BACKGROUND: Since 2016, the Tennessee Department of Health (TDH) has used text messaging for routine foodborne disease surveillance interviews. TDH recently implemented text messaging to investigate large-scale outbreaks using the Tennessee Health Alert Network (TNHAN). HAN systems disseminate alerts to local, state and federal partners to respond to public health events. TNHAN has the ability to send mass messages, through text, email and prerecorded call. We describe use of the TNHAN to send mass text messages to individuals in two different Shiga toxin-producing *Escherichia coli* (STEC) outbreaks in 2018.

METHODS: TDH's Public Health Emergency Preparedness Program TNHAN system protocols were followed. A 250 character text message including a link to an outbreak questionnaire, public health prevention messages, and contact information was sent. STEC Outbreak 1 was restaurant associated. Phone numbers of patrons were obtained from online reservation lists. The electronic outbreak questionnaire capturing symptoms and menu items was accessed by patrons via link sent through the TNHAN. STEC Outbreak 2 was associated with raw milk from a cow share program. We obtained phone numbers for members of the cow share program. In addition to a questionnaire link, cow share members were notified with urgent prevention messaging.

RESULTS: TNHAN messaging was easily accessible with minimal technical support needed. During the STEC Outbreak 1 investigation, 51 (40%) of 127 restaurant patrons responded to the text message. For STEC Outbreak 2, 33 (24%) of 138 cow share participants responded. Through the web-based surveys we identified 4 additional cases in STEC Outbreak 1 and 7 additional cases in STEC Outbreak 2. Exposure data was successfully collected and analyzed, and prevention messages were received advising individuals of ongoing risk and appropriate public health actions.

CONCLUSIONS: Use of an existing HAN to send mass text messages supported both STEC outbreak investigations. Inclusion of an electronic questionnaire link facilitated case finding and collection of exposure data used in epidemiology studies. We observed slightly lower response rates than previous electronic surveys sent via email. However, in the absence of email addresses, this method provided enough responses to proceed with the investigation, implicate food items and inform the at-risk population of urgent health threats and prevention measures. Text messaging is common and may reach individuals who are more comfortable with this form of communication. Although character limits can be a challenge, HAN text messaging can be used to investigate and respond to foodborne outbreaks successfully.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Emergency Preparedness & Response; Outbreaks; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kailey.lewis@tn.gov
Presenting Author(s)	Kailey Lewis
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10617
Abstract Type	Poster
Abstract Title	A Collaborative Outbreak Investigation of Salmonella Enteritidis Linked to Chicken with Multiple Exposure Locations

Abstract

BACKGROUND: In April of 2018, an outbreak of *Salmonella* Enteritidis associated with a local deli and caterer in Newton County, Georgia was investigated. This outbreak was identified when a private citizen called Gwinnett, Newton and Rockdale County Health Departments (GNR) and reported multiple cases of gastrointestinal illness among private event attendees. GNR conducted a collaborative outbreak investigation to identify potential sources of infection and limit the spread of illness. **METHODS:** GNR conducted cohort studies including risk-based interviews with both well and ill event attendees and food service facility patrons. Using event-specific information provided by interviewees and menus collected, surveys were created and distributed to the cohort electronically. Statistical analyses were performed using Open Epi and Epi Info version 7. Stool and food specimens were collected and tested via culture, pulsed-field gel electrophoresis (PFGE), and whole genome sequencing (WGS) for the suspect pathogen at Georgia Public Health Laboratory. Environmentalists conducted facility inspections to identify risk factors. When new cases associated with the facility continued to be identified, GNR requested that the deli close for deep cleaning and additional on-site staff education.

RESULTS: Ninety-five illnesses and five locations associated with the outbreak were identified from April-May, 2018. These locations included the deli, a private event on April 28th (where 67 cases were identified), two private luncheons on May 9th, and a secondary exposure. Median case age was 37 years (range eight days–88 years). Sixty-one percent were female; 39% were male. Thirty-seven people (38.9%) sought medical attention; six (6.3%) were hospitalized. No deaths were reported. Stool cultures from 28 individuals were positive for *Salmonella*; 18 specimens yielded *Salmonella* Enteritidis. Fifteen isolates matched PFGE pattern four; 13 were closely related by WGS. Three isolates matched PFGE pattern 21; three were closely related by WGS. Violations observed during facility inspections included separation and protection and inadequate spacing between hand sink and prep table. Consuming grilled chicken at the catered event on April 28th (RR 1.49 95% CI: 1.01, 2.19), or eating chicken salad prepared by the local deli and caterer the between April and May of 2018 (RR 1.75 95% CI: 1.21, 2.53), were statistically associated with illness.

CONCLUSIONS: Based on epidemiologic and laboratory evidence, this outbreak of *Salmonella* Enteritidis was associated with consumption of food items prepared by a local deli and caterer. Though no common food item was reported by all ill individuals, all statistically significant food exposures contained chicken as an ingredient.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Foodborne Disease; Food Safety
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	keisha.francis@gnrhealth.com
Presenting Author(s)	Keisha K. Francis
Institution Affiliation	Gwinnett, Newton and Rockdale County Health Departments Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	An Outbreak of Gastrointestinal Illness Associated with a Thanksgiving Potluck, Williamson County, Texas, 2018

Abstract

BACKGROUND: On Friday, November 16th, the Williamson County and Cities Health District was notified that multiple people had become ill after eating at a Thanksgiving potluck. The turkey, ham, turkey gravy and stuffing were provided by a catering company; other dishes were brought by potluck attendees. Ill attendees reported diarrhea and abdominal cramps within 24 hours after eating at the potluck. An investigation was initiated to define the extent of the outbreak, identify the causative agent, determine mode of transmission, source of infection, and implement control measures. **METHODS:** Potluck attendees were interviewed by telephone using an Excel-based survey to collect information on demographics, symptoms, and food consumed. A case was defined as a potluck attendee reporting diarrhea and/or abdominal pain $\leq$ 24 hours of the potluck. Epi Info was used to calculate risk ratios (RRs), 95% confidence intervals (CIs), and chi-square (p-values) for all food items consumed. Turkey and ham samples were sent to the Centers for Disease Control and Prevention (CDC) for testing. An environmental assessment was performed by Austin Public Health.

RESULTS: A total of 81 people attended the potluck on November 15th, 2018. Attempts were made to call all attendees and 70 attendees completed the interview; 44 (54%) met the case definition. The predominant symptoms reported among cases included diarrhea, abdominal cramps, and nausea. Stool collected was negative for enteric pathogens. Food items associated with an increased risk of illness were turkey (RR = undefined; $p = 0.01$), turkey gravy (RR = 1.7; CI = 1.03-2.79; $p = 0.02$) and stuffing (RR = 1.5; CI = 1.03-2.16; $p = 0.04$). One of the turkey samples sent to CDC grew a few *C. perfringens* colonies, but these lacked the *C. perfringens* enterotoxin gene. The environmental assessment found dented cans and items in the cooler that were not properly dated. Unfortunately, hot holding temperature, cooking time and temperature and reheating procedures were not observed during the inspection.

CONCLUSIONS: Although we were unable to identify the causative agent, the results from our epidemiologic investigation suggested that the illness was consistent with *Clostridium perfringens*. Outbreaks of *C. perfringens* are commonly associated with beef, poultry, and gravies and often occur at events where food is prepared in large quantities, such as catered events. We hypothesize that the catered turkey, gravy, and/or stuffing was cooled too slowly or reheated insufficiently, leading to the consumption of large amounts of *C. perfringens* by potluck attendees.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Infectious Diseases; Enteric Infectious Diseases; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nicole.evert@wilco.org
Presenting Author(s)	Nicole Marie Evert
Institution Affiliation	Williamson County and Cities Health District Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	Campylobacteriosis Outbreak at a Workplace Cafeteria in Pennsylvania – August 2018

Abstract

BACKGROUND: On August 20, 2018, the Allegheny County Health Department (ACHD) was notified of three cases of campylobacteriosis among employees of a Pennsylvania workplace (Company A). Company A revealed that about 30 employees who ate at the workplace cafeteria reported gastrointestinal symptoms. A majority experienced onset between August 10 and August 11. ACHD investigated to identify a source and implement control measures.

METHODS: ACHD sent a survey to all employees (~500), inquiring about symptoms and food histories. The investigation focused on cafeteria meals served from Monday, August 6 to Wednesday, August 8 given campylobacteriosis' usual incubation period of 2-5 days. The cafeteria is closed on weekends. A case was defined as anyone who worked at Company A and had diarrhea or had abdominal cramps with nausea, vomiting, or fever for >2 days with onset between August 8 and August 18. Laboratory results, shared by employees seeking medical care, were verified using Pennsylvania's reportable disease database. Descriptive statistics were calculated, and a retrospective cohort analysis was performed. Fisher's exact tests were used to assess statistical significance of relative risks. ACHD's Food Safety Program inspected the cafeteria and interviewed management. Cafeteria employees were surveyed separately regarding job duties, symptoms, and food histories.

RESULTS: Of 219 Company A survey respondents, 30 (14%) fit the case definition. Of cases providing demographic information, 76% were male and 69% reported an age between 30-49 years old. Sixty percent reported symptoms lasting ≥6 days and 40% reported symptoms lasting 3-5 days. Most (87%) experienced onset from August 10 through August 12. Four individuals shared laboratory results, all positive for *Campylobacter*. All cases ate at the cafeteria at least once from August 6 to August 8. There was an increased, but not significant risk from eating lunch at the cafeteria on August 8 (RR 3.6, p=0.25). Those who ate a cheesesteak sandwich on August 8 were significantly more likely to become ill (RR 5.8, p<0.01). Cafeteria management revealed that cheesesteaks contained chicken pate and sat at room temperature for extended periods. No food was available for testing. No cafeteria workers reported illness before, during, or after August 6 through August 8.

CONCLUSIONS: Chicken pate has been associated with numerous campylobacteriosis outbreaks. Given investigation results, ACHD believes this campylobacteriosis outbreak was the result of undercooked chicken pate used on cheesesteaks, but the source cannot be confirmed. All chicken products should be cooked to 165°F and refrigerated after preparation.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	molly.nace@alleghenycounty.us
Presenting Author(s)	Molly E. Nace
Institution Affiliation	Allegheny County Health Department CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11297
Abstract Type	Poster
Abstract Title	Characteristics of Infections with Common Salmonella Serotypes in Georgia, 2000-2018

Abstract

BACKGROUND: Over 2,500 *Salmonella* serotypes have been identified, though most human infections are caused by fewer than 100 serotypes. Of *Salmonella* infections reported to the Georgia Department of Public Health (GDPH) since 2000 with serotype data, more than 80% were attributed to 20 serotypes. GDPH utilizes a random selection scheme to prioritize 60% of *Salmonella* case-patients for interview. We examined whether certain serotypes are associated with specific demographics, exposures, or outcomes to better prioritize our interviews to learn more about cases with severe outcomes or that are outbreak related.

METHODS: GDPH collects *Salmonella* case-patient demographic and exposure data for all interviewed cases. *Salmonella* case-patient data from 2000 through 2018 were reviewed and serotype frequencies were calculated. Analyses of hospitalization, outbreak status, travel history, and demographics were limited to cases infected with the 20 most-common serotypes. Missing responses were excluded from analysis. Descriptive statistics were calculated in Microsoft Excel and bivariate analysis using chi-square to compare characteristics of different serotypes was calculated in OpenEpi 3.01. Travel was defined as travel outside of community in the week before illness onset.

RESULTS: From 2000 through 2018, 31,854 *Salmonella* infections from the 20 most-common serotypes were reported. The median age of case-patients was 10 years; those with serotype Rubislaw had the lowest median age (0.54 years) while case-patients with serotype Infantis had the highest (34 years). Female gender was reported by 15,756 (49.9%) case-patients. Serotypes Thompson (152, 61.8%) and Hartford (138, 60.3%) had significantly higher proportions of females ($p < .0001$). Travel was reported by 2,269 (17.2%) case-patients. Serotype Oranienburg (34, 31.2%) infected persons were significantly more likely to report travel ($p < .0001$). Seven hundred (3.6%) case-patients were outbreak-associated. Serotypes of case-patients most likely to be outbreak-associated include: Thompson (72, 44.7%), Montevideo (135, 17.2%), Heidelberg (41, 13.3%), Infantis (39, 12.8%), and Saint Paul (74, 11.0%). Hospitalization was reported by 8,423 (30.1%) case-patients. Serotype Heidelberg case-patients (216, 37.3%) were significantly more likely to be hospitalized ($p < .0001$).

CONCLUSIONS: Demographics, exposures, and hospitalization status vary significantly among Georgia's 20 most-common *Salmonella* serotypes. Tracking these differences and changes over time may provide epidemiologists historical context and inform interview prioritization. For example, case-patients with serotypes that have been previously associated with outbreaks should be prioritized for interview within 2 days of report to potentially prevent a new or recurring outbreak. Targeting education messages, including risk reduction measures, to case-patients with serotypes with higher proportions of hospitalization could prevent future serious illness.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiology; Foodborne Disease; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lana.jones@dph.ga.gov
Presenting Author(s)	Lana Holley Jones
Institution Affiliation	Georgia Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11519
Abstract Type	Poster
Abstract Title	Ciguatera Fish Poisoning in Puerto Rico

Abstract

BACKGROUND: Ciguatera fish poisoning occurs after eating reef fish contaminated with ciguatoxins and is widespread in tropical and subtropical waters. In October 2018, seven (7) ciguatera suspected cases with gastrointestinal and neurological symptoms were reported to the Puerto Rico Department of Health from various hospitals in the area of those, six required hospitalization. Cases developed symptoms two to three hours after consumption of “*picúa*” (barracuda) fish obtained from a local fish market.

METHODS: All cases were interviewed and a questionnaire was completed regarding fish consumption, disease manifestation and possible risk factors for exposure. Frozen leftover fish was sent to the Food and Drug Administration (FDA) Laboratories for analysis.

RESULTS: Two of the seven cases became severely ill and died 24-48 hours after onset of symptom. Fish samples tested positive for Caribbean ciguatoxin-1 (C-CTX-1). Health inspections were performed by the Environmental Health Division and corrections where enforced at the local fish markets.

CONCLUSIONS: There is a need for education and awareness among fishermen, fish market owners and general population. It is important to be able to identify the epidemiology of ciguatera and the gastrointestinal and neurological symptoms associated with it in order to provide treatment in a timely manner.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email	anibal.cruz@salud.pr.gov
Address(es)	
Presenting Author(s)	Anibal Cruz-Sanchez
Institution	Puerto Rico Department Of Health
Affiliation	Territorial public health agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11865
Abstract Type	Poster
Abstract Title	Evaluating Impacts of Enhanced Salmonella Surveillance By Student Disease Investigation at the Hawaii State Department of Health, 2018

Abstract

BACKGROUND: Hawaii has had higher rates of salmonellosis illness than the national average throughout the last 10 years, and salmonellosis cases represent 20% of our non-vaccine-preventable reportable illnesses. In 2017, the Hawaii Department of Health (HDOH) joined CDC's OutbreakNet Enhanced (OBNE) Program to improve salmonellosis case and outbreak detection and increase response capacity. This facilitated hiring a student disease investigator, who would conduct salmonellosis investigations occurring on Oahu once trained. Priority objectives were to enhance investigation speed and efficiency, increase investigation completion rates, and strengthen salmonellosis surveillance strategies.

METHODS: Through the OBNE grant, one student was recruited from a local university Master of Public Health Program from mid-January through mid-December 2018. The student was trained by HDOH disease investigation staff on interviewing salmonellosis cases, tracking laboratory reports, entering data into surveillance systems, and conducting analyses. From February 1, the fully trained student disease investigator began interviewing all salmonellosis cases on Oahu. Observed performance metrics included case load relief for the five full-time Oahu disease investigators during this period as well as timeliness (time from start of investigation to first attempt to reach the case) and proportion of cases considered lost to follow-up (ability to complete interviews) comparing 2018 with the same time period in 2017.

RESULTS: The student disease investigator conducted 207 salmonellosis investigations; full-time investigators each conducted an average of 286 reportable non-vaccine preventable infectious disease cases in the same time period. Approximately 41 salmonellosis investigations or 13% more case load would have been assigned to each investigator. From 2017 to 2018, timeliness of salmonellosis case investigations improved by 27% (from median 1.1 days to 0.8 days), and the proportion of cases considered lost to follow up decreased by 40% (6.3% to 3.8%). Additionally, being the sole investigator for all Oahu salmonellosis cases facilitated the student disease investigator's identifying case and exposure commonalities to determine epi links.

CONCLUSIONS: Hawaii's site participation in OBNE directly benefited the health department in streamlining salmonellosis investigation through ensuring a dedicated student disease investigator. Investigation efficiency and completeness with decreased burden on current staff were enhanced. As incident rates of all reportable illnesses increase overtime, the decrease case load burden to full-time investigators offered by a student disease investigator is of great benefit and ensures the completeness of each investigation of salmonellosis. OBNE participation contributed to the real-time needs of HDOH to improve speed and efficiency of response for sporadic and outbreak salmonellosis events.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email	desireetupas@gmail.com
Presenting Author(s)	Desiree Tupas
Institution Affiliation	Hawaii Pacific University Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11515
Abstract Type	Poster
Abstract Title	Evolving Epidemiology of Reported Giardiasis Cases in the United States, 1995–2016

Abstract

BACKGROUND: Giardiasis is the most common intestinal parasite of humans identified in the United States and an important infection potentially transmitted by water. Giardiasis was under standardized surveillance from 1995 to 2002, when it became nationally notifiable. The national case definition changed in 2010 to reflect changing diagnostic practices. States voluntarily report giardiasis cases to CDC and can change this requirement each year. Our objectives were to describe the evolving epidemiology of US giardiasis cases for 1995–2016 using National Notifiable Disease Surveillance System (NNDSS) data.

METHODS: We used negative binomial regression models to compare incidence by age (0–4, 5–9, 10–19, 20–29, 30–39, 40–49, 50–64 and ≥65 years) across three time periods (1995–2001, 2002–2010, 2011–2016) over the study period. We calculated incidence rate ratios (IRR) and 95% confidence intervals.

RESULTS: During 1995–2016, the average number of reported cases were 19,778 per year (range: 14,623–27,778 cases). Compared to 1995–2001, incidence was lower in 2002–2010 and 2011–2016 across all age groups. The smallest decrease from the referent period was seen amongst cases aged 40–49 in 2002–2010 (IRR 0.83 [0.78–0.89]) and the largest decrease from the referent period was seen amongst those aged 0–4 (IRR 0.30 [0.20–0.44]) in 2011–2016.

CONCLUSIONS: The incidence of reported giardiasis in the United States is decreasing. This decrease differs by age group and may reflect either changes in surveillance methods (e.g., changes in case definitions or changes in reporting practices of states to CDC) or differences in exposures by age group. Incidence in older age groups has not decreased as much as incidence in children, suggesting that differences in exposures and immunity by age group are important to the epidemiology of giardiasis. Investigation of risk factors for sub-populations with higher rates may facilitate prevention and control efforts.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Surveillance; Epidemiology; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	wte7@cdc.gov
Presenting Author(s)	Katharine M Benedict
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11452
Abstract Type	Poster
Abstract Title	Foodborne Outbreak Shows Gaps in Food Safety

Abstract

BACKGROUND: *Salmonella* Enteritidis is one of the most common serotypes of *Salmonella* reported in the United States that cause human illness. *Salmonella* is commonly associated with foodborne illnesses that is widely prevailed as a preventable public health problem, highlighting the importance of food safety knowledge including excluding ill food service workers who have diarrhea of any cause from duty to reduce and stop transmission of disease. Likewise, in early food preparation stages, contamination can occur when there is inadequate food storage, inappropriate cold/hot food holding, and poor work space sanitation. This investigation details how the Florida Department of Health in Orange County (DOH-Orange) pursues to determine a causal relationship between food safety practices and an outbreak of *Salmonella* at local food establishment.

METHODS: DOH-Orange conducted a joint environmental assessment of the local food establishment with aid of environmental health (EH) and department of business and professional regulation (DBPR) on February 14, 2018. The assessment included the process and preparation of each food item, ingredient lists, itemized receipts of grocery purchases, and methods of food storage and hot/cold holding, and a walk through of the facility to observe general food preparation and storage practices. Active and passive surveillance was conducted via multiple surveillance systems throughout the investigation. Previously reported salmonellosis cases were reviewed to identify additional cases related to this outbreak investigation. Food worker interviews were conducted and schedules and call off logs assessed. Stool specimen collection kits were distributed during the joint environmental inspection to food service workers who stated they consumed and prepared meals from the days the implicated food item was served. Clinical specimens were forwarded to the Florida Department of Health Bureau of Public Health Laboratories Jacksonville (BPHL-Jacksonville) for confirmatory test where pulsed-field gel electrophoresis (PFGE) pattern testing was performed to determine genetic relatedness.

RESULTS: Case-patients had illness onsets ranging between January 27 and 28, 2018 and consumed similar meals. One food service worker, an asymptomatic prep cook provided a stool specimen for testing who's PFGE pattern matched that of the ill case-patients. In addition, there were multiple food items that violated time/temperature controls for safety during the joint environmental assessment.

CONCLUSIONS: Onsite recommendations were given post-observations or either corrected onsite by DOH-Orange and DBPR. Interventions to prevent foodborne diseases in food service establishments should be consistent with federal food safety policies, therefore food service employers should ensure that workers engage in and follow standard comprehensive guidance regarding food safety rules.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Food Safety
Consider for Different Presentation?	No
Presenting Author Email Address(es)	Michelle.Persaud@flhealth.gov
Presenting Author(s)	Michelle Persaud
Institution Affiliation	Florida Department of Health Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	11038
Abstract Title	Poster
Abstract Title	Giardiasis Reported to the National Notifiable Diseases Surveillance System — United States and the Commonwealth of Puerto Rico, 2017

Abstract

BACKGROUND: Giardiasis, a disease caused by the parasite *Giardia duodenalis*, is among the most frequently reported human intestinal parasite infections in the United States. Each year, U.S. jurisdictions and territories voluntarily report giardiasis cases to the National Notifiable Diseases Surveillance System (NNDSS). This descriptive analysis summarizes the 2017 giardiasis cases reported in the United States and its territories.

METHODS: In 2017, forty-two U.S. states, the District of Columbia (DC), New York City (NYC), and the Commonwealth of Puerto Rico voluntarily reported giardiasis cases to NNDSS. Giardiasis case reports were downloaded from NNDSS Link and analyzed using the statistical software R and SAS 9.4. Nonconfirmed cases included probable, suspected, and unknown cases, according to CSTE-approved case definitions from 2011. Incidence per 100,000 persons were calculated by dividing the number of cases by mid-year census estimates for reporting jurisdictions and multiplying by 100,000.

RESULTS: In 2017, there were 15,236 giardiasis cases (5.9 cases per 100,000 persons per year, 97.1%, confirmed and 2.9%, nonconfirmed) reported to NNDSS. An average of 15,480 cases per year were reported from 2011 to 2017 (range: 14,657 – 16,870 cases), and an average of 21,748 cases per year were reported from 1995 to 2010 (range: 19,153 – 27,799 cases). Jurisdictions with the highest reported incidence of giardiasis included Alaska (12.2), South Dakota (12.0), Montana (11.9), Wisconsin (11.7), Minnesota (11.5), and NYC (11.3). Most case-patients were male, (n=9,384; 61.6%), white, (n=7,753; 50.9%), and non-Hispanic (n=8,454; 55.5%). A substantial number of reports did not include race (n=4,911; 32.2%) or ethnicity (n=5,708; 37.5%). By age, incidence rates were highest among children aged 1-4 years (n=1,404; 8.8 r) and men 25-29 years (n=890; 7.48). Among cases that had a reported date of symptom onset in 2017 (n=14,020; 92.0%), the number of cases ranged from 907 (6.5%) in February, to 1,678 (12.0%) in August.

CONCLUSIONS: The incidence of reported giardiasis in the United States and its territories declined substantially since 1995 and has remained relatively stable since 2010. Differences in reporting requirements for giardiasis, which differ by state and can change from year to year, may influence these rates. Despite this recent stabilization in reported giardiasis, elevated rates continue to occur in the northern states and predominantly among men, and children aged 1 to 4 years. Identification of these high-risk groups through national surveillance remains essential for guiding giardiasis prevention efforts.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	osr7@cdc.gov
Presenting Author(s)	Michelle E Gleason
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11430
Abstract Type	Poster
Abstract Title	How Often Did PFGE Identify Clusters Worth Investigating? A Cluster Comparison of Indistinguishable PFGE Patterns and Whole Genome Sequencing Analysis

Abstract

BACKGROUND: Pulsed-field gel electrophoresis (PFGE) has been used in Tennessee (TN) for over two decades to identify molecular clusters of salmonellosis. Indistinguishable PFGE patterns focused investigation efforts to identify common source exposures. Whole genome sequencing (WGS) is scheduled to replace PFGE in 2019 as the primary method for molecular cluster detection. We reviewed sequence data for indistinguishable PFGE patterns to determine if epidemiological investigations were indicated based on WGS results.

METHODS: PFGE and WGS were performed on 829 *Salmonella* isolates with collection dates in 2017 at the TN Department of Health State Laboratory. PFGE data were analyzed using BioNumerics version 6.6. Duplicate isolates were removed from analysis. Sequence data for clusters with an indistinguishable PFGE XbaI pattern and ≥ 3 isolates were reviewed in the National Center for Biotechnology Information (NCBI) Pathogen Detection Isolates Browser. A threshold of ≤ 10 single nucleotide polymorphisms (SNPs) and ≥ 2 isolates was used to define a WGS cluster of related isolates.

RESULTS: Forty-six clusters with indistinguishable *Salmonella* PFGE patterns, containing 338 isolates, were identified in 2017. Twenty-nine (63%) PFGE clusters contained at least one WGS cluster with ≥ 2 isolates and ≤ 10 SNPs. In total, 41 WGS clusters were identified (137 isolates). Median WGS cluster size was 3, ranging from 2 to 26 isolates. Time between earliest collection date and latest collection date for WGS clusters ranged from 0 to 326 days with a median of 45 days. Serotypes such as Enteritidis (JEGX01.0004) and Typhimurium (JPXX01.0038) had as many as five separate WGS clusters. Seventeen (37%) clusters with indistinguishable patterns did not contain related isolates (≤ 10 SNPs).

CONCLUSIONS: Review of WGS analysis determined 63% of *Salmonella* clusters with indistinguishable PFGE patterns contained isolates highly related by WGS. This was particularly the case for clonal and high volume PFGE patterns, such as *Salmonella* Enteritidis (JEGX01.0004). Conversely, over one-third of identical PFGE patterns had considerable SNPs differences indicating low epidemiological connection among isolates. Cluster investigation paradigms will change with WGS providing greater resolution. Epidemiologists in foodborne disease programs can anticipate an increase in accuracy and quantity of detected clusters with a continued need for more detailed exposure data. Future studies should consider exposure data review, creating specific SNP thresholds based on *Salmonella* serotypes and developing prioritization strategies for WGS cluster investigations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epi / Lab Capacity (ELC); Surveillance; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Lisha.Constantine-Renna@tn.gov
Presenting Author(s)	Lisha Constantine-Renna
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11135
Abstract Type	Poster
Abstract Title	Is Less Really More? an Analysis of Georgia's Routine Salmonella Case Interview Protocols

Abstract

BACKGROUND: Approximately 2500 *Salmonella* cases are reported to the Georgia Department of Public Health (GDPH) annually. Case interviews are conducted to determine demographics, travel history, possible exposures, and risk factors for illness. Due to Georgia's salmonellosis burden, a selection scheme (60%) is utilized. With new initiatives to perform whole genome sequencing (WGS) on all *Salmonella* isolates and obtain corresponding exposure data, we intend to increase the number of interviewed *Salmonella* cases. We sought to determine the most efficient interview attempt protocol for *Salmonella* cases.

METHODS: We compared two interview attempt protocols used for *Salmonella* cases selected for interview during October 25th through November 29th, 2018. The Traditional Protocol (Protocol 1) included up to 6 interview attempts (calls or texts) within 8 weeks of specimen collection date. The Comparison Protocol (Protocol 2) included up to 3 interview attempts (call and text on attempts 1 and 3; call only on attempt 2), each attempt within 1 week of the last. Protocols were randomly assigned. Data were collected on paper and electronic tracking sheets and analyzed in Microsoft Excel and Epi Info 7. T-tests were used to compare means.

RESULTS: Ninety *Salmonella* cases were initially included in the study; duplicate and out of state cases as well as cases for which interview attempts did not meet study parameters were excluded. Seventy-seven cases met study protocol criteria; 37 in Protocol 1 and 40 in Protocol 2. Interviews were completed on 26 cases from Protocol 1 and 25 from Protocol 2; proportion with completed interview did not vary significantly between groups. Mean number of days from specimen collection date or notification date to first attempt date did not vary significantly between study groups. The mean number of interview attempts to secure interview completion was 2.5 for Protocol 1 and 2.2 for Protocol 2 ($p=0.374$). Mean days from notification to interview completion was 25.3 for Protocol 1 and 17.4 for Protocol 2 ($p=0.043$). Mean days from first interview attempt to interview completion was 15.5 for Protocol 1 and 7.8 for Protocol 2 ($p=0.038$).

CONCLUSIONS: The new Comparison Protocol resulted in more timely interviews. GDPH will adjust routine case interview protocols from the traditional to the comparison protocol to decrease the time from report to completed interview and the staff time required for individual case follow-up. We seek to complete risk assessments, provide prevention information, and identify possible clusters in a timelier manner as more case interviews are completed faster.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email	hope.dishman@dph.ga.gov
Address(es)	
Presenting Author(s)	Hope Dishman
Institution	Georgia Department of Public Health
Affiliation	State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	10652
Abstract Title	Poster
	Myth Busting the "R" Months: Analysis of Florida Vibriosis Cases with Oyster Consumption

Abstract

BACKGROUND: There is an old piece of advice for oyster consumption: only eat oysters in the months that contain the letter “R” in the name. However, vibriosis cases associated with consumption of raw oysters occur year-round, indicating that regardless of the month consumed, raw oysters can cause illness. The Food and Drug Administration (FDA), reports that 40% of cases occur during the colder months of September through April. The Florida Department of Health evaluated vibriosis cases who reported oyster consumption to determine Florida’s monthly distribution and provide data to use in educational messaging

METHODS: Cases of vibriosis reported in Florida between 2013–2017 were extracted from Florida’s reportable disease database, Merlin. The data were analyzed to determine oyster consumption, month of consumption, case outcomes, *Vibrio* species and source of oyster.

RESULTS: There were 1,014 vibriosis cases reported during the study period and of those, 190 (19%) reported consumption of oysters. Sixty (32%) cases reported consuming oysters between May–August while 124 (65%) consumed oysters between September–April (six cases have unknown dates of consumption). Of the 190 cases, the months with the most cases reported on average were April and July (4.6 cases/month) followed by September (4 cases). For cases who consumed oysters, 98 were hospitalized for their illness with 62 hospitalizations occurring in September - April. There were 18 deaths reported out of the 190 cases with a higher proportion of deaths occurring in May–August (15%) versus September–April (7%). *Vibrio parahaemolyticus* was identified in 28% of cases, *Vibrio vulnificus* in 21% and *Vibrio cholerae* non-O1/non-O139 in 14%. Oyster harvest area information was available for 125 cases and most oysters (65%) were harvested in the Gulf of Mexico region.

CONCLUSIONS: Out of the vibriosis cases who consumed oysters, consumption of oysters during non-summer months, September–April, was linked to 65% of those cases identified in Florida, which is higher than the 40% nationally reported by FDA. More deaths were attributed to oyster consumption in summer months, May–August, but deaths still occurred during the cooler months (7%). Further examination of epidemiological and underlying health condition risk factors should be considered for the cases occurring in the cooler months. Public health messaging can be targeted to educate people on the risks of infection with *Vibrio* year-round and that eating raw oysters can lead to significant illness any time of year.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Waterborne Disease; Disease Prevention; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Laura.Matthias@flhealth.gov
Presenting Author(s)	Laura P Matthias
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11227
Abstract Type	Poster
Abstract Title	Norovirus and Acute Gastroenteritis-Associated Deaths — United States, 2001-2015

Abstract

BACKGROUND: Norovirus is a leading cause of acute gastroenteritis (AGE) in the United States. While most norovirus infections result in self-limited illness, severe outcomes including death do occur. With multiple norovirus vaccines progressing through clinical development, updated national estimates of norovirus mortality are needed to inform future vaccine programs and impact assessments.

METHODS: AGE-associated deaths in the United States during July 2001–June 2015 were identified from the National Center for Health Statistics multiple-cause-of-mortality dataset using *International Classification of Disease* 10th edition (ICD-10) codes for all causes of AGE, including bacterial, viral, parasitic, and unspecified gastroenteritis. Time-series negative binomial regression models fit monthly counts of cause-unspecified AGE deaths to ICD-10 coded *Clostridium difficile*, other bacterial, rotavirus, and parasitic AGE deaths. Excess seasonal variation in the remaining unattributed AGE deaths (i.e., model residuals) was used to predict the number of norovirus-associated deaths. Norovirus-associated deaths among persons aged <5, 5–64, and ≥65 years were modeled and estimated separately.

RESULTS: There were 223,705 ICD-10 coded AGE deaths in the U.S. during June 2001–July 2015, resulting in an average rate of 49 deaths per million person-years (PY). A mean of 893 norovirus-associated deaths (95% Confidence Interval [CI]: 676–1139) were predicted annually, including 33 deaths (95% CI: 26–41) in children <5 years old, 83 deaths (95% CI: 66–102) in persons aged 5–64 years, and 777 deaths (95% CI: 584–995) in older adults aged ≥65 years. The overall predicted norovirus mortality rate was 2.74 deaths per million PY. Age-specific norovirus mortality rates were 1.55 deaths per million PY among <5 year olds, 0.32 deaths per million PY among 5–64 year olds, and 18.23 deaths per million PY among those ≥65 years old. Norovirus-associated deaths demonstrated distinct seasonality in persons ≥5 years old, with 45% of such deaths occurring during December–February. Overall, norovirus accounted for 5.6% of all-cause AGE deaths, ranging from 4.1% to 7.0% between age groups.

CONCLUSIONS: Norovirus is an important cause of AGE-associated mortality, resulting in approximately 900 deaths per year in the United States. Nearly 90% of these deaths occur among older adults aged ≥65 years old. These mortality estimates can help prioritize and target prevention strategies, including future norovirus vaccines.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; ICD
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lkz5@cdc.gov
Presenting Author(s)	Claire P Mattison
Institution Affiliation	Oak Ridge Institution for Science and Education CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11350
Abstract Type	Poster
Abstract Title	Outbreak of Salmonella Typhimurium Linked to Chicken Salad

Abstract

BACKGROUND: Iowans became ill with *Salmonella* Typhimurium after consuming chicken salad produced by Triple T Specialty Meats, Inc. (Triple T) and sold at Fareway Stores, Inc. (Fareway). The Iowa Department of Public Health (IDPH) identified the outbreak through routine disease surveillance on February 9, 2018. After notification by IDPH, Iowa's food retail and manufacturing regulatory agency, the Iowa Department of Inspections and Appeals (DIA), notified Fareway about the findings. Within hours, Fareway voluntarily suspended the sale of chicken salad products company-wide. Fareway is a Midwest grocery company with over 121 store locations in five states. It is the second largest grocery chain in Iowa.

METHODS: A cohort study was conducted. Interviews were performed via phone by IDPH's epidemiologists, student interview team, and LPHA partners using the routine IDPH *Salmonella* follow-up questionnaire, the national hypothesis generating questionnaire, and an outbreak specific supplemental questionnaire. DIA responded to Fareway locations across the state and collected 14 chicken salad samples from seven stores. The samples were sent to the State Hygienic Laboratory (SHL) for testing.

RESULTS: Two hundred and eighty illnesses were identified as part of the investigation. Of these, 240 were laboratory confirmed and 15 were probable. In addition, 25 suspect cases were identified through the Iowa illness complaint line. A confirmed case was defined as a person with *Salmonella* Typhimurium infection, with an isolate matching PFGE pattern xbal JPXX01.075 or JPXX01.1896 and collection dates between January 12, 2018 - March 20, 2018. A total of 240 (86%) cases met this case definition from 64 Iowa counties. Of these, 157 (65%) were females. The median age among confirmed cases was 77 years (range 0-89 years). Eighty-one (34%) individuals were hospitalized and one death was reported. Of the 240 confirmed cases identified, 176 (73%) reported eating chicken salad sold at Fareway. *Salmonella* Typhimurium was identified in two chicken salad samples. PFGE testing identified the chicken salad *Salmonella* strain as JPXX01.0275 which matched the clinical isolates. Whole Genome Sequencing (WGS) performed on a subset of clinical isolates showed that they were closely related genetically to the food isolates.

CONCLUSIONS: This outbreak demonstrated a coordinated rapid response between multiple agencies. Strong relationships with partners, especially Fareway, were instrumental in reducing further spread. PFGE and WGS performed on the clinical and environmental isolates showed they were closely related. This further supports the strong epidemiological correlation between cases and exposure to chicken salad produced by Triple T and sold at Fareway.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiology; Food Safety
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Oluwakemi.Oni@idph.iowa.gov
Presenting Author(s)	Kemi Oni
Institution Affiliation	Iowa Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10638
Abstract Type	Poster
Abstract Title	Post-Infectious Sequelae after Campylobacter Enteric Infection: A Pilot Study in Maricopa County, Arizona, USA

Abstract

BACKGROUND: Infection with *Campylobacter* is usually self-limiting, but severe cases may develop post-infectious sequelae (PIS) such as gastrointestinal disorders, neurological disorders, and joint disorders. The objective of this study was to estimate a crude incidence rate for PIS among Campylobacter cases in Maricopa County, Arizona, USA.

METHODS: The pilot study was conducted from August 1, 2016 to August 31, 2017. During this time, cases of campylobacteriosis were reported to the Maricopa County Department of Public Health and interviewed by trained public health students at the University of Arizona. Following an initial routine enteric surveillance interview, cases who were 18 years of age or older and who could speak English or Spanish were recruited and consented into the pilot study. Follow-up with the PIS questionnaire occurred four to six weeks after the date of each case's initial interview. Data analysis was conducted using STATA SE 14 and included chi-squared tests to determine differences in demographics between enrolled and non-enrolled and crude rates with 95% confidence intervals to estimate PIS.

RESULTS: Of the eligible routine surveillance cases (n=286), 36% (n=102) enrolled into the pilot study. Of enrolled participants, 68.6% completed the follow-up questionnaire. Most participants were non-Hispanic White, female, and aged 60+ years. Those who reported mucousy diarrhea (χ^2 (1, N = 87) = 4.54, p=0.03), fever (χ^2 (1, N = 68) = 3.86, p=0.05), and chills (χ^2 (1, N = 21) = 14.7, p=0.0001) were significantly more likely to enroll into the study. Over half (52.8%, 95% CI: 41.1, 64.5) of cases experienced PIS approximately four to six weeks after acute onset of campylobacteriosis. At the time of the follow-up questionnaire, 24 patients (34.3%, 95% CI: 23.2, 45.4) sought additional medical care and 16 of those (66.6%) received a medical diagnosis (e.g. Crohn's disease, gastric cirrhosis, colitis, fibromyalgia, irritable bowel syndrome). Seventeen cases (24.3%, 95% CI: 14.3, 34.3) had new or continuing GI symptoms, nine (12.8%, 95% CI: 5.0, 20.6) had new or continuing joint symptoms, four (5.7%, 95% CI: 0.3, 11.1) had new or continuing neurological symptoms, and seven (10.0%, 95% CI: 3.0, 17.0) had other symptoms (i.e. headaches, swelling, fatigue, etc).

CONCLUSIONS: Our crude estimate that over half of participants experienced PIS following campylobacteriosis contradicts current scientific literature (10-15% estimates on average). The results from this pilot study will be used to address the larger issue of determining the true burden of disease following campylobacteriosis in a larger study.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Research; Chronic Disease; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	barrette@email.arizona.edu
Presenting Author(s)	Erika Austhof
Institution Affiliation	University of Arizona Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	10895
Abstract Type	Poster
Abstract Title	Potential Impact of Multiplex Molecular Panel Testing on Surveillance of Cyclosporiasis, 2018

Abstract

BACKGROUND: Cyclosporiasis, caused by infection with the coccidian parasite *Cyclospora cayetanensis*, is a foodborne disease of public health concern in the United States. *Cyclospora* infections can be identified through morphologic examination (O&P), real-time polymerase chain reaction assay (RT-PCR); and multiplex molecular panels (also referred to as culture-independent diagnostic tests or CIDs). The BioFire FilmArray GI Panel is currently the only Food and Drug Administration cleared CIDT that includes a target for *C. cayetanensis*. In 2018, a marked increase in cases of cyclosporiasis reported in the United States led the Centers for Disease Control and Prevention (CDC) to assess the potential impact of FilmArray GI panel-based diagnosis on case detection and reporting of cyclosporiasis.

METHODS: The Cyclosporiasis National Hypothesis Generating Questionnaire (CNHGQ) is used to collect extended information on cases of cyclosporiasis. In 2018, the CNHGQ was revised to include questions about diagnostic testing methods and laboratory type (i.e., clinical, commercial, or state). We assessed the completeness of reported laboratory data (laboratory type and/or diagnostic method), the number of states that reported use of the FilmArray GI panel as a diagnostic tool, and the proportion of *Cyclospora* infections identified by the FilmArray GI panel compared to other methods for cases reported in 2018.

RESULTS: Thirty-three states submitted laboratory data for 1,439 cases to CDC, using the CNHGQ. Among the 1,408 cases with reported diagnostic methods, 30% (n=424) were tested by O&P, 7% (n=101) by RT-PCR, 57% (n=804) by the BioFire FilmArray GI panel, 2% (n=21) by other or unknown methods, and 4% (n=58) were tested by two or more methods. Thirty states (91%) reported at least one case in their state were tested by the FilmArray GI panel. Approximately 82% (n=693) of the FilmArray GI panel assays were performed by clinical laboratories.

CONCLUSIONS: Extensive food contamination with *C. cayetanensis* may have contributed to the high number of reported cases in 2018; however, since a large proportion of cases were diagnosed using the FilmArray GI panel, this CIDT could have played a role in increasing case detection of cyclosporiasis and enhancing disease surveillance. The FilmArray GI panel potentially detected cases that conventional testing methods would have missed due to improved sensitivity. CDC will continue to collect laboratory data to help monitor trends over time to further understand how use of CIDs may impact cyclosporiasis surveillance.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Surveillance; Foodborne Disease; Data Collection
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nuw8@cdc.gov
Presenting Author(s)	Carolyn Bennett
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11857
Abstract Type	Poster
Abstract Title	Risk History Surveillance Assessment of Campylobacteriosis Cases in Hawaii from August 2018 to November 2018

Abstract

BACKGROUND: Hawaii has an annual *Campylobacter* infection incident rate 3.3 times higher (44.1 per 100,000 persons) than the national average (13.4 per 100,000 persons). Factors contributing to this elevated rate have not been assessed in the last 20 years. As campylobacteriosis cases are not routinely interviewed, the Hawaii Department of Health (HDOH) conducted a focused risk history surveillance assessment (RHSA) over a 3-month period in an effort to identify risk factors associated with campylobacteriosis among Hawaii residents.

METHODS: This RHSA was conducted from 08/29/18 to 11/30/18. After creating a campylobacteriosis interview form, which included Hawaii specific exposures, phone interviews were conducted with cases, and data entered into the electronic disease case management system, Maven. Epi Info™ 7 was used to calculate frequencies of risk history variables including recent travel, environmental factors, and food exposures. A chi-square test with a significance level of .05 was used to examine the relationship between cases by county and environmental exposures including live animal contact. Aggregated baseline food item consumption rates reported in the 2007 FoodNet Atlas of Exposures were used to conduct binomial probability analysis to identify possible foods associated with a higher risk for contracting *Campylobacter*.

RESULTS: During the assessment period, HDOH received laboratory confirmation of 144 cases. We were able to contact 134 and successfully interviewed 114 (84%). Of the interviewed cases, 37 (33%) stated they travelled (20 internationally, 17 within the U.S.) during the incubation period. Among in-state cases, 35 (46%) claimed to have direct or indirect close contact with live chickens and/or droppings. Cases residing on islands other than Oahu were significantly associated ($p<0.01$) with having more live chicken exposure (87%) than cases residing on Oahu (30%). Comparison between 86 foods listed on our questionnaire and FoodNet Atlas showed chicken ($p<0.01$), pork ($p<0.01$), hamburger ($p<0.05$), and eggs ($p<0.05$) were foods likely to be associated with campylobacteriosis in our study population.

CONCLUSIONS: This RHSA identified nearly a third of campylobacteriosis cases in Hawaii during this study period were attributable to exposures outside the state and suggests non-Hawaii exposures inflate our perceived incidence rates. Additionally, obtaining live chicken exposure information will support focused, culturally appropriate education regarding safe practices in prevention of campylobacteriosis via animal interactions and potentially contribute to a reduction in *Campylobacter* infection rates. Food exposure analysis did not identify any additional foods other than previously recognized high risk food items as likely contributing factors to *Campylobacter* infections.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Foodborne Disease; Surveillance; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	aswanso2@my.hpu.edu
Presenting Author(s)	Adam Swanson
Institution Affiliation	Hawaii Pacific University Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	10740
Abstract Type	Poster
Abstract Title	Salmonella Outbreak in an Elementary School from Home-Made Ice-Cream, Nebraska - October 2018

Abstract

BACKGROUND: In October 2018, the Nebraska Department of Health and Human Services (NDHHS) was notified by North Central District Health Department (NCDHD) of an outbreak of gastroenteritis at a Nebraska elementary school. Several students and two teachers reported developing diarrhea, vomiting, or fever. School officials reported a teacher had prepared home-made ice-cream for the 3rd grade class and that multiple illnesses were being reported by persons who consumed it. An epidemiologic investigation was initiated to identify cases, establish etiology, and prevent further illnesses.

METHODS: NCDHD worked closely with school officials to collect epidemiologic data including basic demographics, date of illness onset, illness history, and number of days absent and to confirm that both 3rd grade teachers and all students consumed the ice-cream. NCDHD collected ingredient and preparation information from the teacher. We quickly confirmed that all ill persons were exposed and all exposed became ill (100% attack rate) with illness characterized by diarrhea or vomiting. Accordingly, a formal study was not conducted. NDHHS facilitated testing of stool specimens at Nebraska Public Health Laboratory (NPHL). Nebraska Department of Agriculture (NDA) collected leftover food product for culture; isolates were forwarded to NPHL for Whole Genome Sequencing (WGS).

RESULTS: All 20 persons (two teachers, 18 students) who consumed the ice-cream experienced illness with onsets during early morning hours the next day (12–24 hours after exposure) and were absent from school that day. Two people sought medical care; one was hospitalized. NCDHD confirmed ingredients used were sugar, vanilla, pudding mix, pasteurized milk, pasteurized cream, and locally sourced raw eggs; no heating process was employed. Six stool specimens were tested; five were positive by culture and one was positive by culture independent diagnostic testing. NPHL confirmed *Salmonella* Typhimurium from five human and eight food product isolates which all genetically matched (i.e. 0–3 single nucleotide polymorphisms).

CONCLUSIONS: Our findings demonstrate this outbreak was caused by consumption of home-made ice-cream contaminated with *Salmonella* Typhimurium, presumably from raw eggs. All 20 individuals who consumed the ice-cream reported incubation periods and symptoms consistent with salmonellosis and WGS confirmed human and food isolates matched genetically. *Salmonella* Typhimurium has been frequently identified in egg-related outbreaks and associated with the consumption of raw or undercooked eggs. Public health prevention should continue to inform and educate consumers on risks of raw or unpasteurized food products of animal origin and encourage safer options such as well-cooked or pasteurized products.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiology; Foodborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Brianna.Loeck@nebraska.gov
Presenting Author(s)	Brianna K. D. Loeck
Institution Affiliation	University of Nebraska - Lincoln Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11049
Abstract Type	Poster
Abstract Title	Shigellosis Prevention and Control Efforts: A Needs Assessment of State and Local Health Departments

Abstract

BACKGROUND: Shigellosis is a highly contagious enteric disease that causes about 500,000 cases of diarrhea in the United States annually. Populations at particular risk for shigellosis include children, travelers, individuals with weakened immune systems, and gay, bisexual, and other men who have sex with men (MSM). The Centers for Disease Control and Prevention (CDC) *Shigella* program supports states in detecting, investigating, and preventing shigellosis clusters and outbreaks. This includes interaction with state and local health departments to provide technical assistance, consultation, and health promotion materials. Through these interactions, ongoing challenges related to state and local shigellosis prevention and control were identified. To better understand these challenges and identify areas for CDC to improve support of state and local prevention activities, the *Shigella* program conducted a formal Community Needs Assessment (CNA) with health department partners.

METHODS: Participants engaging in *Shigella* -related work were identified through convenience and snowball sampling techniques. For example, participants were identified through their participation in FoodNet, PulseNet, or whether the state has a Center of Excellence. In-depth telephone interviews took place after an initial email exchange that included an invitation to participate, privacy and confidentiality statements, and an affirmation of consent to participate. In the telephone interview a second project member took detailed field notes. Resulting qualitative data were imported into MAXQDA software and analyzed using thematic analysis.

RESULTS: Interviews identified ongoing challenges with shigellosis prevention and control, and several ways CDC could better support state and local efforts. Participants identified challenges with controlling childcare-associated outbreaks due to limited existing evidence, and balancing patient confidentiality when collecting comorbidity and exposure data. Interviewer capacity to complete sexual histories was identified as a challenge for controlling MSM-associated outbreaks. Overall, improved CDC support was requested for clinician communication and education, questionnaire or data collection instrument development, subject matter consultation, and general health education about diarrheal disease. These suggestions included assistance with exposure risk assessment in MSM-associated clusters and outbreaks, application of exclusion policies in childcare-associated outbreaks, isolate testing, and development of health promotion materials for specific populations, including low-literacy and multi-lingual populations.

CONCLUSIONS: The CNA with state and local partners revealed information on the scope of shigellosis prevention and control work being conducted, challenges related to this work, and key areas where CDC could better support state and local efforts. Activities and priorities of the *Shigella* program at CDC will be updated to address the areas identified by participants.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	oby5@cdc.gov
Presenting Author(s)	Elise C. Caruso
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10817
Abstract Type	Poster
Abstract Title	Timely Identification of Alfalfa Sprouts As the Source of a <i>Salmonella</i> Newport Cluster Prevents Ongoing Cases -- Nebraska, 2018

Abstract

BACKGROUND: On April 3, 2018, the Nebraska Department of Health and Human Services (NDHHS) was notified of a multistate outbreak of *Salmonella* Newport cases with matching Pulsed-Field Gel Electrophoresis (PFGE) patterns and the majority were from the Omaha, Nebraska metropolitan area. NDHHS, in collaboration with Nebraska local health departments (LHD), initiated an investigation into locally occurring cases to identify the source. **METHODS:** The Centers for Disease Control and Prevention (CDC) provided the 14-page National Hypothesis Generating Questionnaire (NHGQ) on April 9, 2018 to obtain detailed information on illness and exposure histories including multiple foods. A confirmed case was defined as illness in a person infected with *Salmonella* Newport, with outbreak-matching PFGE patterns, with laboratory isolation date on or after March 12, 2018. LHDs were able to interview/re-interview all Nebraska cases using the NHGQ; data were shared with CDC to be included with the multistate exposure data for comparison against expected background rates of consumption in FoodNet Population Survey data. NDHHS worked with Environmental Health Officials in the Nebraska Department of Agriculture and Lincoln-Lancaster and Douglas County Health Departments (Omaha) to conduct traceback investigations. **RESULTS:** Of 41 confirmed cases in 10 states, 18 were identified in Nebraska residents who reported illness onset dates during March 9-30, 2018. By April 13, 2018, LHD interviewers had completed interviews with all but one patient and data were shared with CDC whose preliminary results indicated only alfalfa sprouts to be statistically significant ($p<0.0001$) amongst multiple food item exposures. Among Nebraska's 17 patients, 7 reported eating sprouts at two local restaurant chains. Later that day, Nebraska Environmental Health Officials obtained supply records from the implicated restaurants which traced back to a single Nebraska producer. A Douglas County inspector visited the growing facility and this firm voluntarily stopped sprout production and distribution that same day (April 13). **CONCLUSIONS:** Timely conducted interviews successfully identified sprouts as a possible common exposure to enable rapid traceback investigations completed by Nebraska Environmental Health Officials. Given the epidemiologic link between 7 Nebraska cases to locally produced sprouts and suspicion that other ill persons might have consumed sprouts unknowingly, our environmental partners were able to convince the firm to voluntarily stop production thus preventing additional cases in Nebraska and likely elsewhere. Our findings supported CDC and FDA efforts to identify and recall a contaminated lot of sprout seeds from a non-Nebraska supplier to ultimately bring an end to the larger multistate outbreak.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Foodborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	samir.koirala@nebraska.gov
Presenting Author(s)	Samir Koirala
Institution Affiliation	Nebraska Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10892
Abstract Type	Quick
Abstract Title	A Multi-Disciplinary Response to a <i>Shigella</i> Flexneri Outbreak Among Persons Experiencing Homelessness in Long Beach, CA

Abstract

BACKGROUND: On the week of October 8, 2018, the Long Beach Department of Health and Human Services (LBDHHS) received four reports of *Shigella* flexneri among persons experiencing homelessness (PEH) in Long Beach. Given the sudden reported increase in a vulnerable population and the potential for the disease to quickly spread in the encampments, an outbreak investigation was initiated. LBDHHS led the response and prevented further spread by collaborating with Long Beach Police, Fire, and the Parks, Recreation and Marine (PRM) Departments.

METHODS: Outbreak response teams distributed hand sanitizing wipes and information on *Shigella* to PEH in the encampments. Police responders offered security when conducting the outreach, and Fire's homeless outreach teams helped outbreak responders locate and interview cases who were difficult to find. The Parks, Recreation, and Marine Department installed soap dispensers in the commonly named public bathrooms and worked with a cleaning contractor to re-evaluate restroom disinfection protocols. Several of the cases reported practicing open defecation, and those who used public park restrooms reported no soap available to wash hands, and stated the restrooms often had visible feces on the floors and walls.

RESULTS: Nine cases of outbreak-related *Shigella* flexneri and an additional 12 PEH with gastrointestinal illness among persons with no laboratory results available were reported in the encampments as early as August. Eight (89%) of the confirmed cases were hospitalized, and an additional eight (38%) symptomatic cases were also hospitalized but never tested for *Shigella*. Laboratory results showed there were multiple *Shigella* serotypes circulating, including four serotype 7 (provisional 88-803), four serotype 2a, and one serotype 1. Pulse field gel electrophoresis (PFGE) was conducted on three of the specimens, and found two of the serotype 7 cases to be indistinguishable. The third PFGE that resulted was serotype 2a and could not be tied to another isolate.

CONCLUSIONS: There were likely numerous contributing factors to this outbreak, given that *Shigella* is easily transmitted among those living in close contact with no access to hand hygiene and among those practicing open defecation. Although case counts remained small, this response was aggressive and multi-faceted due to the vulnerable population involved and the potential for the outbreak to spread quickly. Outbreaks in PEH present unique challenges, as common interventions such as education on washing hands after using the restroom present difficulties for those living in encampments. Utilizing the resources of multiple City Departments from the beginning of the response proved successful in controlling this outbreak.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Outbreaks; Special/Vulnerable Populations
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	emily.holman@longbeach.gov
Presenting Author(s)	Emily Holman
Institution Affiliation	Long Beach Department of Health and Human Services Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11477
Abstract Type	Quick
Abstract Title	Coordinating Chaos: Strategies Utilized during a Large Cluster of Cyclosporiasis Outbreaks, Illinois, 2018

Abstract

BACKGROUND: Cyclosporiasis is caused by the parasite *Cyclospora cayetanensis*. From 2013 to 2017, Illinois reported a median number of 18 confirmed cyclosporiasis cases per year (range 9 to 44). In the summer of 2018, the Illinois Department of Public Health (IDPH) investigated over 800 domestically-acquired cyclosporiasis cases linked to 20 outbreaks, including an outbreak associated with salads served at a fast food restaurant chain. IDPH and local health departments investigated cases to identify outbreaks and sources of illness and implemented various strategies for outbreak data collection and management.

METHODS: The Cyclospora National Hypothesis Generating Questionnaire, Illinois' National Electronic Disease Surveillance System questionnaire and/or other outbreak specific surveys were used to collect case information. IDPH implemented staff surge capacity and a student interview team to assist local health departments (LHDs) with interviews. The Research Electronic Data Capture (REDCap) application was used to assign interviews, interview cases and controls, collect case data and track staff time. IDPH conducted binomial analysis to identify risk factors and analyzed case data to identify common source outbreaks. Once outbreaks were identified, invoices for suspect produce items were collected and provided to the U.S. Food and Drug Administration for traceback efforts.

RESULTS: From May to August 2018, Illinois identified 1045 confirmed cyclosporiasis cases, 892 of which were domestically acquired. IDPH coordinated with and assisted 54 LHDs during the investigation. Interviews were completed for 921 cases, including 167 completed by a student team. REDCap projects were used to collect and analyze case and outbreak information. An outbreak of 275 confirmed cases was linked to a common fast food chain resulting in the company pulling salads from their menu. An outbreak was reported in persons who attended a large event and an on-line REDCap survey collected data from 268 attendees. Eighteen additional outbreaks associated with restaurants were identified, 16 of which were linked to Mexican style foods. Outbreak cases accounted for only 44 percent of the domestically acquired cases. Based on outbreak investigations, product testing, and traceback information, several produce items distributed in Illinois were the suspected sources of illnesses but a source was not determined for 85 percent of the outbreaks.

CONCLUSIONS: Illinois had a large increase in cyclosporiasis cases in 2018. Collection and management of case and outbreak investigation data was challenging. Implementation of staff surge capacity, assigning interviews to a student team and utilization of the REDCap tool improved the response.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Epidemiology; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lori.saathoff@illinois.gov
Presenting Author(s)	Lori Saathoff-Huber
Institution Affiliation	Illinois Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11328
Abstract Type	Quick
Abstract Title	Cracking an Outbreak of Salmonellosis Associated with Hazelnuts; Mining National Data and Analyzing with Genetic Sequencing

Abstract

BACKGROUND: In 2009, investigation of a multi-state outbreak of *Salmonella* Typhimurium infections implicated Oregon hazelnuts; however, there were no Oregon cases. Environmental testing at the processing facility identified *Salmonella* Typhimurium with a pulse field gel electrophoresis pattern (PFGE) indistinguishable from the human cases. Seven years later, in November 2016, two Oregon *Salmonella* infections were identified with PFGE patterns matching those of the 2009 outbreak, and a cluster investigation ensued.

METHODS: Cases were interviewed using Oregon's hypothesis-generating questionnaire. The binomial probability statistic was used to compare exposures among cluster cases to those of previously reported cases. Oregon State Public Health Laboratory genetically sequenced isolates from both the 2016 cases and from environmental samples associated with the 2009 outbreak. Samples of hazelnuts purchased from a roadside farm stand were sent to Institute of Environmental Health (IEH) for molecular testing and genetic sequencing. National PulseNET databases were queried for matching isolates, genetic sequencing (hqSNP/cgMLST) analyses were performed on isolates from the current cluster and from the 2009 outbreak.

RESULTS: Isolates from 6 Oregon cases were identical by PFGE. Illness onsets ranged from October 15–December 13. Cases ranged from 54–74 years; four were female. Cases were significantly associated (<0.0001) with consumption of hazelnuts and other items. Querying the national databases for this PFGE pattern identified 46 PFGE matching isolates in 2016. CDC opened a cluster investigation including of 17 cases with onsets from August–December. Genetic analysis of the cluster case isolates (MD[1], OR[5], WA[1], OH[1], CA[1]) indicated that 3 of the OR isolates and the WA isolate were indistinguishable (0 SNPs). Two of the other OR isolates (clade 2) were highly similar (4 SNPs different). Clades 1 and 2 appeared unrelated, differing by 473–475 SNPs. The CA isolate was in another unrelated clade. The MD and OH isolates were unrelated to each other (34 SNPs), and unrelated to both clades 1 and 2 (184–494 SNPs).

CONCLUSIONS: Hazelnuts sold at a roadside stand from a single farm were implicated as the source of this salmonellosis outbreak. Using historical PFGE data, we strengthened our hypotheses, and genetic analyses refined the cluster investigation. *Salmonella* isolates from hazelnut consumers were highly related genetically, and unrelated to other PFGE matching cases without hazelnut exposure, demonstrating how PFGE can be insufficiently specific in determining which cases are part of a common-source exposure.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Genomics; Epidemiologic Methods
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	june.e.bancroft@state.or.us
Presenting Author(s)	June Bancroft
Institution Affiliation	Oregon Health Authority State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11821
Abstract Type	Quick
Abstract Title	Differential Food and Non-Food Exposures Reported By Pennsylvania Salmonella and Campylobacter Case-Patients in Urban and Rural Areas, 2011-2016

Abstract

BACKGROUND: *Salmonella* and *Campylobacter* are the two most commonly reported bacterial enteric diseases in Pennsylvania. During 2001-2015, *Salmonella* rates were 28% higher in rural counties (95% CI:12-46%) and *Campylobacter* rates were 74% higher in rural counties, (95% CI:53%-96%) suggesting exposure sources may vary by rurality. Differences in reported food and non-food exposures by rurality have not been previously well characterized in Pennsylvania. The objective of this study was to describe food and non-food exposures reported by *Salmonella* and *Campylobacter* case-patients overall and by rurality.

METHODS: Reported confirmed and probable cases of *Salmonella* and *Campylobacter* during 2011-2016 in Pennsylvania were included. Cases were excluded if outbreak-linked, not interviewed, missing home address, or if they reported international travel. Demographics included age, sex and race/ethnicity. *Campylobacter* exposures included ≥ 1 restaurant meal, eggs, meat/poultry/fish, unpasteurized dairy/juice, well water, recreational water, any animal(s), cat/dog(s), reptile(s), livestock. *Salmonella* exposures also included any poultry, beef, or fresh produce. Chi squared or Fisher's Exact tests were used to determine if any exposures differed by rurality, stratified by pathogen.

RESULTS: A total of 6489 *Salmonella* and 8099 *Campylobacter* cases were included in final analyses. More *Salmonella* case-patients reported any meat/poultry/fish (*Salmonella* :61% vs. *Campylobacter* :14%) or eggs (*Salmonella* :41% vs *Campylobacter* :11%). More *Campylobacter* case-patients reported unpasteurized dairy (*Salmonella* :2% vs. *Campylobacter* :4%). More *Campylobacter* case-patients reported well water (*Salmonella* :16%vs. *Campylobacter* :26%). More *Salmonella* case-patients reported reptile exposure (*Salmonella* :7% vs. *Campylobacter* :1%). 95% of *Salmonella* and 91% of *Campylobacter* cases resided in urban areas. Rural cases were younger (*Salmonella* urban mean age=36, rural=26, $p<0.0001$; *Campylobacter* urban mean=43 years, rural=40, $p=0.0014$) and more likely to be non/Hispanic white (*Salmonella* $p<0.0001$; *Campylobacter* $p<0.0001$). Urban *Salmonella* cases more frequently reported poultry ($p=0.0009$) and urban *Campylobacter* cases more frequently reported eggs ($p=0.0019$) or meat/poultry/fish ($p<.0001$). Rural *Campylobacter* cases were more likely to drink unpasteurized milk/juice ($p<.0001$). Rural cases of both pathogens were more likely to drink well water (*Salmonella* $p<0.0001$; *Campylobacter* $p<0.0001$). Rural *Salmonella* cases were more likely to report contact with livestock ($p<0.0001$) and rural *Campylobacter* cases were more likely to report contact with any animal ($p<.0001$).

CONCLUSIONS: These results suggest that food and non-food exposures may differ by rurality and pathogen in Pennsylvania. Urban cases appeared to report food exposures like chicken, eggs and meat more frequently, while rural cases more commonly reported unpasteurized dairy/juice, well water, and animal exposure. Public health programs to control bacterial enteric diseases should be tailored for differential food and non-food exposures in rural and urban areas.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	Epidemiology; Foodborne Disease; Rural Health
Presenting Author Email Address(es)	Yes
Presenting Author(s)	ees73@drexel.edu
Institution Affiliation	Erica Smith
	Drexel University School of Public Health Student

Submission Type	Breakout/Quick/Lightning/Poster
ID	11743
Abstract Type	Quick
Abstract Title	Do Cantaloupes Grow on Trees?—a Food Production Wiki for Public Health Professionals

Abstract

BACKGROUND: Many different types of foods have been implicated in foodborne disease outbreaks, including an increasing variety of produce items. Access to food production information can aid outbreak responders in identifying the implicated food and determining how it became contaminated. The Food Source Information Wiki (<http://fsi.colostate.edu/>) is an online, Wikipedia-style resource for public health professionals, providing ready access to essential information on production practices and food safety hazards for a range of agricultural food products, from farm to fork.

METHODS: The Food Source Information Wiki was developed by Colorado State University and the Colorado Integrated Food Safety Center of Excellence. The Wiki includes food-specific articles written by individuals or groups working in food production, food safety, and outbreak response and externally reviewed by experts in the field. Information on production practices, food safety, past outbreaks, food consumption, and nutrition are included in each 'article' for a given food. Google Analytics is being used to track website traffic. User feedback and a website evaluation to assess website layout and organization was done using Optimal Workshop with targeted public health professionals to improve the Wiki website. An evaluation of the added benefit of the Wiki, compared to a general web search, is being conducting through key informant interviews and quiz-style assessments.

RESULTS: The Wiki currently hosts over 30 food articles, including articles on produce items (e.g., avocados, cantaloupes), animal-food products (e.g., beef, cheese), and complex foods (e.g., kombucha, marijuana edibles). In 2018, there were ~85,000 page views and almost 70,000 individual sessions. An assessment of the layout of the website solidified the organization of the site and provided insight into changes needed. Key informant interviews will provide more information about specific information needs with regard to food production information and challenges or resources for accessing this type of information. Results of the evaluation will be discussed.

CONCLUSIONS: By centralizing this information and delivering it in a format that meets the needs of public health professionals, we aim to bridge an important knowledge gap and improve outbreak response nationwide. Delivering information via online websites is a proactive tactic for meeting the needs of public health professionals responding to foodborne illness outbreaks.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Collaboration; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	allison.seidel@ucdenver.edu
Presenting Author(s)	Allison K Seidel
Institution Affiliation	Colorado School of Public Health Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	10983
Abstract Type	Quick
Abstract Title	Evaluating the Impact of Multiplex PCR Use on Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) Surveillance, New York City, 2016–2018

Abstract

BACKGROUND: Historically, diagnostic testing for Shiga toxin-producing *Escherichia coli* (STEC) infections included antigen detection of Shiga toxin or PCR-based testing for Shiga toxin genes, and bacterial culture. In June 2015, laboratories in New York City (NYC) began adopting multiplex PCR (mPCR) panels for enteric diseases, including STEC. We assessed the impact of mPCR on surveillance activities for STEC cases.

METHODS: Health care providers and laboratories must report STEC infection among NYC residents to the NYC Health Department, with specimens forwarded to the NYC Public Health Laboratory for additional testing. We attempt to interview all patients with STEC. Cases with only an antigen or PCR-based test were classified as unconfirmed, while cases with a positive culture were classified as confirmed. We analyzed confirmed and unconfirmed STEC cases among NYC residents diagnosed during 2016–2018. Risk ratios (RRs) were used to assess differences (1) by case classification in age, sex, race/ethnicity, residential county, census tract poverty level, diagnosis year, and international travel history, and (2) by first reported test type (mPCR or non-mPCR) in case classification and interview completeness. Wilcoxon rank-sum tests were used to assess differences by first reported test type in days between first specimen collection and report dates, and first report and interview attempt dates.

RESULTS: mPCR was the first test reported for 62% of 1,011 cases (confirmed: 344; unconfirmed: 667). Annual confirmed case numbers remained stable across the three years (range: 109–123). Cases first reported by mPCR increased from 36% (91/253) in 2016 to 76% (343/453) in 2018. Unconfirmed cases occurred more frequently among Hispanic vs. white, non-Hispanic patients (RR: 1.21, 95% confidence interval (CI): 1.10–1.34), ≥20 year-olds vs. <20 year-olds (RR: 1.49, 95% CI: 1.32–1.67), Manhattan vs. Queens residents (RR: 1.24, 95% CI: 1.09–1.39) and those diagnosed in 2018 vs. 2016 (RR: 1.27, 95% CI: 1.12–1.43). Cases first reported by mPCR were more likely to be unconfirmed (RR: 2.19, 95% CI: 1.90–2.51) and reported more quickly (median days from collection to report date, mPCR: 2, non-mPCR: 3, $p < 0.0001$). No difference by first reported test was observed for interview completeness or timeliness of first attempted interview.

CONCLUSIONS: mPCR testing increased reporting of only unconfirmed cases. Geographic areas served by labs performing mPCR may explain demographic differences in culture confirmation. Cases reported first by mPCR did not differ in interview timeliness or completeness. We are evaluating methods to address the increased staff burden of investigating unconfirmed cases.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Enteric Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	bталbot@health.nyc.gov
Presenting Author(s)	Brooke M Talbot
Institution Affiliation	New York City Department of Health and Mental Hygiene CDC/CSTE Fellow

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	False-Positive Culture-Independent Diagnostic Test Reports and Effects on <i>Vibrio</i> Surveillance — Nebraska, 2017–2018

Abstract

BACKGROUND: In August 2018, Nebraska public health officials identified a gastrointestinal illness cluster where stool from 4 patients who resided in close proximity tested positive for *Vibrio cholerae* and vibriosis on culture-independent diagnostic testing (CIDT), but reflex cultures were negative. Patients lacked known exposures for vibriosis or cholera (e.g., travel, saltwater exposure, or seafood consumption), indicating false-positive CIDT results. To determine effects of false-positive results on surveillance, we analyzed *Vibrio* detections in Nebraska.

METHODS: We analyzed *Vibrio cholerae* and vibriosis surveillance data to compare 2017 with 2018 counts of probable (detected only by CIDT) and culture-confirmed *Vibrio* cases consistent with national case definitions. After determining initial test type, we calculated proportion of those initially positive by CIDT where attempted culture was negative. We also assessed reported exposures for patients diagnosed by CIDT only.

RESULTS: During January 1–December 31, 2017, a total of 9 *Vibrio* or *Vibrio cholerae* cases were reported, including 4 culture-confirmed (1 initially CIDT-positive) and 5 probable. Of 6 initially CIDT-positive specimens, reflex culture was attempted on 4 and negative on 3 (75%). Overall, 3/5 (60%) probable case reports documented vibriosis or cholera exposures. During January 1–October 31, 2018, a total of 23 *Vibrio* or *Vibrio cholerae* cases were reported, including 1 culture-confirmed and 22 probable. Of 22 initially CIDT-positive specimens, reflex culture was attempted on 21 and negative on 21 (100%). Overall, 5/22 (23%) probable case reports documented exposures. The change from 3 CIDT-positive, culture-negative detections in 2017 to 21 by October 31, 2018, represents a 700% increase.

CONCLUSIONS: *Vibrio* detections through CIDT have increased substantially; some are likely false-positives, highlighting the importance of reflex culture. *Vibrio* CIDT results should be interpreted along with clinical, epidemiologic, and culture findings. For culture-negative patients lacking known exposures, utility of probable case classifications in *Vibrio* surveillance is unclear.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Waterborne Disease; Surveillance; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rebecca.free@nebraska.gov
Presenting Author(s)	Rebecca J. Free
Institution Affiliation	Nebraska Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11744
Abstract Type	Quick
Abstract Title	Gastrointestinal Illness Associated with a Community Food Truck Event — Nebraska, 2018

Abstract

BACKGROUND: In May 2018, a community organization reported a gastrointestinal illness cluster after an employee appreciation meal with 3 food truck vendors. We investigated to identify cases, assess etiology, and prevent further illnesses.

METHODS: A cohort study was performed using a menu- and symptom-specific Internet-based questionnaire disseminated to ~900 employees by the organization. Cases were defined as diarrhea (≥ 3 stools < 24 hours) among attendees who reported symptom onset < 24 hours after the event. We calculated relative risks (RRs) for all food items, comparing ill and non-ill attendees. Vendor A, who served the implicated food, was interviewed.

RESULTS: Of 228 respondents, 208 attended and were included for analysis. Forty-one (20%) cases were identified; two (5%) sought medical care. Ill persons reported diarrhea (41, 100%), abdominal cramps (32, 78%), and vomiting (5, 12%). Illness occurred 4–22 hours (median: 11 hours) after the event. No stool samples were collected. Consuming Vendor A's pork (RR: 6.1; 95% CI: 3.7–10.0), bun (RR: 3.4; 95% CI: 1.9–6.1), condiment 1 (RR: 2.9; 95% CI: 1.7–4.8), or condiment 2 (RR: 3.3; 95% CI: 1.7–6.4) demonstrated significant associations with illness. Two days before the event, pork was cooked, placed in plastic bins, and transferred to noncommercial grade refrigerators; the cooling process was not monitored. The day of the event, pork was reportedly reheated to 145 degrees. No foods were leftover for testing.

CONCLUSIONS: Our findings demonstrate foods from Vendor A, particularly pork, as likely causative vehicles. The reported clinical presentations and timing of symptom onsets suggest *Clostridium perfringens*, a ubiquitous spore- and enterotoxin-forming bacteria, as a potential cause. We suspect improper handling led to contamination of pork; cross-contamination during serving could explain other Vendor A food items demonstrating associations with illness. Although not required in Nebraska, the vendor agreed to complete food safety training.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Outbreaks; Food Safety
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rebecca.free@nebraska.gov
Presenting Author(s)	Rebecca J. Free
Institution Affiliation	Nebraska Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11318
Abstract Type	Quick
Abstract Title	Impact of Culture-Independent Diagnostic Tests (CIDTs) on Vibriosis Surveillance and Epidemiological Factors Associated with Culture Confirmation, Illinois, 2016–2018

Abstract

BACKGROUND: Culture-independent diagnostic tests (CIDTs) are commonly used by clinical laboratories to diagnose *Vibrio* infections, although culturing remains the gold standard for case confirmation. In 2017, the Vibriosis nationally notifiable disease surveillance system (NNDSS) case definition expanded, including persons with positive CIDT results as probable cases, regardless of culture result, clinical symptoms or relevant exposures. Consequentially, there is concern for false positives being reported and the burden this may place on health departments when conducting investigations. We examined the impact of CIDTs on the volume of Vibriosis cases in Illinois, the frequency of false positives and epidemiological factors associated with culture confirmation.

METHODS: Vibriosis cases reported to the Illinois National Electronic Disease Surveillance System during January 2016–November 16, 2018 were analyzed. Cases were classified as confirmed or probable following the NNDSS Vibriosis case definition. The false-positive rate was defined as the proportion of CIDT-positive cases that were culture-negative. Relevant *Vibrio* exposure was defined as reported consumption of raw oysters, mussels, clams or scallops; or saltwater exposure. Patients with specimens collected during May–October were considered peak season; those with specimens during November–April were classified as non-peak. False-positive rates were stratified by relevant *Vibrio* exposure, symptom presence and peak season. Chi-squared tests were used to determine significant associations ($\alpha=0.05$).

RESULTS: Overall, 174 Vibriosis cases were reported during January 2016–November 16, 2018. Probable cases increased from zero in 2016 to 29 in 2017 and to 52 in 2018, whereas culture-confirmed case counts remained relatively stable (33, 31 and 29 respectively). Seventy-two percent of probable cases were culture-negative, 23% CIDT-positive only and 5% symptomatic contacts. Among cases with both CIDT and culture results ($n=65$), 52 were culture-negative and 13 were culture-positive, yielding a false-positive rate of 80%. When stratifying by relevant *Vibrio* exposure, cases with exposures ($n=14$) had a significantly lower false-positive rate compared to cases with no or unknown *Vibrio* exposures ($n=51$): 36% vs. 92% ($p<0.0001$). Asymptomatic cases ($n=11$) had a false-positive rate of 91% compared to 78% for symptomatic cases ($n=54$) ($p>0.05$). The false-positive rate for cases tested in peak season ($n=51$) versus non-peak ($n=14$) were not significantly different: 80% vs. 79% ($p>0.05$).

CONCLUSIONS: Vibriosis case counts have increased in Illinois due to probable, CIDT-positive cases, with no increase in culture-confirmed cases. The high false-positivity rate of CIDTs in diagnosing *Vibrio* infections is a concern for detecting true infections. Health departments should prioritize culture-confirmed cases and probable cases with relevant *Vibrio* exposures in public health investigations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epi / Lab Capacity (ELC); Waterborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kelly.walblay@illinois.gov
Presenting Author(s)	Kelly Walblay
Institution Affiliation	Illinois Department of Public Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11272
Abstract Type	Quick
Abstract Title	Implementation of Prospective Whole Genome Sequencing for Enteric Pathogens: The Canadian Experience

Abstract

BACKGROUND: The Public Health Agency of Canada implemented prospective whole genome sequencing (WGS) for *Listeria monocytogenes* (LM) and *Salmonella* in 2017 and *E. coli* in 2018; providing increased resolution compared to the previous methods of pulsed field gel electrophoresis (PFGE), phage typing, and multiple-locus variable-number of tandem-repeats analysis (MLVA). The impact of this change on multi-jurisdictional cluster detection and outbreak investigations in Canada will be described.

METHODS: Multi-jurisdictional WGS clusters of LM, *Salmonella* and *E. coli* are identified by the National Microbiology Laboratory. Clusters are assessed and epidemiologic information is obtained to determine possible sources of illnesses. Non-human isolates are routinely sequenced by national and provincial laboratories for real-time integration with human isolates. The characteristics and trends of multi-jurisdictional LM, *Salmonella* and *E. coli* clusters and outbreaks identified in the two years pre-WGS implementation were examined and compared to post-WGS implementation results gathered to date.

RESULTS: The number of multi-jurisdictional clusters detected and outbreak investigations conducted decreased for LM post-WGS implementation (clusters: 24 vs. 4; outbreaks: 2 vs. 0). In contrast, an increase in both clusters and outbreak investigations was seen for *Salmonella* post-WGS implementation (clusters: 164 vs. 348; outbreaks: 5 vs. 16). Since WGS implementation, 32% of multi-jurisdictional *Salmonella* clusters have been found to be associated with poultry. Collaborative response to the multi-jurisdictional poultry-associated *Salmonella* outbreaks investigated post-WGS implementation resulted in a new requirement for industry to reduce *Salmonella* to below detectable amounts in frozen raw breaded chicken products (FRBCP) packaged for retail sale, which will come into effect April 1, 2019. Based on preliminary data, the number of multi-jurisdictional *E. coli* clusters detected and outbreak investigations conducted has remained consistent pre and post-WGS implementation.

CONCLUSIONS: WGS has changed the landscape of foodborne illness cluster detection and outbreak investigation in Canada, decreasing the number of LM clusters/investigations, but increasing the number of clusters/investigations for *Salmonella*. The first six months of prospective WGS for *E. coli* has shown that the impact may not be as substantial as it has been for the other pathogens. For *Salmonella*, WGS has highlighted the burden of salmonellosis infections associated with poultry, resulting in a new industry requirement within the first year of implementation. While WGS has improved the detection of, and response to, foodborne outbreaks, it has not come without challenges. Epidemiologic assessment and outbreak response procedures have been adapted, resulting in evolving cluster assessment criteria, new investigative approaches and changes in resource allocation.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Genomics; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email	tanis.kershaw@canada.ca
Address(es)	
Presenting Author(s)	Tanis Kershaw
Institution	Public Health Agency of Canada
Affiliation	International Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10907
Abstract Type	Quick
Abstract Title	Improving Inclusion and Exclusion Criteria in Foodborne Illness Outbreak Investigations: A Case Study

Abstract

BACKGROUND: The practice of foodborne illness outbreak investigations has evolved, shifting away from large-scale community case control studies towards more focused case exposure assessments and sub-cluster investigations to identify contaminated food sources. Criteria to include or exclude cases are established to increase the efficiency of traceback activities and etiologic analyses. A 2010 outbreak of *Salmonella* ser. Hvitittingfoss associated with quick-service restaurants (Chain A) provides a useful case study on the impact of exclusion criteria on the ability to identify a food vehicle. In the original investigation, produce tracebacks identified green peppers as a likely source, but no specific food item was associated with illness in the final analysis. The objective of our study was to examine how exclusion criteria affected these results.

METHODS: De-identified exposure information for 85 cases and 33 well-meal companions associated with the 2010 Chain A outbreak were obtained. Because of uncertainty about which exposure may have led to illness, the investigating agency excluded any cases (n=18) or well-meal companions (n=8) who reported eating at Chain A restaurants more than once in the 15 days before illness onset. We compared results of multi-variable analyses of food items for patrons with single eating dates with analyses including those with multiple eating dates. We also conducted a sub-analysis restricted to patrons who had eaten at a Chain A restaurant where well companions had eaten.

RESULTS: Including all cases, green peppers were associated with illness (OR: 3.7; 95%CI: 1.3, 10.6). Excluding patrons with multiple Chain A meals, lettuce (OR: 4.1; 95%CI: 1.4, 11.8), tomatoes (OR: 3.4; 95%CI: 1.1, 9.9), and olives (OR: 7.9; 95%CI: 1.7, 37.5) were significantly associated with illness, while green peppers were not (OR: 2.1; 95%CI: 0.7, 6.4). In a sub-cluster analysis restricted to restaurants with well-meal companions, green peppers were associated with illness when all patrons were included (OR: 4.3; 95%CI: 1.2, 15.0), but were not when excluding cases who had multiple exposures (OR: 2.8; 95%CI: 0.7, 10.7).

CONCLUSIONS: Despite being initially suspected, green peppers were not epidemiologically linked to illness when Chain A patrons with multiple eating dates were excluded. Including these patrons showed that green peppers were most strongly associated with illness, as initially suspected by traceback. As outbreak investigation practices shift with application of whole genome sequencing (WGS), improving exposure assessments, conducting sub-cluster analyses with food item tracebacks, and using all available case data will be critical to the success of outbreak investigations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	fire0018@umn.edu
Presenting Author(s)	Melanie J. Firestone
Institution Affiliation	University of Minnesota Student

Submission Type	Breakout/Quick/Lightning/Poster
ID	10894
Abstract Type	Quick
Abstract Title	Multiple Cyclosporiasis Outbreaks, United States, 2018

Abstract

BACKGROUND: Cyclosporiasis is a gastrointestinal illness caused by the parasite *Cyclospora cayetanensis*, primarily found in the tropics and subtropics. Previous U.S. outbreaks have been linked to imported fresh produce (e.g., basil, cilantro, raspberries). Foodborne outbreaks of cyclosporiasis are challenging to investigate, in part because molecular typing methods, which could facilitate linking cases to each other and to food sources, are not yet available. Typically, increased numbers of cases are reported during the spring and summer months.

METHODS: The Centers for Disease Control and Prevention (CDC) received reports of cases through the National Notifiable Diseases Surveillance System and the Cyclosporiasis National Hypothesis Generating Questionnaire (CNHGQ). Data received through these methods were combined and analyzed in aggregate. Clusters and outbreaks were detected through use of the CNHGQ or state-adapted questionnaires; investigations were led by state or local public health partners in collaboration with the CDC and Food and Drug Administration (FDA).

RESULTS: CDC was notified of 2,328* laboratory-confirmed, domestically acquired cases in persons with illness onset during May–August, 2018. These cases were reported by 34 states. The median patient age was 49 years (range: <1–103) and 56% were female (n=1,308/2,321). At least 164 patients were hospitalized; no deaths were reported. Approximately one third of cases were linked to either of two large multistate outbreaks: 250 cases associated with prepackaged vegetable trays (containing broccoli, cauliflower, and carrots) sold at a convenience store chain in the Midwest; 511 cases associated with salads (containing carrots, romaine, and other leafy greens) sold at a fast food chain in the Midwest. Additional clusters of cases associated with other types of fresh produce were investigated, including basil (two clusters, 16 cases) and cilantro (three clusters, 53 cases). Traceback investigations conducted by FDA did not identify a single source or potential point of contamination for these clusters or outbreaks.

CONCLUSIONS: The number of domestically acquired, laboratory-confirmed cases (n=2,328) of cyclosporiasis reported during May–August, 2018 is markedly higher than the number reported during the same time in 2016 (n=174) and 2017 (n=623). The extent to which changes in diagnostic testing practices, including use of gastrointestinal molecular testing panels, may have contributed to this increase is unknown. While a substantial proportion of cases were linked to identified outbreaks, many could not be directly linked. For some identified clusters, a single vehicle of infection could not be identified because of small case counts, limited exposure information, or because produce items were served comingled. *As of 12/21/2018.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	yqj1@cdc.gov
Presenting Author(s)	Shannon Casillas
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10904
Abstract Type	Quick
Abstract Title	Multistate Outbreak of <i>Listeria Monocytogenes</i> Infections Linked to Ready-to-Eat Country Deli Ham

Abstract

BACKGROUND: In July 2018, three *Listeria monocytogenes* (*Lm*) clinical isolates were identified that were highly related to one another by whole genome sequencing (WGS) and to three US Department of Agriculture Food Safety and Inspection Service (USDA-FSIS) isolates from ready-to-eat (RTE) deli ham products. CDC, USDA-FSIS, and state and local public health officials investigated to determine if the RTE products were the source of the outbreak and to prevent additional illnesses.

METHODS: We defined a case as infection with *Lm* with a clinical isolate closely related to the outbreak strain by WGS from July 2017 to November 2018. Ill people or their surrogates were interviewed using the standard *Listeria* Initiative questionnaire and asked specific additional questions about ham exposure. State and local health departments and USDA-FSIS collected and reviewed food records from an assisted living facility where one patient resided, as well as from retailers where ill people reported purchasing ham products.

RESULTS: We identified four ill people from North Carolina (1) and Virginia (3) with the outbreak strain. Ill people ranged in age from 70 to 81 years, and two were female. All four ill people were hospitalized, and one death was attributed to listeriosis. Two ill people specifically reported consuming country ham products before becoming ill. One of the two reported consuming a country ham roll. Records from the ham roll producer indicated that ham was supplied by Establishment A, a producer of RTE pork products that yielded the same strain of *Lm*. Records from an assisted living facility where one patient resided indicated that the facility also received country ham products from Establishment A. On October 3, 2018, Establishment A voluntarily recalled 89,096 pounds of RTE deli ham products produced April 3, 2017 to October 2, 2018 due to potential contamination with *Lm*.

CONCLUSIONS: This is the first multistate outbreak of listeriosis linked to a deli meat product identified in the United States since 2005. Although outbreaks linked to deli meat products have become rare, deli meat remains a possible vehicle for infection with *Lm*. Persons at higher risk of listeriosis (e.g., older adults, pregnant women, immunocompromised persons) should avoid deli meats and cold cuts unless they are heated to a temperature of 165°F immediately before serving. Producers of deli meat products should be aware of the potential for environmental contamination and harborage in the production environment and mitigate these risks through proper environmental controls.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kse1@cdc.gov
Presenting Author(s)	Jessica R. Marus
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11100
Abstract Type	Quick
Abstract Title	Multistate Outbreak of Multidrug-Resistant <i>Salmonella</i> Infections Linked to Raw Chicken Products – United States, 2018

Abstract

BACKGROUND: In May 2018, PulseNet, the national molecular subtyping network for foodborne disease surveillance, identified an increase in *Salmonella* Infantis isolates with a rare pulsed-field gel electrophoresis (PFGE) pattern. Prior to this outbreak, there were only 164 isolates with this rare PFGE pattern in the PulseNet database. Approximately sixty percent of these historical isolates were from chicken and had been collected from 2016 to 2018. CDC investigated to determine the outbreak source and prevent additional illnesses.

METHODS: A case was defined as infection with the outbreak strain of *Salmonella* Infantis occurring since January 19, 2018. Case-patients were identified via PulseNet and interviewed to determine common exposures. A subset of isolates identified as part of the cluster underwent whole genome sequencing (WGS). Isolate sequences were analyzed for relatedness and antibiotic resistance determinants.

RESULTS: As of October 15, 2018, we had identified 92 cases from 29 states. The median age was 36 years (range <1–105 years); 69% were female. Of the 62 patients with available information, there were 21 (34%) hospitalizations and no deaths. Of 54 patients interviewed, 48 (89%) reported exposure to a variety of chicken products both at home and in restaurants. These included chicken breasts, chicken parts, and rotisserie chickens. Three case-patients were infants who lived in homes where raw chicken was prepared. In addition, one case-patient became sick after feeding their pet a raw chicken pet food that had been recalled, and another case-patient lived in the same household as a family member who worked on a poultry farm. The outbreak strain was identified in raw chicken pet food, raw chicken products from 58 slaughter or processing establishments, and from live chickens. Isolates were related by WGS. Isolates from humans and chickens were resistant to antibiotics from up to eight classes, including ceftriaxone and ciprofloxacin, both commonly used to treat severe salmonellosis infections. A single, common chicken supplier was not identified. Representatives from the poultry industry were notified.

CONCLUSIONS: Further work with industry is needed to better understand the emergence and spread of this strain of multidrug-resistant *Salmonella* Infantis. Clinicians should be aware that this strain of *Salmonella* is resistant to many common first-line antibiotics and should consider susceptibility testing for suspected *Salmonella* infections. Consumers should handle raw chicken carefully to avoid cross-contamination, cook chicken to an internal temperature of 165°F, and avoid feeding raw poultry diets to their pets.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Antimicrobial Resistance; Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	wjq3@cdc.gov
Presenting Author(s)	Colin A. Basler
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10995
Abstract Type	Quick
Abstract Title	Novel Serotype of Enteroinvasive <i>Escherichia coli</i> Associated with a Party — North Carolina, June–July 2018

Abstract

BACKGROUND: On July 2, 2018, the North Carolina Division of Public Health was notified that ~38 members of an ethnic Nepali immigrant community were transported to area hospitals for severe gastrointestinal illness after consuming food at a potluck on June 30. We investigated to identify the cause of the outbreak.

METHODS: We reviewed medical records, conducted a retrospective cohort investigation, and coordinated laboratory testing. A case of gastroenteritis was defined as diarrhea, vomiting, or temperature $\geq 100^{\circ}\text{F}$ in a person who consumed food from the party. One hospital used a commercial multiplex polymerase chain reaction (PCR) assay; the State Laboratory of Public Health (SLPH) employed culture for enteric pathogens and PCR for Shiga toxin genes *stx*₁ and *stx*₂; and CDC used a molecular guided approach for isolation.

RESULTS: Fifty-two of ~100 attendees met the case definition; 28 (54%) were hospitalized and 8 (15%) admitted to intensive care. Forty-nine attendees (35 ill) were interviewed. Although no specific food was statistically associated with illness, persons who ate chicken curry were more likely to become ill than those who did not (risk ratio: 1.47; 95% CI: 0.76–2.83). Food was not available for testing. Stool PCR assays from 25 persons were positive for *Shigella* /Enteroinvasive *Escherichia coli* (EIEC). However, among 24 specimens tested at SLPH, no enteric pathogens grew on culture media and all were PCR-negative for Shiga toxin genes. Ultimately, CDC identified novel EIEC serotype O8:H19 from 12 patient specimens.

CONCLUSIONS: A novel EIEC serotype caused the outbreak, likely through a food vehicle. This represents the first reported U.S. outbreak of EIEC in >40 years. *Shigella* was initially suspected based on preliminary PCR results and because domestic EIEC infections are rare. However, clinical and epidemiologic findings appeared more consistent with EIEC leading to use of advanced molecular methods and detection of a novel organism.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nqw6@cdc.gov
Presenting Author(s)	Carolyn Herzig
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	11447
Abstract Type	Quick
Abstract Title	Outbreak of <i>Staphylococcus Aureus</i> and <i>Clostridium Perfringens</i> Associated with a Meal Served at a Workplace, Kansas 2018

Abstract

BACKGROUND: On November 9, 2018, a Local Health Department notified the Kansas Department of Health and Environment of at least 20 individuals with vomiting 2-4 hours after eating a pre-made plate of food delivered to a workplace by a vendor.

METHODS: An outbreak-specific, self-administered, questionnaire was distributed to the workplace employees. A case was defined as diarrhea and/or vomiting in a person within eight hours of eating food from the vendor on November 9th. Stool specimens were sent to the Minnesota Department of Health – Public Health Laboratory (MDH-PHL) for toxin testing. Food samples were sent to Food Microbiological Laboratories, Inc. (FMS) and Food Safety Net Service (FSNS). Pulsed-field gel electrophoresis (PFGE) was performed at MDH-PHL on human specimens and food samples. The Kansas Department of Agriculture (KDA) interviewed the vendor.

RESULTS: Surveys were completed by 143 employees. Sixty persons reported consuming the pre-made plate and 42 (70%) persons reported illness, and all met the outbreak case definition. Median incubation period was three hours (range: 30 minutes-eight hours). Thirty-seven (98%) ill persons experienced vomiting and diarrhea. No cases were hospitalized; however, 26 (62%) sought care at an emergency department or urgent care. Of eight stool specimens submitted for testing, four were positive for *C. perfringens* enterotoxin A, one was positive for *C. perfringens* by culture but negative for enterotoxin A, one was positive for *S. aureus* enterotoxin A, and two were co-infected with both organisms. Two separate plates of food were submitted for testing. A meat sample (cow cheek) from one plate tested by FMS was positive for *S. aureus* by culture (900,000,000 cfu/g), the staphylococcal enterotoxin, and *C. perfringens* by culture (28,000,000 cfu/g). Food samples from the second plate tested by FSNS were negative. Four *S. aureus* isolates (3 stool, 1 food) were indistinguishable by PFGE. Results for PFGE of *C. perfringens* are pending. Upon interview, the unlicensed vendor reported the meat was prepared the evening prior to serving and left in an unrefrigerated, unplugged crockpot overnight.

CONCLUSIONS: *C. perfringens* and *S. aureus* were confirmed as causative agents in this outbreak. Temperature abuse contributed to the magnitude of this outbreak. Due to majority of ill persons reporting very short incubation periods and experiencing both vomiting and diarrhea, it was impossible to distinguish cause of illness in persons who were not tested. Comprehensive toxin testing, including *C. perfringens*, should be considered in outbreaks with reported incubation periods of <6 hours.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	amie.cook@ks.gov
Presenting Author(s)	Amie Cook
Institution Affiliation	Kansas Department of Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11818
Abstract Type	Quick
Abstract Title	Outbreak of Cryptosporidiosis Associated with Dining at a Taco Restaurant – San Diego, California, 2018

Abstract

BACKGROUND: In September 2018, the County of San Diego Health and Human Services Agency identified five confirmed and two probable cryptosporidiosis cases among recent patrons of a San Diego restaurant. Cryptosporidiosis is a parasitic intestinal illness caused by *Cryptosporidium* species commonly associated with recreational water exposure. This was the first restaurant-associated cryptosporidiosis outbreak detected in the county and the first identified by routine enteric polymerase chain reaction (PCR) testing.

METHODS: A confirmed case was defined as laboratory-confirmed *Cryptosporidium* infection and diarrheal illness in a person who ate at the restaurant within ten days prior to symptom onset. A probable case was defined as diarrhea onset within seven days of dining with a confirmed case-patient. All case-patients were interviewed using a standard questionnaire. Four cases were diagnosed using PCR and one using direct fluorescent antibody (DFA); the DFA-positive specimen was genotyped at CDC using PCR. Persons with recent cryptosporidiosis were re-interviewed to determine if they had eaten at this restaurant during their exposure periods. Restaurant employees were interviewed, and Environmental Health Specialists (EHS) conducted a restaurant field investigation. Employees' stool specimens were tested using DFA to determine ongoing risk to restaurant patrons.

RESULTS: The seven case-patients had a median age of 56 years (range = 33–59 years); five were male. All experienced diarrhea, two had bloody diarrhea, five had fever, and two had vomiting. Six reported dining at the restaurant during August 28–September 1; one could not recall the specific date. Genotyping of one case-sample identified *C. hominis* as the likely etiologic agent in this outbreak. The only common exposure among cases was the restaurant salsa bar. Two restaurant cooks were identified who worked while symptomatic with diarrheal illness during the exposure period. EHS observed dirty water in the salsa bar cooling unit and 50–100 houseflies throughout kitchen, front desk, and dining areas. The restaurant was directed to stop serving food, kill flies, sanitize surfaces and equipment, and replace cooling unit water before reopening. All eight employee specimens tested negative for *Cryptosporidium*.

CONCLUSIONS: Although the specific outbreak source was not identified, investigation of lab-reported cases identified a common restaurant exposure, enabling public health action. Between 1998 and 2016, only two restaurant-associated cryptosporidiosis outbreaks were reported to CDC's National Outbreak Reporting System. As routine *Cryptosporidium* PCR testing increases, surveillance systems may detect additional clusters, including restaurant-associated clusters.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Local Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	cory.arrouzet@sdcounty.ca.gov
Presenting Author(s)	Cory J Arrouzet
Institution Affiliation	County of San Diego, Health and Human Services Agency CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11583
Abstract Type	Quick
Abstract Title	Outbreak of Cyclospora Cayetanesis at a Wedding Linked to Cilantro Consumption from a Mexican-Style Restaurant — Indiana, 2018

Abstract

BACKGROUND: On July 11, 2018, the Indiana State Department of Health (ISDH) Rapid Response Team was notified of an outbreak of gastrointestinal illness following a wedding ceremony on June 23, 2018. This event was catered by a Mexican-style restaurant, and 154 people attended.

METHODS: The ISDH obtained a catering menu, and foodborne illness surveys were e-mailed to all wedding attendees with available contact information. An outbreak case was defined as any wedding attendee who developed gastrointestinal symptoms on or after June 23, 2018. A cohort study was performed using survey data. Stool specimens from two wedding attendees were tested using a BioFire® FilmArray® Gastrointestinal (GI) Panel. The ISDH collected leftover pico de gallo, onions, and green sauce samples from a wedding attendee. Food samples were shipped to the United States Food and Drug Administration (FDA) Laboratories for testing.

RESULTS: The ISDH received surveys from 90 wedding attendees (58%). Of the respondents, 49 (54.4%) from eight states reported illness. Cases ranged in age from 16 to 72 years, and 63.3% were female. Primary symptoms included fatigue (51.1%), diarrhea (51.1%), watery stool (46.7%), nausea (41.1%), abdominal cramps (40%), and weight loss (24.4%). Dates of onset of watery stool ranged from 6/28/18-7/11/18. The median incubation period was nine days. Stool specimens from two wedding attendees tested positive for *Cyclospora cayetanesis*, which confirmed outbreak etiology. The cohort study yielded a strongly significant relationship between cilantro consumption and illness onset (risk ratio, 10.7; 95% confidence interval [CI], 3.6-31.8). All leftover food samples from the wedding tested negative for *Cyclospora*. The ISDH traced the cilantro served at the wedding event back to a farm in Mexico. This region had an import alert by the FDA that referenced *C. cayetanesis* outbreaks from 2012-2015.

CONCLUSIONS: Symptom descriptions, median incubation period, and laboratory evidence confirmed that the causative etiologic agent of this outbreak was *C. cayetanesis*. This was one of several outbreaks of cyclosporiasis that occurred in the summer of 2018, many of which were linked to fresh produce items. It was one of three outbreaks associated with Mexican-style restaurants in the Midwest. Increased case detection of *Cyclospora* has occurred nationally, partially due to changes in laboratory testing methods. Public health practitioners should continue to pursue vehicle identification to determine outbreak sources given that molecular subtyping is unavailable for *Cyclospora*.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Waterborne Disease; Food Safety
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	MSundararajan@isdh.IN.gov
Presenting Author(s)	Madhura Sundararajan
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11561
Abstract Type	Quick
Abstract Title	Outbreaks Associated with Untreated Recreational Water — United States, 2000–2014

Abstract

BACKGROUND: Outbreaks associated with untreated recreational water can be caused by pathogens, toxins, or chemicals in fresh water (e.g., lakes, rivers) or marine water (e.g., ocean). It is estimated we enter, swim, or wade in the water in these venues on 280 million days each year. Thus, it is imperative to better understand the epidemiology of these outbreaks to optimize prevention efforts.

METHODS: Public health officials in the 50 states, the District of Columbia, and U.S. territories voluntarily report outbreaks associated with recreational water to CDC via the Waterborne Disease and Outbreak Surveillance System. Poisson regression analysis was conducted to assess the trend in the overall annual counts of outbreaks during 2000–2014.

RESULTS: Public health officials from 35 states and Guam reported 140 untreated recreational water–associated outbreaks. These outbreaks resulted in at least 4,958 cases of disease and two deaths. Among the 95 outbreaks with a confirmed infectious etiology, enteric pathogens caused 80 (84%); 21 (22%) were caused by norovirus, 19 (20%) by *Escherichia coli*, 14 (15%) by *Shigella*, and 12 (13%) by *Cryptosporidium*. Investigations of these 95 outbreaks identified 3,125 cases; 2,704 (87%) were caused by enteric pathogens, including 1,459 (47%) by norovirus, 362 (12%) by *Shigella*, 314 (10%) by *Cryptosporidium*, and 155 (5%) by *E. coli*. Avian schistosomes were identified as the cause in 345 (11%) of the 3,125 cases. The two deaths were in persons affected by a single outbreak (two cases) caused by *Naegleria fowleri*. Public parks (50 [36%]) and beaches (45 [32%]) were the leading settings associated with the 140 outbreaks. Overall, the majority of outbreaks started during June–August (113 [81%]); 65 (58%) started in July. Poisson regression analyses indicated the overall annual outbreak count did not change significantly over the 15 years ($p = 0.477$).

CONCLUSIONS: Untreated recreational water–associated outbreaks were predominantly caused by enteric pathogens, indicating fecal contamination of water; however, environmental pathogens (e.g., avian schistosomes, *Naegleria fowleri*) not transmitted fecally-orally can also contaminate untreated recreational water. Swimmers and parents of young swimmers can take steps to minimize the risk for exposure to pathogens toxins, and chemicals in untreated recreational water by not swimming while sick with diarrhea and heeding posted advisories (e.g., closing the beach to swimming).

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Infectious Diseases; Outbreaks; Waterborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	acz3@cdc.gov
Presenting Author(s)	Michele C. Hlavsa
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11483
Abstract Type	Quick
Abstract Title	Pull Your Pork Properly: A Large Salmonellosis Outbreak at a Picnic, Pennsylvania 2018

Abstract

BACKGROUND: In July 2018, the Pennsylvania Department of Health was notified of multiple cases of salmonellosis among attendees of a picnic affiliated with a small private school. Foods included a main dish of roasted pulled pork plus multiple other pot-luck items, all brought by attendees. The picnic was held at a farm where attendees had access to several farm animals including poultry, peacocks, horses, a llama, and a donkey as well as a goshawk brought by the individual who prepared the pork. We investigated to determine the source of this outbreak.

METHODS: We conducted a case-control study to identify exposures potentially associated with illness. Picnic attendees were interviewed with a targeted questionnaire to collect demographics, clinical details, food history, and animal exposures during the picnic. Case-patients were defined as picnic guests who developed symptoms consistent with salmonellosis within ten days following the picnic. Confirmed cases had *Salmonella* isolated from clinical specimens; probable cases had consistent symptoms without laboratory confirmation. Environmental assessment included review of cooking procedures for approximately 200 pounds of pork prepared for the picnic and collection of raw and cooked pork samples for laboratory testing.

RESULTS: Approximately 148 people attended the picnic and 109 met the case definition (17 confirmed and 92 probable) for an 82.0% attack rate among all attendees. Median age was 21 and ranged from <1 to 77 years and median incubation period was 12 hours and ranged from 30 minutes to 160.75 hours. Sixty-one (56.0%) case-patients sought medical care and 11 (10.1%) were hospitalized. Blood and stool revealed *Salmonella* Typhimurium with pulsed-field gel electrophoresis pattern JPXX01.0146. Pulled pork was strongly associated with illness, with 103 ill of 107 who consumed pork affected (attack rate 96.3%; odds ratio = 171.7 [95% CI: 35.7-826.6]). *Salmonella* matching the clinical strain was isolated from leftover cooked pork but not frozen raw pork. Review of cooking and serving techniques suggested multiple potential routes for cross-contamination of raw with finished product and time-temperature abuse in the kitchen and during the picnic. Contact with animals during the picnic was not associated with illness.

CONCLUSIONS: Improperly handled pork was the source of this *Salmonella* outbreak with a high attack rate. These findings underscore the importance of adhering to food safety guidelines including use of adequate commercial facilities to prepare large volumes of food, avoiding cross-contamination and ensuring proper times and temperatures are reached when cooking, serving and reheating food.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Zoonotic Diseases; Enteric Infectious Diseases; Food Safety
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	c-chributl@pa.gov
Presenting Author(s)	Christina Butler
Institution Affiliation	Pennsylvania Department of Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11618
Abstract Type	Quick
Abstract Title	Raw Milk Outbreaks in Pennsylvania – a Systematic Review, 2005-2018

Abstract

BACKGROUND: Consumption of unpasteurized milk (“raw milk”) carries inherent risk of infection. Before widespread adoption of pasteurization across the United States, contaminated milk was one of the most common causes of foodborne illness. Today, it is estimated that less than 1% of outbreaks are milk-related, and almost all are due to raw milk or its derivatives. The burden of raw milk outbreaks in Pennsylvania is high. Data published in 2015 show that Pennsylvania had the highest number of reported raw milk outbreaks in the United States from 2007-2012. Pennsylvania law allows in-state sale of raw milk, which requires permitting by the Pennsylvania Department of Agriculture.

METHODS: We conducted a systematic review of raw milk-related outbreaks across the state from 2005-2018 using data from PA-NEDSS, Pennsylvania’s electronic disease surveillance system and the National Outbreak Reporting System. A confirmed outbreak was defined as an outbreak in which raw milk produced from a Pennsylvania farm was implicated as the outbreak vehicle, either through epidemiologic or laboratory evidence. A possible outbreak was defined as a household cluster in which raw milk was a possible vehicle, but there was not sufficient evidence to implicate it due to multiple shared exposures among cases. Cases could be residents of any state.

RESULTS: From 2005-2018, we investigated 22 confirmed raw milk outbreaks with 491 cases, representing 8% of reported foodborne outbreaks in Pennsylvania. Etiologies included 14 (64%) *Campylobacter*, 6 (27%) *Salmonella*, 1 (5%) *Cryptosporidium*, and 1 (5%) *Listeria monocytogenes* outbreaks. There was a median of 8 cases per outbreak (range: 2-148). Seven (41%) outbreaks caused illness in residents outside of Pennsylvania, 9 (41%) caused illnesses in residents of multiple counties within Pennsylvania, and 6 (27%) were confined to residents of a single county. Most were caused by raw milk from a permitted dairy (68%), while 4 (18%) were from an unlicensed farm, 2 (9%) were from an unnamed farm, and 1 (5%) was from a private farm (owned by friends or family). Four dairies were implicated in multiple outbreaks. Additionally, there were 22 possible raw milk outbreaks investigated. These outbreaks occurred exclusively in a single county (100%) and the majority (82%) were from a private farm.

CONCLUSIONS: Raw milk outbreaks comprise a significant portion of foodborne investigations in Pennsylvania. Given the disproportionate volume of outbreaks, the fact that most implicated dairies were permitted, and multiple outbreaks associated with the same dairy, additional control strategies are needed.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Food Safety; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	keeklin@pa.gov
Presenting Author(s)	Kelly E Kline
Institution Affiliation	Pennsylvania Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11059
Abstract Type	Quick
Abstract Title	Shigellosis at a Wedding — Oregon, 2018

Abstract

BACKGROUND: On August 13, 2018, Oregon Health Authority received reports of gastroenteritis among persons attending a wedding, including a woman aged 92 years who was hospitalized. The Oregon State Public Health Laboratory (OSPHL) identified *Shigella flexneri* type 3a in stool samples. In the United States, <3% of *S. flexneri* are type 3a; foodborne shigellosis outbreaks are uncommon. We investigated to determine the cause of the outbreak and prevent further transmission.

METHODS: We performed a cohort study by emailing surveys to wedding attendees, asking about exposures and illness; the bride provided addresses. A presumptive case was diarrhea ≤ 5 days in an attendee; confirmed cases had *S. flexneri* isolation from stool. Multnomah County Health Department and Oregon Department of Agriculture (ODA) officials inspected the caterer and venue, respectively. Specimens were tested at OSPHL and ODA.

RESULTS: Of 263 wedding attendees, 198 (75%) responded; 107 (54%) cases were identified, including 23 (21%) confirmed. Patient age range was 2–93 years; 60 (56%) were female. Eighty-four (90%) of 93 patients with onset information reported illness 12–72 hours after the wedding. Among 107 patients, 91 (85%) reported fever, 51 (48%) vomiting, and 49 (46%) bloody diarrhea. Of 106 patients, healthcare was sought by 57 patients, and 10 were hospitalized; none died. No additional cases were reported. Only asparagus consumption was associated with illness; 64% of those consuming asparagus versus 12.5% of those who denied it became ill (relative risk: 5.1; 95% CI: 2.0–12.9). The caterer served the same foods at other events that day without illnesses reported. No food handling violations were observed during the caterer’s inspection. A contamination source was not identified. No related outbreaks were reported.

CONCLUSIONS: The epidemic curve indicated a point source, and asparagus was implicated. Poor food-handler hygiene may be the most likely cause of contamination.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	wny6@cdc.gov
Presenting Author(s)	Steven I Rekant
Institution Affiliation	Oregon Public Health Division EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	10678
Abstract Type	Quick
Abstract Title	Stec O157:H7 Outbreak in Childcare Provides Opportunity for Infection Control Education

Abstract

BACKGROUND: During May 2018, the Knox County Health Department (KCHD) noted an increase in laboratory-confirmed Shiga toxin-producing *Escherichia coli* (STEC) cases. Preliminary investigation identified additional cases reporting attendance to Childcare Facility A. KCHD worked closely with the Tennessee Department of Health to interview cases, ensure clinical isolates were collected and sent to the state public health laboratory, conduct an environmental investigation, and consider any possible exposures and/or links between cases.

METHODS: Active case finding was conducted using enrollment rosters and all persons reporting symptoms were interviewed via telephone using a standard questionnaire. Facility visits were conducted to assess infection control practices, interview and educate staff, and collect environmental samples from both the interior classroom areas and the onsite goat paddock. Pulsed-field gel electrophoresis (PFGE) and whole genome sequencing (WGS) were performed on isolates obtained from clinical and environmental samples.

RESULTS: A total of five confirmed cases, four probable cases, and one secondary case were identified during the investigation. Of confirmed and probable, cases had an average age of 1.7 years and five cases were male. Two cases were hospitalized, and one case developed HUS. All cases reported diarrhea; three cases reported bloody diarrhea during illness. All cases reported one common exposure: attendance at Childcare Facility A. One case returned to the facility while symptomatic prior to public health approval. Clinical specimens from five cases yielded STEC O157:H7 STX 2 with indistinguishable PFGE patterns. Four of 26 environmental samples, three from goat feces, also yielded the outbreak strain of *E. coli* O157:H7. All clinical and environmental isolates were highly related by WGS.

CONCLUSIONS: An outbreak of *E. coli* O157:H7 associated with attendance at Childcare Facility A was identified. Epidemiologic evidence implicating the facility and its goat paddock was supported by the environmental investigation and the isolation of the outbreak strain from goat manure and clinical specimens. Lack of communication and enforcement of exclusion criteria for ill childcare attendees could have contributed to transmission in this setting. Recommendations related to infection control policy were made, and a quick guide to exclusion criteria was created and distributed widely to childcare facilities in the county. This outbreak created opportunity to provide infection control education where it is greatly needed. The KCHD intends to expand its efforts to this setting in the future.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Infection Control; Local Epidemiology; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	becky.meyer@knoxcounty.org
Presenting Author(s)	Rebecca Ann Meyer
Institution Affiliation	Knox County Health Department Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Testing 1-2-3: Benefit of Water Testing during the Investigation of Three Large Waterborne Outbreaks, Tennessee, 2017-2018

Abstract

BACKGROUND: Tennessee Department of Health (TDH) officials investigated three large waterborne outbreaks responsible for over 800 illnesses during 2017-2018. TDH utilized water sampling and testing during responses. We describe the benefits and limitations of water sampling during these three outbreaks.

METHODS: Water sources identified during the investigations were sampled, including wells, recreational water features and building plumbing. Samples were collected and transported to the state public health laboratory. Testing varied by outbreak and included: coliform and *Escherichia coli* (*E. coli*) enzyme substrate test, polymerase chain reaction, gastrointestinal pathogen panel and bacterial culture. Water testing results were incorporated into the investigation to complement epidemiologic, environmental and clinical results.

RESULTS: During June 2017, we sampled recreational and building water to investigate a large Legionnaires' disease outbreak at a hotel. *Legionella* bacteria were detected in pool water and a pool sand filter and *Legionella pneumophila* was isolated from the hot tub sand filter. Ninety-two ill persons were identified, including one death. Ill persons were significantly more likely to have spent time in or around the aquatics area (pool, hot tub) than well people (odds ratio [OR] = 11.2; 95% confidence interval [CI] = 3.4-37.4). Environmental and epidemiologic results converged implicating the aquatics area as the outbreak source. During July 2018, we sampled untreated well water during a multi-pathogen outbreak investigation at a zip line facility. A total of 693 ill persons with confirmed or suspected norovirus or enteropathogenic *E. coli* (EPEC) illnesses were identified. Water samples tested positive for total coliforms, EPEC and *E. coli* O45. Water testing supported the epidemiologic finding that ill persons were more likely to have consumed onsite water than well persons (OR=4.4, CI=3.1-6.3). During August 2018, we sampled untreated well water during a multi-pathogen outbreak at a restaurant and kayak rental facility. Eighty-nine ill persons with gastrointestinal illnesses were identified. Clinical testing detected norovirus, EPEC, enterotoxigenic *E. coli* and *Clostridium difficile*. Water tested positive for total coliforms and *E. coli*, but samples for additional pathogen-specific tests were not collected. Epidemiologic and environmental results converged to indicate water contamination.

CONCLUSIONS: Water testing supported three large waterborne outbreak investigations by detecting contamination and outbreak pathogens in implicated water sources. Water testing complemented the epidemiologic, environmental and clinical testing results. Limited training and staff availability for general and pathogen-specific water sample collection were primary barriers to water testing. Expanding capacity and training for water sampling could improve future waterborne outbreak investigations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Waterborne Disease; Outbreaks; Water
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jane.yackley@tn.gov
Presenting Author(s)	Jane Yackley
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11286
Abstract Type	Quick
Abstract Title	Using Student Interviewers to Enhance Capacity for Salmonellosis Investigations in Texas

Abstract

BACKGROUND: Detailed interviewing of case-patients with foodborne conditions is the best way to identify contaminated foods and exposures that may have caused illness. However, not all health departments have sufficient capacity to interview all case patients. In Texas, one of the most common foodborne pathogens is *Salmonella*, with more than 5,000 reported cases annually. Health departments interview case patients when clusters or outbreaks are identified but some report they lack sufficient personnel or resources to interview all sporadic cases of salmonellosis. The Texas Department of State Health Services, Emerging and Acute Infectious Disease Branch, created a student interview team pilot project to improve statewide capacity for interviewing *Salmonella* case patients.

METHODS: Each student was trained in foodborne illness interviewing and completed practice interviews with staff members. After the practice interview, students received a debriefing session to discuss strengths, weaknesses and issues. Students also conducted their first interviews under supervision. Finally, the students received training about patient confidentiality and the Health Insurance Portability and Accountability Act (HIPAA) of 1996. Confirmed cases were referred by a regional health department that was short-staffed. Students used a shortened *Salmonella* interview form to conduct telephone interviews. Completed forms were reviewed for accuracy and completeness, then scanned and emailed securely back to the region.

RESULTS: A total of 37 cases of confirmed *Salmonella* infections were referred to the student team between late June and mid-August 2018. Of those, 18 interviews were successfully completed, 11 cases were unable to be reached, and eight patients refused. Overall, the student team made 87 attempts to contact case patients, for an average of 2.4 attempted phone calls per case. At least three attempts were made to contact each patient and some cases received more than three attempts if the case indicated they were willing to do the interview the next day or at another time. On average, successful interviews were completed within an average of 2 days from first attempt at contact with the case (range 0 – 10 days).

CONCLUSIONS: This pilot project provided a viable option for offering additional interviewing capacity to health departments with insufficient staff or resources. Future plans include a paid internship for student interviewers during the fall and spring semesters; expanding the project to other local and regional health departments across Texas; development of a web-based survey tool; creation of a student interviewer training manual; and allowing the students to work after-hours and/or weekends.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiology Capacity; Foodborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	vivienne.heines@dshs.texas.gov
Presenting Author(s)	Vivienne Heines
Institution Affiliation	Texas Department of State Health Services State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Using Whole Genome Sequencing to Uncover a Prolonged Multistate <i>Shigella Sonnei</i> Cluster, United States, 2017 — 2018

Abstract

BACKGROUND: An estimated 500,000 cases of shigellosis occur annually in the United States. Although the majority of shigellosis cases are sporadic, i.e., not cluster-associated, some are involved in single state or multistate clusters. PulseNet, the national network for foodborne disease surveillance, currently uses pulsed-field gel electrophoresis (PFGE) to detect multistate *Shigella* clusters. However, whole genome sequencing (WGS) of distinct clusters occurring in 2017 and 2018 demonstrated that PFGE alone was insufficient to detect a prolonged, multistate *Shigella sonnei* cluster primarily among men who have sex with men (MSM).

METHODS: PulseNet detects multistate clusters of *Shigella sonnei* by comparing the frequency of uploaded PFGE patterns to the national baseline for that PFGE pattern. Case-patients whose isolates had matching PFGE patterns were interviewed to determine demographic characteristics and exposures of interest in the seven days before illness onset, such as travel and sexual activity. Additional characterization of selected isolates was performed using WGS with high quality single nucleotide polymorphism (hqSNP) analysis to assess relatedness between isolates.

RESULTS: Four clusters were detected using PFGE from August 2017 to October 2018 and were initially investigated as distinct clusters because they had different PFGE patterns. A total of 222 cases from the four clusters were reported by 26 states with the most in CA (46, 21%), CO (24, 11%), and MO (23, 10%). A majority of the case-patients from these clusters were young to middle-aged men (overall median age: 44 years, range: 3-83 years; overall percent male: 95%, range: 92-96%). Across the four clusters, 55 (90%) of the 61 case-patients for whom MSM status was known were reported as MSM. Finally, domestic or international travel was reported for 25 (40%) of the 63 case-patients for whom recent travel history was known. Out of the 177 isolates from four PFGE clusters sequenced, 168 were closely related, clustering within 23 SNPs. The remaining nine isolates formed a separate single state clade.

CONCLUSIONS: WGS demonstrated that four seemingly different clusters by PFGE were likely caused by the same *S. sonnei* strain. PulseNet's transition from PFGE to WGS may prove beneficial to detecting larger multistate *Shigella* clusters as we learned from this investigation. Therefore, state and local health departments should continue allocating WGS resources to detect *Shigella* clusters, particularly given the anticipated resource constraints and competing pathogen priorities during the WGS transition.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Surveillance; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ksf6@cdc.gov
Presenting Author(s)	Zachary A. Marsh
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Best Practices for Identifying, Communicating with, and Surveying Clinical Laboratories

Abstract

Key Objectives:

The objective of this roundtable is to share methodology, successes, and challenges in routinely surveying clinical laboratories to assess diagnostic testing practices. Moderators from the Foodborne Diseases Active Surveillance Network (FoodNet) will share practices used in the 10 FoodNet sites, and participants will be encouraged to share their own practices. Discussion topics will include identifying clinical laboratories, communicating with clinical laboratory staff, developing and implementing laboratory surveys, and using the data.

Brief Summary:

The increased development and availability of culture-independent diagnostic tests (CIDTs) and uptake by clinical laboratories continue to change the landscape of enteric pathogen detection. In 2012, FoodNet implemented a standardized, pathogen-specific survey of clinical laboratories in FoodNet catchment to capture onsite testing protocols, primary detection methods, and specimen submission practices. The survey is conducted for *Campylobacter*, *Cyclospora*, *Listeria*, *Salmonella*, Shiga toxin-producing *E. coli*, *Shigella*, *Vibrio*, *Yersinia*, and norovirus. These surveys help address gaps in surveillance data, encourage specimen submission, and anticipate changes in surveillance. Identifying clinical laboratories for surveys has been challenging as testing is now available where it previously was not. In several FoodNet sites, CIDTs are now being used by outpatient clinics. Traditionally, outpatient clinics are not included in these surveys. During the roundtable, we will discuss ways to identify these types of practices and develop communication channels between the laboratories and public health. Additionally, at-home nucleic acid-based microbiome tests are newly available and can be ordered directly by consumers or remotely by providers. Because these tests are not typically used by a facility for diagnostic purposes and are not FDA-approved, they present challenges for tracking diagnostic testing practices and ensuring reporting of pathogens under surveillance. Participants can share their experiences with these tests and we will identify next steps needed in determining how to incorporate new diagnostic testing methods into surveillance. In upcoming cycles, the FoodNet laboratory survey will be conducted in conjunction with laboratory surveys for other Emerging Infectious Disease Programs. This will streamline data requests to clinical laboratories, which may increase their willingness to respond. We will also discuss opportunities for collaboration and best practices for communicating with clinical laboratories and creating standardizing surveys. Standardized surveys within FoodNet have allowed us to monitor the transition to CIDTs on a broader level as well as inform changes in other non-FoodNet sites that are served by the same laboratories.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Surveillance; Foodborne Disease
Consider for Different Presentation?	No
Presenting Author Email Address(es)	elisha.wilson@state.co.us; uyk1@cdc.gov
Presenting Author(s)	Elisha Wilson; Ellyn Marder
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Novel Approaches in Multistate <i>Shigella</i> Cluster Investigations

Abstract

Key Objectives:

- Provide an update on recent multistate shigellosis clusters.
- Discuss successes and challenges of investigating multistate shigellosis clusters at the state, local, and federal level.
- Discuss new approaches in case follow up, including the *Shigella* hypothesis generating questionnaire.

Brief Summary:

An estimated 500,000 people become sick with shigellosis annually in the United States. Populations at particular risk for shigellosis include children, travelers, individuals with weakened immune systems, and gay, bisexual, and other men who have sex with men. Shigellosis is typically self-limiting; however, treatment is an option for severe cases and immunocompromised individuals. There is growing concern about drug resistant shigellosis, particularly multidrug resistance, which can result in more severe illness and potentially worse outcomes. It is critical that effective prevention and control efforts be developed and applied at the state, local, and federal level. State and local health departments, researchers, and CDC engage in a range of public health activities to prevent and control shigellosis. These include surveillance, cluster and outbreak investigations, health promotion communications development, behavioral science, and research. Activities related to shigellosis cluster and outbreak investigations, particularly multistate clusters, can be especially challenging. These clusters are challenging to investigate because known cases occur sparsely over space and time, are spread by person-to-person transmission, and represent only a fraction of the true number of cases. The purpose of this roundtable is to provide a forum for state and local health departments, researchers, and CDC to share experiences, challenges, and successes in *Shigella* multistate investigations. Participants will discuss current trends in large multistate clusters and novel approaches to better detect, characterize, and disrupt these clusters. This includes use of behavioral science strategies for prevention and control of shigellosis. Feedback will be sought on the newly developed *Shigella* hypothesis generating questionnaire and the potential for future investigation approaches.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	Behavioral Health; Enteric Infectious Diseases; Outbreaks
Presenting Author Email Address(es)	No
Presenting Author(s)	ksf6@cdc.gov
Institution Affiliation	Zachary A. Marsh
	Centers for Disease Control and Prevention
	CDC

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Preventing Norovirus Transmission in Schools.

Abstract

Key Objectives:

- Quantify the impacts norovirus outbreaks have on schools and the community at large
- Recognize the value of disinfection BEFORE outbreaks occur
- Identify a low-cost intervention for norovirus outbreaks in schools.

Brief Summary:

Norovirus outbreaks in schools have significant impacts on school operations, and are costly. Approximately 92% of outbreaks are non-foodborne. Contact with contaminated fomites is a known route of norovirus transmission. Two epidemiological studies assessed the impact of disinfecting wipes used to disinfect desks after school dismissal over a seven week period. High touch objects were sampled weekly for human norovirus using PCR (polymerase chain reaction). The first study was conducted in 3rd and 4th grade classrooms at the same school. Three served as a control. The other three were treated with disinfecting wipes. Absenteeism records for illness were kept for both classrooms. Children in control classrooms were 2.32 times more likely to be absent due to illness than children in intervention classrooms ($p = 0.026$, 95% CI=1.03–5.28, odds ratio). Norovirus was commonly detected in non-treated classrooms. We then conducted a more defined study in which 1) impact of disinfecting wipes on absenteeism due to gastroenteritis was determined, 2) monitoring wipes' usage ensured compliance 3) use of qPCR quantified concentration of noroviruses on fomites. This cluster-randomized trial studied 3rd through 5th grade classrooms over a period of eight weeks (March–May) and adjusted for family size, race, health status, and home sanitizer use. The adjusted absenteeism rate for gastrointestinal illness was significantly lower in the intervention-group subjects compared with control subjects (Rate Ratio: 0.91, 95% confidence interval (CI): 0.79–0.94; $p < 0.01$). Norovirus was found less frequently on surfaces in intervention classrooms compared with control classrooms (9% vs 29%; $p < 0.01$). Concentration of noroviruses on fomites was 90% less in the classrooms using disinfecting wipes. Use of disinfecting wipes with EPA registration for norovirus on key surfaces in elementary school classrooms is effective in reducing norovirus exposures at school, resulting in lower absenteeism. Information on this easy, affordable intervention can be relayed to schools before and following outbreaks and as part of routine interactions and inspections.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	School Health; Enteric Infectious Diseases; Infection Control
Presenting Author Email Address(es)	No
Presenting Author(s)	JudiA@KroegerPR.com
Institution Affiliation	Charles P. Gerba
	University of Arizona
	Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11146
Abstract Type	Breakout
Abstract Title	Candida Auris Colonization in the Community Setting — New York City (NYC), 2017-2018

Abstract

BACKGROUND: *C. auris* is a multidrug resistant yeast that can spread in healthcare settings and cause invasive infections. It emerged in NYC in 2016. In healthcare settings, most patients remain colonized for months, but it is unclear if patients remain colonized after discharge. NYC Department of Health and Mental Hygiene (DOHMH) piloted a case management program for people colonized with *C. auris* in the community setting to alert healthcare facilities where patients may seek care and monitor colonization status longitudinally.

METHODS: Starting October 4, 2017, New York State Department of Health referred people colonized with *C. auris* to DOHMH when they were informed of community discharges from healthcare facilities. DOHMH case managers collected clinical information through patient interview and medical record review and informed the patient's providers and healthcare facilities about the patient's *C. auris* status and infection control needs. Case managers coordinated colonization testing with the patient's providers every 3 months. Colonization testing included swabs of axillae, groins and nares and when applicable a culture of previously *C. auris* positive body site. If *C. auris* was not detected, testing was repeated at least one week later to confirm results.

RESULTS: By October 16, 2018, DOHMH received 59 referrals, performed 33 patient interviews, and sent 89 reports to health care facilities regarding a patient's *C. auris* status. Twenty-nine (49%) patients had at least 2 colonization tests after initial *C. auris* diagnosis, of whom 9 (31%) no longer had *C. auris* detectable on 2 consecutive assessments.

CONCLUSIONS: An ongoing pilot case management program supports infection control for people colonized with *C. auris* by informing a person's healthcare facilities of needed infection control. Some people no longer had *C. auris* detectable on repeat colonization testing. Continued data collection is needed to identify factors associated with persistent *C. auris* colonization.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Emerging Infections; Healthcare Associated Infections (HAI); Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nqw9@cdc.gov
Presenting Author(s)	Genevieve Bergeron
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	11547
Abstract Type	Breakout
Abstract Title	Challenges and Successes in Investigating a Concurrent Outbreak of Invasive <i>Escherichia coli</i> K1 and Methicillin-Resistant <i>Staphylococcus Aureus</i> (MRSA) in a Hospital Neonatal Intensive Care Unit (NICU), Kansas 2017

Abstract

BACKGROUND: In November 2017, the Kansas Department of Health and Environment (KDHE) notified Centers for Disease Control and Prevention (CDC) of three invasive *E. coli* K1 infections and an increase in MRSA colonization and infection within one NICU. Cohorting and MRSA decolonization were recommended to prevent further transmission; concern remained that infants colonized with *E. coli* K1 without signs of infection could be sources of transmission. Identifying specific *E. coli* strains using traditional methods is challenging. CDC's novel approach combined whole genome sequencing (WGS) with culture-independent metagenomic sequencing (CIMS) to identify colonized infants.

METHODS: In the *E. coli* K1 outbreak, a case was defined as *E. coli* K1 isolated from an infant in the NICU from September 2017 to December 2017. NICU infants were routinely screened for MRSA colonization; therefore, in the MRSA outbreak a case was defined as infection or colonization in an infant in the NICU occurring above 12-month baseline rate. WGS of *E. coli* K1 isolates and MRSA isolates was performed. To inform cohorting, stool specimens from non-case-patients with close contact with infants with *E. coli* K1 underwent CIMS for microbiome analysis to detect whether the outbreak strain was present. KDHE staff conducted an on-site assessment of infection prevention and control.

RESULTS: Five infants in the NICU met the *E. coli* K1 outbreak case definition and 11 infants met the MRSA outbreak case definition. Two infants had both organisms isolated. Infants with *E. coli* K1 were hospitalized for a median of 70 days (55-117 days) and infants with MRSA were hospitalized a median of 29 days (4-161 days). All isolates were *E. coli* O75:K1:H5 with *bla*_{CMY-2} gene, were identical by MLST, and differed by 0-1 SNPs. CIMS identified one infant that was colonized with the outbreak strain. MRSA isolates from seven infants differed by 0-13 SNPs; four were unrelated by WGS and likely represent sporadic MRSA infection or colonization. KDHE observed poor hand hygiene compliance among ancillary staff which likely contributed to person-to-person transmission. Cohorting recommendations were not strictly followed and MRSA decolonization was not implemented. After no additional *E. coli* K1 cases and MRSA monthly incidence returned to baseline, the outbreaks ended in December 2017.

CONCLUSIONS: The facility's poor adherence to recommendations potentially prolonged transmission during the concurrent outbreaks. However, our novel approach combining WGS and CIMS can be useful in outbreak response and infection control efforts by effectively identifying colonized patients that could serve as potential reservoirs.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Justin.Blanding@ks.gov
Presenting Author(s)	Justin Blanding
Institution Affiliation	Kansas Department of Health and Environment State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Establishing a Baseline of Infection Prevention Practices and Carbapenemase Producing Organisms (CPO) Colonization Rates in Tennessee Skilled Nursing Facility Ventilator Units—Tennessee, 2018–2019

Abstract

BACKGROUND: Carbapenemase Producing Organisms (CPO), including carbapenemase-producing carbapenem-resistant Enterobacteriaceae (CP-CRE) are a public health threat of increasing concern in healthcare settings that provide care for medically complex populations. Data from other states suggest that residents of ventilator skilled nursing facilities (vSNFs) appear to be at increased risk for CPO. Facilities that care for these patients can potentially serve as amplifiers for infection and colonization with multidrug-resistant organisms. Point prevalence surveys for CPOs have been limited in Tennessee’s long term care facilities. A baseline assessment of CPO colonization and infection control programs in this setting is needed to inform future prevention and control efforts.

METHODS: All eleven licensed Tennessee vSNFs were recruited for on-site infection control assessments, followed by colonization screening for CPOs of residents on the ventilator unit. Tennessee Department of Health (TDH) staff performed assessments specific to ventilator units and community areas such as, dining room and rehabilitation gym. Facility observations were collected in REDCap by TDH staff. Rectal swabs were collected by facility staff. Testing of swabs was performed using reverse transcription-polymerase chain reaction (RT-PCR) on the Cepheid Gene-X at the Southeast Antimicrobial Resistance Laboratory Network (ARLN) in Nashville, Tennessee.

RESULTS: Infection control assessments have been completed at seven of eleven facilities. Common infection control gaps included lack of infection control risk assessments, low compliance with hand hygiene, limited hand sanitizer dispensers and hand washing sinks, lack of standardized surveillance processes, inadequate use of signage for transmission based precautions, low compliance with oral care of ventilated residents, lack of training programs for environmental cleaning and no oversight of contracted services offered at facilities. Colonization screening has been completed at four of eleven facilities with screening currently scheduled at one of the seven remaining facilities. 115 residents have been screened to date. Two of 115 (2%) rectal swabs were PCR positive for *Klebsiella pneumoniae* Carbapenemase (KPC). Eight (7%) residents refused screening.

CONCLUSIONS: This project highlights the need to improve various infection prevention practices in Tennessee vSNFs. We continue to work proactively with these vSNFs to address identified gaps. Facilities receive ongoing infection prevention support and resources. Although screenings will continue over the next two months, so far we have seen lower rates of colonization than expected. This project establishes a baseline of the prevalence of CPO colonization among residents in Tennessee vSNFs.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Infection Control; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	sandra.pena@tn.gov
Presenting Author(s)	Sandra Adrienne Peña
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Fatal <i>Acinetobacter Baumannii</i> Complex-Associated Septicemia Following Transfusion of Bacterial Contaminated Platelets

Abstract

BACKGROUND: In May 2018, the American Red Cross (ARC) notified the Utah Department of Health (UDOH) of a patient that died of *Acinetobacter baumannii* complex-associated septicemia following platelet transfusion. Platelet products pose an increased infection risk because they cannot typically be refrigerated, but are stored at room temperature, and routinely come into contact with non-sterile surfaces. Potential bacterial contamination of platelets from the exterior of the bag is extremely rare, so these events necessitate a multifaceted investigation.

METHODS: Investigators worked with the transfusion facility to review patient charts and assess transfusion documentation for protocol deviations. The investigation team worked with the ARC and transfusion facility to conduct infection control assessments, observations, and environmental sampling. The donor was also screened for urine, rectal and skin colonization. All samples were cultured by the Utah Public Health Laboratory (UPHL) for organism isolation and identification. Whole-genome sequencing (WGS) was conducted at UPHL to determine relatedness between patient and environmental bacterial isolates.

RESULTS: Patient record and transfusion documentation reviews indicated platelet contamination likely happened prior to the transfusion event based on the time between transfusion and symptom onset (~1 hr). The investigation revealed no deviations in blood supplier or hospital procedures, and donor screening swabs tested negative for *Acinetobacter*. The initial platelet bacterial surveillance sample demonstrated no growth. The co-collected platelet component was re-sampled (interior and exterior), with no bacterial growth detected. Environmental sampling at both the ARC and transfusing facility revealed environmental contamination of multiple locations which came into contact with platelets (receiving station at the transfusing facility, and platelet agitators at both facilities). A rare species of the *Acinetobacter baumannii* complex was identified from patient samples, residual platelet component and environmental samples. WGS and phylogenetic analysis indicated all isolates were highly related and nearly identical at the nucleotide level. Infection control assessments revealed that the transfusing facility did not have a routine cleaning schedule in place for platelet agitators. We determined there were no routine cleaning recommendations for platelet agitators in transfusion facilities, representing a significant gap in blood product infection control recommendations.

CONCLUSIONS: Bacterial contamination of platelets, although rare, can have severe consequences. Efforts should be taken to reduce potential bacterial contamination of the exterior surfaces of platelet bags. We recommend national infection control groups consider implementing standardized cleaning guidelines for platelet processing equipment in transfusion facilities. Facilities with blood banks should implement routine cleaning schedules for all blood product processing equipment.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	amandarsmith@utah.gov
Presenting Author(s)	Amanda R Smith
Institution Affiliation	Utah Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Improving Infection Control through Non-Regulatory Infection Control Assessments in Long-Term Care Facilities in Orange County, Florida

Abstract

BACKGROUND: Infection control (IC) and prevention aim to inhibit the transmission of healthcare-associated infections. Recently, regulatory agencies have developed regulations to enforce IC best practices in nursing homes and assisted living facilities (ALFs). From December 2017 to June 2018, lack of an infection control and prevention program was the most common citation in nursing homes reported by the Agency for Health Care Administration. To close this gap, the Department of Health in Orange County (DOH-Orange) aimed to conduct 15 IC assessments within one year and evaluate its efficacy in changing IC practices.

METHODS: From January 2017 to November 2018, 27 nursing homes and 4 ALFs had outbreaks of infectious diseases. Recruitment of 23 facilities (5 facilities had ≥ 1 outbreak) began March 2018. Assessments were conducted using the Infection Control Assessment and Response (ICAR) tool developed by the Centers for Disease Control and Prevention.

RESULTS: From March to December 2018, ICARs were conducted at 3 ALFs and 8 nursing homes. Of the 11 facilities, 9 (81.8%) were able to identify a specific person responsible for leading the IC program and activities, and of those 100% provided documentation of IC training by the state or recognized professional societies. All nursing homes (100%) and one ALF (33%) had written IC policies/procedures. Annual training on hand hygiene and personal protective equipment (PPE) was conducted in 66% of ALFs and 87.5% of nursing homes. Only one ALF required hand hygiene competency validation. Among nursing homes, 75% and 37.5% required return demonstrations for hand hygiene and PPE competency, respectively, after each training. Only 50% of nursing homes conducted audits (monitoring and documenting) on adherence to both hand hygiene and PPE, whereas 33% and 0% of ALFs conducted audits on adherence to hand hygiene and PPE, respectively.

CONCLUSIONS: To evaluate the facility's uptake of recommendations provided by DOH-Orange, one-month follow up calls are being conducted. A post-test survey will be distributed at the end of the project to evaluate the ICAR tool's efficacy in improving IC practices. The ICAR assessment is a sustainable tool that increases collaboration between healthcare facilities and local health departments. Future goals aim to utilize the ICAR assessment as a prequel to regulatory visits by state agencies, to improve IC policies/procedures and decrease IC citations. Continuing efforts will be made to build partnerships between local health departments, regulatory agencies, and healthcare facilities to strengthen IC practices for the safety of residents and healthcare workers.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Risk Assessment
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	danielle.walden@flhealth.gov
Presenting Author(s)	Danielle L. Walden
Institution Affiliation	Florida Department of Health Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Infection Control Assessments in Response to Novel/Targeted Multidrug-Resistant Organisms: Addressing Identified Gaps across the Continuum of Care in the State of Florida, 2018

Abstract

BACKGROUND: The field of public health is continuously faced with new challenges despite rapid advancements in medical knowledge and health practices. Microbes that were previously sensitive to treatment are becoming increasingly resistant to antibiotics. Florida's Health Care-Associated Infection (HAI) Prevention Program has been actively responding to contain transmission of novel/targeted multidrug-resistant organisms (MDROs). During 2018, we responded to a total of 27 novel/targeted MDROs, of which 16 responses warranted an infection control assessment and response (ICAR) using the Centers for Disease Control and Prevention ICAR form. Throughout our ICAR assessments we have identified consistent gaps across the continuum of care by collecting data on measurable indicators. This data is used to formulate infection control trainings for health care facilities across our state to address the identified gaps.

METHODS: For each ICAR assessment, we conduct a representative sample of hand hygiene and personal protective equipment (PPE) observations at each facility by using "My 5 Moments of Hand Hygiene" method from the World Health Organization. All observations are recorded on iScrub Lite mobile phone application (version 1.5.3, 2018, SwipeSense, Inc.). Adherence rates are aggregated by discipline type and opportunity type (e.g., "My 5 Moments of Hand Hygiene") in Microsoft Excel 2016. Additionally, during the administrative portion of the ICAR assessment, we determine the method each facility uses to evaluate competency following each hand hygiene and PPE training.

RESULTS: Out of the 16 ICARs, we collected representative samples of hand hygiene and PPE observations based on unit bed size for 13 facilities (acute-care hospitals=9; long-term acute-care hospitals=3; long-term care facility=1). Our analysis identified the lowest hand hygiene and PPE adherence rates occur during the "after body fluid exposure risk" opportunity (median hand hygiene rate: 55%, range: 0-80%; median PPE rate: 34%, range: 0-61%). Physicians and respiratory therapist had the lowest hand hygiene and PPE compliance rates (physician compliance rate=70%; respiratory therapist compliance rate=57%). Out of the 13 ICARs conducted, 15% required return demonstration of hand hygiene and PPE competency; 69% of facilities provide hand hygiene and PPE training through computer-based modules.

CONCLUSIONS: As our MDRO responses increase, our program aims to mitigate fundamental infection control gaps to decrease the risk of horizontal transmission. The consistency toward passive training and lack of return demonstration of competency may directly relate to the deficiencies identified in hand hygiene and PPE compliance. These findings provide us with ample opportunities to provide awareness, education, and behavior changes across the continuum of care.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infection Control; Healthcare Associated Infections (HAI); Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	danielle.rankin@flhealth.gov
Presenting Author(s)	Danielle A. Rankin
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11314
Abstract Type	Breakout
Abstract Title	Injection and Needle Use Practices By Healthcare Facility Type in Rural Jackson County, Oregon

Abstract

BACKGROUND: A 2015 investigation of an Oregon prolotherapy clinic delivering needle-based care was found to be placing patients at risk for infection with blood-borne pathogens as a result of unsafe injection practices. Following this identified risk, staff in the Healthcare-Associated infections (HAI) Program of the Oregon Health Authority (OHA) surveyed healthcare personnel (HCP) countywide across the continuum of care to identify potential future risks related to injection and needle use practice.

METHODS: We developed and distributed a survey by mail to all licensed HCP and businesses/facilities ("facilities") in Jackson County, Oregon that might provide care involving needles. We developed Oregon's Injection and Needle Safety Toolkit containing injection safety-related resources, which was distributed to all survey respondents. Responses were stratified by setting type: non-acupuncture inpatient; non-acupuncture outpatient; and acupuncture. Fisher's Exact Test comparisons and odds ratio calculations were conducted in SAS Version 9.4.

RESULTS: Respondents detailed the types of licensed HCP employed and procedures performed at the facility. Needle use and injection practices varied between inpatient and outpatient facilities. Nurses were less likely to administer the majority of injections in outpatient facilities than in inpatient facilities (OR 0.0445, 95% CI 0.0087 , 0.2280). Outpatient facilities were less likely to offer assistance to staff with substance use issues than inpatient facilities (OR 0.078, 95% CI 0.0089 , 0.6819). Outpatient facilities were more likely to report ever using vials of medication on more than one patient (OR 11.7857, 95% CI 1.3419 , 103.5147). Facilities reported interest in receiving education regarding topics including disease transmission and outbreaks associated with injection and needle use as well as needlestick injury.

CONCLUSIONS: The survey provided a number of tangible benefits for fostering injection safety in Oregon. Survey responses provided valuable insight regarding differences in injection and needle-based care by facility type as well as common practices involving needles and the types of licensed provider engaged in this care in one of Oregon's rural counties. The results of this survey are being used to develop targeted educational approaches and materials. Oregon's Injection and Needle Safety Toolkit has been viewed by 444 unique users since posting in May 2018. Furthermore, we have now established a network of providers who we can work with in future efforts focused on safe injection practices.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control; Rural Health
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	roza.p.tammer@state.or.us
Presenting Author(s)	Roza Tammer
Institution Affiliation	Oregon Public Health Division State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11075
Abstract Type	Breakout
Abstract Title	Multistate Outbreak of <i>Burkholderia cepacia</i> Complex Infections Among Non-Cystic Fibrosis Patients - United States, 2018

Abstract

BACKGROUND: *Burkholderia cepacia* complex (Bcc) is an emerging cause of healthcare-associated outbreaks often due to contamination of aqueous medical products. In February and March of 2018 a Pennsylvania hospital and a California hospital notified public health authorities of clusters of suspected healthcare-associated Bcc infections among non-cystic fibrosis patients, predominantly in intensive care units. Product testing at the Pennsylvania facility resulted in Bcc growth from cultures of a perineal skin cleanser from Manufacturer X, suggesting infections could be related to a widely distributed product warranting further investigation.

METHODS: A national call for clusters of Bcc recovery from cultures collected from non-cystic fibrosis patients was issued to assist case finding. Data were collected including lot numbers of aqueous products from Manufacturer X used at facilities reporting clusters and clinical data from affected patients. A confirmed case was a patient's first culture collected on or after November 1, 2017, yielding Bcc indistinguishable or closely related to the outbreak strain by molecular typing. A probable case was a patient's first culture collected on or after November 1, 2017, yielding Bcc with unknown strain type, from a patient who received care at a facility utilizing aqueous product from a master lot manufactured at Manufacturer X that tested positive for Bcc. CDC tested products for presence of Bcc and compared clinical and product Bcc isolates by pulsed-field gel electrophoresis (PFGE).

RESULTS: We identified 17 confirmed and 31 probable cases from 13 hospitals in 6 states. Culture site was reported for 43 of 48 cases and included the urogenital tract (27), respiratory tract (9), bloodstream (4), wound (4), and peritoneum (3). Four patients had multiple positive culture sites. Three lots of the skin cleanser from Manufacturer X grew Bcc on culture; the species identified was *Burkholderia cenocepacia*. PFGE identified that product isolates and clinical isolates from patients across states were indistinguishable or closely related. Manufacturer X voluntarily recalled the three lots of the skin cleanser which tested positive for Bcc.

CONCLUSIONS: Epidemiologic and laboratory evidence indicated this large multi-state outbreak of Bcc was due to contamination of a nonsterile skin cleanser. Recognition of clusters of Bcc infections at sites unusual for the pathogen (e.g., non-pulmonary Bcc) can suggest possible product contamination. Contamination of aqueous medical products, including hygiene products, can lead to infections among susceptible patients. Nonsterile, aqueous medical products should therefore be considered as a potential source of Bcc outbreaks in healthcare settings.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Health Care; Outbreaks; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	cwu0@cdc.gov
Presenting Author(s)	Matthew B Crist
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Positive Deviance Study for Timeliness of Mandated Reporting of Carbapenem-Resistant Enterobacteriaceae — Los Angeles County, 2017–2018
Abstract	BACKGROUND: In January 2017, Los Angeles County (LAC) hospitals were mandated to report carbapenem-resistant Enterobacteriaceae (CRE) infections. A November 2018 evaluation of CRE reporting revealed lengthy reporting delays (mean: 40 days) with substantial differences among facilities (mean: 8.8–143 days/facility). The Los Angeles County Department of Public Health (LACDPH) adapted the positive deviance methodology by qualitatively studying performance outliers to identify strategies that improve timeliness. METHODS: The National Healthcare Safety Network (NHSN) was queried for CRE cases reported in LAC during January 2017–September 2018. Reporting delays were calculated as difference between culture collection and report dates. Mean reporting delay and 95% confidence limits (CLs) were generated for each hospital. Positive outliers (POs) and negative outliers (NOs) were defined as hospitals with CLs higher or lower than the grand mean, respectively. A sample was created using maximum variation sampling ensuring heterogeneity for mean reporting delay, case volume, and number of infection preventionists (IPs). Semi-structured interviews were conducted with selected IPs to characterize reporting practices. RESULTS: We detected 2,907 CRE cases from 76 hospitals, and identified 45 POs and 15 NOs with CLs excluding the grand mean (43.5 days). Our sample included 13 POs and 6 NOs. IPs responded from 11 (24%) POs and 5 (33%) NOs. Interviews revealed no novel practices. Common workflow elements were similar between groups, including electronic laboratory notification (PO 82% and NO 80%) and automated NHSN entry (PO 18% and NO 20%). However, internal reporting targets differed between groups. Seven POs targeted reporting ≤5 days; all NOs intentionally batched reporting at least monthly. CONCLUSIONS: Our findings indicate hospitals can improve CRE reporting timeliness with workflow or practice changes alone. LACDPH is designing a campaign with hospital IPs to increase awareness of CRE reporting requirements. This study demonstrates how positive deviance methods can guide intervention design.
Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infectious Diseases; Antimicrobial Resistance; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	okl8@cdc.gov
Presenting Author(s)	Howard Chiou
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	10914
Abstract Type	Breakout
Abstract Title	Prescriber Adherence to <i>Clostridioides Difficile</i> Infection Treatment Guidelines, Minnesota 2013–2017

Abstract

BACKGROUND: In 2010, the Society for Healthcare Epidemiology of America (SHEA) and Infectious Diseases Society of America (IDSA) published clinical guidelines for *Clostridioides difficile* infection (CDI), with updates in 2018. SHEA/IDSA CDI clinical definitions were comprised of clinical presentation, white blood cell count (WBC), and serum creatinine level. Appropriate treatments for clinical infections were defined as follows: asymptomatic, no treatment; mild, metronidazole for 10-14 days; severe, vancomycin for 10-14 days; severe-complicated, vancomycin with or without metronidazole. We evaluated appropriateness of CDI antibiotic treatment in Minnesota during 2013-2017.

METHODS: An incident CDI case was defined as a positive *C. difficile* toxin or molecular assay on a stool specimen from a person without a positive *C. difficile* test in the prior eight weeks. During routine active surveillance, clinical presentation and treatment data were captured through medical record review. Creatinine levels, while included in the 2010 clinical guidelines, were not captured. CDI cases aged ≥ 18 years were assigned clinical infection severity: asymptomatic, no diarrhea documented or asymptomatic; mild, diarrhea with $\text{WBC} \leq 15,000/\mu\text{l}$; severe, diarrhea with $\text{WBC} > 15,000/\mu\text{l}$; and severe-complicated, documented megacolon and/or ileus. We defined treatment appropriateness as correct drug per 2010 SHEA/IDSA guidelines.

RESULTS: During 2013-2017, 3,042 incident adult CDI cases were reported: 284 (9%) asymptomatic, 2,368 (78%) mild, 256 (8%) severe, 50 (2%) severe-complicated, and 84 (3%) unknown. A total of 1,877 (62%) cases received appropriate CDI treatment: 28/284 (10%) asymptomatic (no treatment), 1,668/2,368 (70%) mild, 149/256 (58%) severe, and 32/50 (64%) severe-complicated. Though none was indicated, 249 (88%) asymptomatic cases were prescribed an antibiotic. Of these, 71 (20%) had a recurrent positive test with no clinical symptoms, and 57 (80%) asymptomatic patients received a second antibiotic course. Of the 170 severe cases that received metronidazole, 11 (6%) had recurrent positive tests. Although 30% (17/56) of severe-complicated cases received metronidazole without vancomycin, none had a documented recurrence. Of 1,023 patients receiving care at a hospital and 1,583 at a clinic, 557 (54%) and 1047 (66%) patients received appropriate treatment, respectively.

CONCLUSIONS: Over one-third of CDI cases are inappropriately treated, demonstrating a need for targeted education on appropriate CDI testing and treatment. The lack of data on creatinine might lead to overestimation of both mild cases and the rate of appropriately treated severe disease. Over- and incorrect prescribing of antibiotics might increase the chance of recurrence and increase overall CDI rates. Repeat analysis could assess uptake of the updated 2018 SHEA/IDSA guidelines.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	emma.leof@state.mn.us
Presenting Author(s)	Emma Leof
Institution Affiliation	Minnesota Department of Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11615
Abstract Type	Breakout
Abstract Title	VIM-Crpa in Lubbock, Texas: Conducting the First Antibiotic Resistance Laboratory Network Multi-Site Epi-Aid in the United States

Abstract

BACKGROUND: The Texas Department of State Health Services (DSHS) Antibiotic Resistance Laboratory Network (ARLN) notified the Region 1 Healthcare-Associated Infections (HAI) Epidemiologist of the first four cases of Carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) positive for the carbapenemase VIM, or Verona Integron-Mediated Metallo- β -lactamase, in August 2017. From January 2017 to July 2018, 76 cases of VIM-CRPA were identified through regional laboratories from across the entire United States. Facilities in Lubbock, Texas, voluntarily submitted certain isolates to the ARLN for antibiotic resistance mechanism testing. The DSHS ARLN has tested over 237 CRPA isolates from the Lubbock area and identified 27 cases of VIM-CRPA. The Lubbock isolates were from urine, sputum, wound, tissue, and respiratory sources. On October 8, 2018, the Centers for Disease Control and Prevention (CDC) began an Epi-Aid investigation in the city of Lubbock due to the continued positive results without an identifiable source. The Epi-Aid and ongoing investigation involved the CDC, the Region 1 HAI Epidemiologist, Texas DSHS, the City of Lubbock Health Department, and multiple healthcare facilities in Lubbock.

METHODS: During the Epi-Aid, medical records were reviewed for risk factors, and patients who received outpatient care were interviewed. Pulsed-field gel electrophoresis (PFGE) and whole genome sequencing (WGS) were performed on all VIM-CRPA positive isolates. Site visits were conducted at multiple healthcare facilities in Lubbock where case patients received healthcare; these visits included infection prevention assessments, consultations, and point-prevalence surveys to assess for the presence of VIM within the facilities. Point-prevalence surveys were implemented by obtaining specimens via rectal swabs from 265 patients in seven facilities.

RESULTS: 31 VIM-positive isolates have been identified from Lubbock from June 2017 to October 2018. PFGE revealed 15 unique patterns: seven isolates share a common pattern and two clusters of three isolates share other patterns. WGS showed that VIM-CRPA in Lubbock is unique to the region. Point-prevalence surveys resulted in no additional VIM-positive patients identified. Common infection control gaps identified included hand hygiene, environmental cleaning, and communication during transfers between healthcare facilities.

CONCLUSIONS: The VIM-CRPA outbreak in Lubbock is unique to the area and is characterized by genetically-related cases occurring across multiple closely-connected healthcare facilities. There is currently no identifiable reservoir. A regional containment strategy is being developed and implemented to further contain this outbreak, increase infection prevention across facilities in Lubbock and, upon success, decrease all multidrug-resistant organism prevalence and transmission.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Healthcare Associated Infections (HAI); Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	thi.dang@dshs.texas.gov
Presenting Author(s)	Thi Dang
Institution Affiliation	Texas Department of State Health Services State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Lightning
Abstract Title	Developing a Risk Score to Prioritize Hawaii Dialysis Facilities for State-Led Infection Control Intervention Activities

Abstract

BACKGROUND: Infections are the second leading cause of death among hemodialysis patients. The standard measure for healthcare facilities, excess bloodstream infections (BSI), may not completely describe infection risk and burden for dialysis facilities. The Hawaii Department of Health piloted a modified Targeted Assessment for Prevention strategy, which included additional infection control indicators beyond excess BSI, to identify dialysis facilities with the greatest potential to benefit from state-led infection prevention activities.

METHODS: We identified a list of metrics relevant to infection control in dialysis facilities from the National Healthcare Safety Network (NHSN) and Medicare's Dialysis Facility Compare data. These included census (patient-months), excess BSI, proportion of patients with central venous catheters, access-related BSI (ARBSI) rate, local access site infection (LASI) rate, number of patients with Hepatitis B and C, Dialysis Compare quality of patient care rating, hospitalization rate, and death rate. Each continuous metric was standardized to a Z-score using data from 25 NHSN-reporting dialysis facilities in Hawaii. Z-scores were summed across indicators to compute a total risk score for each facility.

RESULTS: Risk scores ranged from -9.1 to 13.4 (median, -0.15). The four facilities identified with the highest risk scores measured higher on indicators related to potential infection drivers compared with the four lowest ranked facilities: mean LASI rates per 100 patient-months (mean of highest ranked, 0.14 vs. mean of lowest ranked, 0.10), mean proportion of patients on catheters (0.18 vs. 0.11), and mean ARBSI rates per 100 patient-months (0.65 vs. 0.11). Additionally, patients of the four highest ranked facilities had worse outcomes compared with patients of facilities ranked in the four lowest: mean hospitalization rate per 100 patient-years (150.0 vs. 137.0) and mean death rate per 100 patient-years (21.5 vs. 19.2).

CONCLUSIONS: Expanding the standard assessment tool by including additional data elements allowed us to summarize facility performance and identify specified drivers of infection in Hawaii dialysis facilities. In contrast with traditional assessments, our approach offers a more comprehensive and specific assessment of infection drivers at the facility level to inform intervention development and targeting. Use of Z-scores based on a set of carefully selected dialysis-specific infection control metrics can be used to develop standardized summary risk scores which identify facilities of greatest need for infection control activities. Subsequent work can guide state-led efforts by focusing on designing targeted intervention strategies tailored to each of the facilities with the greatest risk of infection.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Epidemiologic Methods; Infection Control
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	audrey.brezak@doh.hawaii.gov
Presenting Author(s)	Audrey Brezak
Institution Affiliation	Hawaii State Department of Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11710
Abstract Type	Lightning
Abstract Title	First Investigation of Healthcare-Associated Legionnaires' Disease in Hawaii

Abstract

BACKGROUND: In June 2018 the Hawaii Department of Health (HDOH) initiated an investigation upon receiving reports of potentially healthcare-associated (HA) Legionnaires' Disease (LD) from a large Honolulu acute care hospital, Hospital A, which is supplied with water from a private well. HA-LD can cause substantial morbidity and mortality, although it had not been previously recognized in Hawaii. This investigation offered the first glance at etiologic agents of HA-LD in Hawaii, and insight into the hospital's and health department's preparedness to prevent, identify, respond to HA-LD.

METHODS: HDOH staff from various branches reviewed Hospital A's existing water management plan, conducted site visits, guided implementation of control measures including water use restrictions, and conducted case finding. Confirmed cases were classified using CSTE's confirmed case definition for Legionnaires' disease with symptom onset during May or June 2018 and inpatient stays at Hospital A the entire 10 days before onset date. Probable cases had inpatient stays for any period of the 10 days before onset date. A consultant collected environmental water samples, which were tested at a private laboratory. Positive results were retested at the Hawaii State Laboratories Division by Legiolert™, culture, MALDI-TOF, and PCR. Select isolates were sent to CDC for whole genome sequencing.

RESULTS: One confirmed case and one probable case were identified. *Legionella pneumophila* serogroup 2, identified via culture from a bronchial wash, was isolated from the confirmed case. The probable case was diagnosed by the urine antigen test, which only detects *L. pneumophila* serogroup 1 (LP1). Various species of *Legionella* were recovered from 16 different water outlets throughout Hospital A. The existing water management plan lacked detail on: target chlorine residual levels among the distribution system, specific response procedures for low chlorine residual, and documentation or reporting requirements. Whole genome sequencing revealed no match between the one clinical isolate and the environmental isolates.

CONCLUSIONS: LP1 causes the vast majority of LD cases. However, one of our two identified HA-LD cases was not LP1, and the environmental investigation revealed a diversity of *Legionella* species and serogroups which pose pathogenic potential. Our findings reveal the need to ensure future HA-LD investigations in Hawaii utilize laboratory testing methods sensitive to all *Legionella* species and serogroups. Additionally, our investigation highlighted that healthcare facilities should ensure their water management plans are both comprehensive and specific enough to prevent *Legionella* proliferation and transmission, and that a robust HA-LD outbreak investigation requires multidisciplinary expertise.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Outbreaks; Waterborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	caitlin.cook@doh.hawaii.gov
Presenting Author(s)	Caitlin Cook
Institution Affiliation	Hawaii State Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11371
Abstract Type	Lightning
Abstract Title	Improving Florida's Capacity to Respond to HAI Outbreaks

Abstract

BACKGROUND: Healthcare-associated infections (HAI) present critical challenges in the field of public health requiring professionals to respond timely and competently to HAI outbreaks. There is a lack of knowledge about the Florida Department of Health epidemiology staff's capacity to respond to HAIs. In this study, we aimed to understand staff's self-efficacy in their ability to 1) respond to HAI outbreaks, 2) identify and help address gaps in a facility's infection control (IC) program, 3) educate medical providers on HAI prevention and response, 4) conduct IC assessments (ICAR), and 5) investigate outbreaks involving contaminated medical equipment.

METHODS: Florida's HAI Prevention Program in collaboration with the Florida Department of Health in Orange County (DOH-Orange) conducted a cross-sectional survey in November 2017 and 2018. The "Certification in Infection Prevention and Control (CIC) Employee Assessment" was administered to epidemiology staff throughout the state of Florida, via SurveyMonkey. Results from respondents were aggregated and analyzed using Microsoft Excel 2016.

RESULTS: In our assessment, those who answered the self-efficacy questions (2017 n=103; 2018 n=53) "strongly agreed/agreed" that they felt confident in their ability to respond to an HAI outbreak (mean=70.3%), identify and help address gaps in a facility's infection control program (mean= 61.2%), and educate medical providers on HAI prevention and response (mean= 63.0%). Whereas, approximately one-third "strongly agreed/agreed" that they felt confident in their ability to conduct an infection control assessment (mean= 36.6%) and investigate an outbreak involving contaminated medical equipment (mean= 33.5%). Among all participants (n=158), only 16 (mean= 10.5%) reported being CIC certified and less than half (mean= 43.9%) of those not certified planned to take the exam in the upcoming 12 months.

CONCLUSIONS: The CIC Employee Assessment illustrated opportunities for improvement in several areas, including improving staff's self-efficacy to respond to HAI outbreaks, accessibility to infection control education/resources, and increasing the number of CIC credentialed staff at local health departments. Interventions developed from these findings included the Florida Department of Health HAI CIC Study Group and access to IC education through a series of trainings dedicated to long-term care facilities with a focus on outbreak prevention and response. Our findings allowed us to clearly and efficiently target gaps in infection control education throughout Florida to improve capacity to respond to HAI outbreaks. Continuing education and resources are warranted for our Florida public health professionals.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infection Control; Healthcare Associated Infections (HAI); Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	luz.caicedo@flhealth.gov
Presenting Author(s)	Luz Caicedo
Institution Affiliation	Florida Department of Health in Orange County Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11367
Abstract Type	Lightning
Abstract Title	Incorporating Electronic Medical Records with National Healthcare Safety Network Data to Characterize Recurrent <i>Clostridioides Difficile</i> Infections Reported at the Ohio State University Medical Facilities, 2014-2016

Abstract

BACKGROUND: Recurrent *Clostridioides difficile* infection (rCDI) occurs among 10-25% of incident cases. All CDI events at Ohio State University Wexner Medical Center (OSUWMC) are submitted to the National Healthcare Safety Network (NHSN) but only incident data is analyzed and publicly reported. Our objective was to reliably merge NHSN CDI laboratory-identified (LabID) events with electronic medical records (EMR) to develop a comprehensive dataset that could be used for epidemiologic investigations.

METHODS: We conducted a retrospective cohort analysis from a major academic medical center in Ohio, United States. CDI data were collected as part of the NHSN surveillance program from 2014 to 2016. We merged CDI LabID events with OSUWMC EMR data for the period January 1, 2014, to December 31, 2016. We matched NHSN records with EMR data by medical record number, admission date, and specimen date. We performed descriptive epidemiologic analyses for rCDI including evaluating trends over time.

RESULTS: Six hospitals within OSUWMC make up 3 unique facilities that submit data separately to NHSN. These separate NHSN facilities were merged before they could then be combined with the patient's electronic record. The 3 different NHSN facilities generated a list of 3,213 patients who were submitted to the NHSN MDRO and CDI database. However, only 2,024 were CDI LabID events that occurred within the study window. One hundred percent of the NHSN cases were able to be merged to EMR data. The resulting comprehensive dataset contained 180 variables. When comparing different follow-up periods for recurrence, 121 (6.5%) patients experienced recurrence within 56 days; 209 (11.8%) patients experienced recurrence within 180 days; and 245 (14.3%) patients experienced recurrence at any point in the study period. We found that patients who experienced recurrence within 56 days were more likely to be older, more likely to be female, and more likely to have an emergency or outpatient status. Finally, there was an increase in the proportion of rCDI between 2014 (6.2%) and 2016 (7.1%).

CONCLUSIONS: Our analysis demonstrates how to use the EMR to supplement NHSN CDI data. Facilities reporting CDI LabID events may be able to extend their own data to further examine CDI outcomes, including recurrence. OSUWMC Clinical Epidemiology and Antimicrobial Stewardship Programs are using these analyses to update provider policy and improve CDI prevention.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infectious Diseases; Hospital Data
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	orellana.4@osu.edu
Presenting Author(s)	Robert Charles Orellana
Institution Affiliation	The Ohio State University Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11804
Abstract Type	Lightning
Abstract Title	The Development of Screening Protocols for Colonization of Contacts with CP-CRE in Non-Acute Care Settings in Nebraska

Abstract

BACKGROUND: Recommendations on colonization screening of CP-CRE (carbapenemase producing carbapenem resistant Enterobacteriaceae) in acute care hospitals are relatively well established. However, there is little published guidance on what factors should be considered in determining who needs such screening in non-acute healthcare settings. After performing several screenings in skilled nursing facilities (SNFs) and assisted living facilities (ALFs), the HAI/AR (Healthcare Associated Infections/Antimicrobial Resistance) team at NDHHS (Nebraska DHHS) developed checklists for approaching colonization screening in these settings.

METHODS: We reviewed the factors that influenced the actual screenings performed in SNFs and ALFs in Nebraska. Discussions with in-state and out-of-state experts as well as infection preventionists (IPs) at various facilities identified the following factors as essential: the overall acuity of the patients in the facility; the source of the CP-CRE; continence; sharing of toileting facilities; common use of bathing, whirlpool and PT/OT equipment; mental capacity of the patient; and overall level of IP practices. Nebraska's largest tertiary care hospital recommends screening individuals located 3 rooms on either side with a 3 day or more overlap. Therefore, we included this recommendation for all NE acute care settings and for SNFs.

RESULTS: In ALFs the stepwise checklist begins with the question: "Does the patient have a roommate?" If the answer is "yes" that person should be screened. Question 2: "Does the index case share toileting facilities?" If "yes" then all those who share toileting facilities are screened. Question 3: Does the patient use common bathing facilities or whirlpool equipment? An affirmative triggers screening those who use the same devices. Additional questions regarding continence, compliance with personal hygiene, and use of PT/OT facilities, contribute to the screening algorithm. In high acuity SNFs the acute care recommendation to screen those in 3 rooms on either side is followed. The SNF checklist intersects the ALF paradigm at Q3: both recommend auditing and documentation of auditing findings for hand hygiene and compliance with contact precautions. Lastly a link to the Nebraska Interfacility Transfer Form is included to encourage transfer communication.

CONCLUSIONS: Since little formal guidance on colonization screening in SNFs and ALFs exists, easy-to-use checklist protocols to determine who to screen for CP-CRE colonization in ALFs and SNFs are necessary, particularly since the staff members tasked with performing the screening in non-acute care settings often lack infection prevention experience.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Healthcare Associated Infections (HAI); Infection Control
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	maureen.tierney@nebraska.gov
Presenting Author(s)	Maureen Tierney
Institution Affiliation	Nebraska Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11311
Abstract Type	Poster
Abstract Title	Carbapenemase-Producing (CP) Carbapenem-Resistant Enterobacteriaceae (CRE) and Carbapenem-Resistant Pseudomonas Aeruginosa (CRPA) Infections in Georgia Long-Term Care Facilities (LTCF), 2018

Abstract

BACKGROUND: CRE and CRPA with carbapenemase-producing enzymes (i.e., CP-CRE and CP-CRPA) represent a serious public health threat, as they have high transmission rates and contribute to antibiotic resistant disease in healthcare settings. The epidemiology of CP-CRE and CP-CRPA are not well characterized in Georgia, particularly in LTCFs. In 2018, the Georgia Public Health Laboratory (GPHL) expanded its capacity to identify CP-CRE and CP-CRPA and initiated a pilot project with a statewide LTCF reference laboratory to test their CRE and CRPA isolates for carbapenemase production and genotypic expression.

METHODS: Data were analyzed using Excel, and urban and rural classifications were assigned to LTCFs. Submitted isolates were tested for carbapenemase production using modified carbapenem inactivation method (mCIM); those positive were tested for resistance genes genotype using the Cepheid GeneXpert® CARBA- R assay.

RESULTS: Between December 28, 2017 and November 28, 2018, the LTCF reference laboratory submitted 215 isolates from 94 LTCFs to GPHL for carbapenemase testing; these isolates were collected between 11/14/2017 through 11/22/2018. Of these 94 facilities, 79% (74) were in urban regions and 21% (20) rural. Urban LTCFs submitted 87% (186) of isolates and rural 13% (29). Twenty-three percent (34/146) of the CRE isolates were carbapenemase producers; 23% (27/118) urban isolates and 25% (7/28) rural. GPHL identified *Klebsiella pneumoniae* in all 7 of the rural CP-CRE isolates, 86% (6) with the *Klebsiella pneumoniae* carbapenemase (KPC) gene and 14% (1) with the New-Delhi metallo-β-lactamase (NDM) gene. GPHL detected more strains of CP-CRE and CP-CRPA from urban LTCF isolates. Of the 27 CP-CRE isolates identified in urban LTCFs, 56% (15/27) were KPC-*Klebsiella pneumoniae*, 19% (5/27) KPC-*Escherichia coli*, 15% (4/27) KPC-*Enterobacter cloacae*, 7% (2/27) NDM-*Klebsiella pneumoniae*, and 4% (1/27) KPC-*Enterobacter asburiae*. Four percent (3/69) of the CRPA isolates were carbapenemase producers, and all were from urban LTCFs. GPHL identified one incidence of Verona integron-encoded metallo-β-lactamase (VIM)-CRPA and two incidences of KPC-CRPA, which are emerging multi-drug resistant organisms (MDROs) in the US.

CONCLUSIONS: Although GPHL identified similar rates of CP-CRE in urban and rural LTCFs, it detected a greater diversity of *Enterobacteriaceae* species harboring carbapenemase genes in urban LTCFs. In addition, GPHL detected the emerging MDROs of CP-CRPA in urban LTCFs, signaling a need for increased infection control training and support in these facilities. The carbapenemase testing capacity at GPHL is essential for DPH to understand CP-CRE and CP-CRPA epidemiology and to direct effective response to antibiotic resistance in Georgia LTCFs.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Surveillance; Antimicrobial Resistance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jeanne.negley@dph.ga.gov
Presenting Author(s)	Jeanne Negley
Institution Affiliation	Georgia Department of Public Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	10908
Abstract Title	Poster
	Data from the 2018 National Healthcare Safety Network (NHSN) Home Dialysis Center Practices Survey: What Can NHSN Tell Us about Home Dialysis Care?

Abstract

BACKGROUND: The number of end-stage renal disease (ESRD) patients who receive dialysis at home has increased over the past decade. Facilities that provide home dialysis services, specifically peritoneal dialysis (PD) or hemodialysis (HD), are less regulated than clinics that perform in-center HD. In addition, these facilities do not report dialysis healthcare-associated infection (HAI) event data to the National Healthcare Safety Network (NHSN), even when the home dialysis services are provided within other healthcare settings, such as long-term care facilities (LTCF). Using data from NHSN, we aimed to describe the characteristics of facilities providing home dialysis (home HD or PD) without in-center HD services.

METHODS: Outpatient dialysis facilities that lack in-center HD services complete an annual Home Dialysis Center Practices Survey as part of their participation in the NHSN Healthcare Personnel Influenza Vaccination Module. We analyzed 2018 survey data, which includes facility characteristics and select patient and staff characteristics that were present during the first week of February. NHSN does not currently collect the location of dialysis services (i.e., a home vs. LTCF) from these facilities.

RESULTS: In 2018, 402 home dialysis facilities completed the annual survey; 384 (95.5%) of these provided PD and 277 (68.9%) provided home HD. Facilities were located in 39 states and Washington, DC. Most facilities were part of a chain (n=385, 95.7%) and had for-profit ownership (n=353, 87.8%). Facilities had a median number of 30 home dialysis patients (26 PD and 6 home HD) and 8 staff. Of home HD programs, 95.3% reported that they tracked patient bloodstream infections; 100% of PD programs reported tracking peritonitis episodes. Of home patients treated by these facilities during the first week of February, 73.1% had received ≥ 3 doses of hepatitis B vaccine, 85.2% had received the 2017-2018 seasonal influenza vaccine, and 81.4% had received ≥ 1 dose of pneumococcal vaccine. Among facility staff during the same time period, 78.1% had received ≥ 3 doses of hepatitis B vaccine and 83.8% had received the seasonal influenza vaccine. Of home HD patients cared for by these facilities, 66.2% used an arteriovenous fistula for dialysis and 20.4% used a central line.

CONCLUSIONS: Home-only dialysis facilities are located in most states and provide care to a large patient population. Extending HAI surveillance at the national level to this at-risk patient population could bolster efforts to track and prevent infections.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	xyb4@cdc.gov
Presenting Author(s)	Preeti Ravindhran
Institution Affiliation	Leidos, Inc. Corporate Settings

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	Examining the Difference in Clostridioides Difficile Incidence By Gender in South Carolina, a Population-Based Study

Abstract

BACKGROUND: *Clostridioides difficile* infection (CDI) has emerged as a significant threat to public health. Cases of CDI have been linked to inappropriate antibiotic prescribing and use. Previous studies have reported higher CDI incidence for women than men. This cross-sectional study seeks to examine if the burden of CDI is higher in women than men in South Carolina as well as any implications of antibiotic use.

METHODS: To assess the antibiotic prescribing rate in South Carolina, 2015 Medicaid and State Health Plan claims data for oral antibiotic prescriptions and associated medical claims were used as a proxy to estimate antibiotic prescription rates for adults age 18-64. Community-onset CDI (CO-CDI) cases were identified through state-mandated reporting in the National Healthcare Safety Network (NHSN) and the South Carolina Infectious Disease and Outbreak Network (SCION). The incidence rates of CO-CDI were obtained in both men and women in two age groups, 18-39 years and 40-64 years. The incidence rates were then adjusted by antibiotic prescription rates within each gender and age group. Ninety-five percent confidence intervals (CI) were constructed to examine statistical significance across genders within the same age group.

RESULTS: In 2015, a total of 1,564 CO-CDI cases were identified in SC residents 18-64 years of age. The CO-CDI incidence rate per 100,000 persons was higher in women than men in each age group: 18-39 years (37.3, 95% CI [32.8, 41.8] vs. 21.0 [95% CI [17.6, 24.4]] and 40-64 years (86.4, 95% CI [80.1, 92.8] vs. 56.6, 95% CI [51.2, 61.9]). Similarly, antibiotic prescription rates per 1,000 person-years were higher in women than men in the two respective age groups (1130.9 [95% CI: 1126.4, 1135.3] vs. 529.8 [95% CI: 525.5, 534.1] and 1283.9 [95% CI: 1278.3, 1289.6] vs. 830.9 [95% CI: 825.1, 836.7]). After adjustments for antibiotic prescriptions, there was no significant difference in the incidence rates of CO-CDI per 100,000 persons between women and men 18-39 years of age (33.0 [95% CI: 29.0, 37.0] vs. 39.6 [95% CI: 33.2, 46.0] and 40-64 years old (67.3 [95% CI 62.4, 72.2] vs. 68.1 [95% CI: 61.7, 74.5]).

CONCLUSIONS: Higher crude incidence rates of CO-CDI in women are associated with higher outpatient antibiotic prescription rates.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Healthcare-Associated Infections
Consider for Different Presentation?	Healthcare Associated Infections (HAI); Surveillance
Presenting Author Email Address(es)	Yes
Presenting Author(s)	waitesks@dhec.sc.gov
Institution Affiliation	Katie Waites
	South Carolina Department of Health and Environmental Control
	State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11788
Abstract Type	Poster
Abstract Title	Management of Extended Spectrum Beta-Lactamase (ESBL)-Producing <i>Proteus Mirabilis</i> in a Long-Term Care Facility in Nebraska

Abstract

BACKGROUND: A cluster of extended spectrum beta-lactamase (ESBL)-producing *Proteus mirabilis* urinary tract infections was reported by Hospital A to be occurring at a long-term care facility, Facility A, in Nebraska. Local health department A (LHD A), the Nebraska Department of Health and Human Services (NDHHS) and the Infection Control Assessment Program (ICAP) team performed a site visit and made recommendations on infection prevention (IP) practices. Cases continued and a repeat visit was made.

METHODS: A team from NDHHS, LHD A, ICAP and ASAP (Nebraska Antimicrobial Stewardship Assessment and Promotion Program) visited Facility A and met with personnel over 2 days for interviews and record review. A review of possible contributing IP concerns and an evaluation of antimicrobial stewardship (AMS) were performed.

RESULTS: Over a 1 year period, there were 27 reports of ESBL-producing *P. mirabilis* with similar resistance patterns from Hospital A, including 23 residents of Facility A. These isolates were resistant to 6 classes (aminoglycosides, cephalosporins, folate-inhibitors, nitrofurantoin, penicillins, and quinolones) of antimicrobials. Initial chart review suggested there may have been an index patient who introduced the pathogen to Facility A. Notably, there were 4 cases reported by Hospital A from patients that live in the region but were not Facility A residents. Although *P. mirabilis* isn't required to be reported to the state, a review of the *P. mirabilis* isolates voluntarily reported state-wide in 2017 found 98% susceptible to ceftriaxone (a proxy marker for ESBL production) compared to 84% based on Hospital A's antibiogram. A number of IP gaps were noted in Facility A that may have facilitated transmission including gaps in cleaning of shared whirlpool devices.

CONCLUSIONS: Our findings suggest this outbreak likely reflects the multiple challenges associated with AMS and IP in a long-term care setting. These facilities can amplify infectious agents due to the presence of inhabitants in close proximity with complex health issues, on multiple medications (including antimicrobials). This investigation provided an opportunity for the mobilization of our ICAP and ASAP (Nebraska Antimicrobial Stewardship Assessment and Promotion Program) team to improve practices (an ongoing effort at Facility A) and the application of our state-wide antibiogram to determine the increased prevalence of this organism both in the surrounding community as well as Facility A.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Healthcare Associated Infections (HAI); Infection Control
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	maureen.tierney@nebraska.gov
Presenting Author(s)	Maureen Tierney
Institution Affiliation	Nebraska Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10828
Abstract Type	Poster
Abstract Title	Validation of Risk Factors for NHSN Colon and Abdominal Hysterectomy Surgical Procedures in Maine Hospitals

Abstract

BACKGROUND: A total of 14 patient, procedure, and facility risk factors are used to calculate the Standardized Infection Ratio (SIR), the risk-adjusted metric used by the National Healthcare Safety Network (NHSN) to track Healthcare Associated Infections (HAIs). This ratio is made available to the public and is used as an indicator of hospital quality by consumers and payers. The objective of this validation was to review a small sampling of surgical procedure risk factors for accuracy and types of errors to determine if a more comprehensive validation should be conducted.

METHODS: Data from NHSN procedure datasets were frozen before the validation was announced so no changes could be made to the data. Nine of the 11 patient and procedure-centric risk factors were evaluated; two risk factors, age and gender, were not included due to restrictions on access to Protected Health Information (PHI). A maximum of two colon and two abdominal hysterectomy procedures, performed between July 2016 and June 2017, were randomly selected from each hospital. Hospitals were asked to submit a copy of the medical record page that contained the risk factor information. Data on each medical record page were compared, manually, to data reported to NHSN. Errors identified were sorted by risk factor and potential for error to decrease or increase surgical procedure risk.

RESULTS: A total of 615 risk factors were reviewed and 43 errors were identified, yielding an accuracy score of 93%. The number of errors by category were: procedure duration (27 errors), body mass index (7), use of scope (3), wound class (3), closure technique (1), diabetic status (1), and wrong procedure reported (1). The percent of errors that decreased or increased surgical procedure risk were 49% (21/43) and 51% (22/43), respectively.

CONCLUSIONS: The accuracy score provided assurance regarding the quality of data being reported by Maine hospitals and identified an opportunity for education to improve procedure duration reporting. The difference in the percent of errors that had the potential to decrease or increase surgical procedure risk did not appear to bias the SIR to the hospital's benefit. The small sample size, however, was not adequate to determine if a single hospital may be using surgical procedure risk factor reporting to deliberately improve their hospital SIR.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Outcome Measures; Surveillance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rita.owsiak@maine.gov
Presenting Author(s)	Rita J. Owsiak
Institution Affiliation	Maine Center for Disease Control and Prevention State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11574
Abstract Type	Quick
Abstract Title	An Outbreak of <i>Enterobacter Cloacae</i> Infections Among Patients Receiving Joint Injections at an Outpatient Clinic in Virginia, 2018

Abstract

BACKGROUND: Numerous outbreaks have been associated with unsafe injection practices in outpatient settings. Few outpatient facilities are licensed in Virginia. On October 19, 2018, the Virginia Department of Health (VDH) was notified of a cluster of *Enterobacter cloacae* joint infections in patients identified at an out-of-state hospital September–October 2018. All patients had received steroid injections at one rheumatologist’s clinic in Virginia.

METHODS: VDH conducted a site visit October 23, 2018 to observe injection practices, interview staff, collect lidocaine and synthetic corticosteroid vials and alcohol and betadine prep pads, and review medical records of patients with laboratory-confirmed infections. VDH conducted active case finding by interviewing patients who had received steroid injections at the clinic during July–October 2018, querying Virginia’s syndromic surveillance system, and requesting that regional hospital and reference laboratories report any detection of *E. cloacae* in wound or joint fluid isolates during July–October. VDH obtained supply invoices identifying vial lot numbers. Virginia’s state public health laboratory and CDC performed pulsed-field gel electrophoreses (PFGE) on isolates from seven patients, and open multi-dose medication vials.

RESULTS: VDH observed injection safety breaches at the clinic, including drawing medications in patient rooms, not dating multi-dose vials, and using one syringe across different multi-dose vials. The clinic did not record vial lot numbers by patient. Injections were performed July 11–October 16. VDH reached 87 of 114 (76%) patients who received intra-articular injections at the clinic; two reported unconfirmed symptoms post-injection. *E. cloacae* was detected in nine patients and the open lidocaine vial. PFGE patterns for six patients and the lidocaine isolates were indistinguishable from each other. The seventh patient isolate was highly related. Retrospective surveillance did not identify any additional cases. There were no known reports of product recall or contaminated lidocaine or steroid vials.

CONCLUSIONS: Contamination of lidocaine likely occurred because of injection safety breaches, although the source was undetermined. VDH provided and followed up on these recommendations to the clinic: use single-dose vials whenever possible; draw up medications in a location separate from the patient room; record when multi-dose vials are opened; log vial lot numbers in patient charts; and conduct post-injection surveillance for infection-related symptoms. Active surveillance is ongoing, with no additional cases reported. Clinic practices may not have been unusual, but were lacking regulatory oversight. Education on safe injection practices to outpatient providers and timely reporting of infections may prevent future outbreaks.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	tisha.mitsunaga@vdh.virginia.gov
Presenting Author(s)	Tisha M Mitsunaga
Institution Affiliation	Virginia Department of Health CDC/CSTE Fellow

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Are Paid Plasma Donors at Increased Risk of Bloodborne Disease Transmission?

Abstract

BACKGROUND: Each year approximately 30 million paid plasma donations are collected in the United States to manufacture plasma protein therapies (PPT). Plasmapheresis is utilized to collect whole blood, plasma is removed for PPT, and remaining components are returned to the donor. Plasma donation centers (PDCs) are not considered healthcare facilities. PDCs are subject to regulations aimed at manufacturers to ensure safe blood products and preventing worker exposure to bloodborne pathogens (BBPs). Following a report of poor glove change practices at two PDCs, we initiated an investigation into their infection prevention (IP) practices; we also sought to gain a general understanding of PDC practices and regulations, as well as populations served by PDCs in Colorado.

METHODS: Phone (two PDCs and corporation) and onsite (one PDC) assessments of IP practices were completed, including hand hygiene (HH), standard operating procedures (SOP), plasmapheresis equipment cleaning, and donor screening. We reviewed current Colorado public health hepatitis B (HBV) and hepatitis C (HCV) surveillance methods. We compared census tract poverty level with locations for all PDCs with paid donors in Colorado.

RESULTS: Assessments identified deficient HH and glove change practices, and HH supplies were not readily available. There was little physical separation between donors, and equipment and donor beds were not cleaned/disinfected between uses. Colorado corporate SOP for HH, glove use and disinfection/cleaning were reviewed and consistent with facility assessments. In Colorado, investigation of HBV and HCV cases reported to public health via surveillance includes follow-up of acute cases with positive confirmatory results, but patients interviewed are not routinely asked about plasma donation. Since PDC donor screening includes only antibody testing, and follow-up confirmatory testing does not typically occur at the PDC, disease surveillance does not currently identify most confirmed cases identified from plasmapheresis. Of 18 paid-donor PDCs in Colorado, 72% are located in areas with the highest levels of poverty.

CONCLUSIONS: IP assessments identified gaps that might place plasma donors at increased risk of BBPs, but current surveillance systems are inadequate to detect cases of BBPs associated with PDCs; we are exploring methods to improve identification of HBV and HCV cases following plasma donation. Current Colorado and federal regulatory oversight focuses on recipient and healthcare worker safety, and paid donors, who might be disproportionately disadvantaged socioeconomically, are likely unaware of possible increased risk for BBPs given current IP practices. Additional assessments of broader PDC practices are necessary to understand the full BBP risk to plasma donors.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control; Social Inequalities
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	april.burdorf@state.co.us
Presenting Author(s)	April Burdorf
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Bacterial Infections Post-Stem Cell Product Procedures, Texas 2018

Abstract

BACKGROUND: On September 17, 2018 the Texas Department of State Health Services (DSHS) received notification of three patients that had developed *Enterobacter cloacae* and *Citrobacter freundii* bloodstream infections after having non-FDA-approved umbilical cord blood-derived stem cell product procedures at the same outpatient clinic. Due to the concern for additional affected patients, DSHS collaborated with the CDC to identify other patients and potential sources of contamination.

METHODS: Patient isolates and remaining product from the same lot that was used on the affected patients were submitted for PFGE and whole genome sequencing (WGS). An epidemiologist certified in infection control conducted two onsite assessments at the outpatient clinic to review infection control practices. Case finding methods included a call-for-cases, investigating reported suspect cases, and active case finding. Active case finding was conducted by contacting the 67 facilities in Texas that received the product of interest between 02/01/18 and 09/26/18 and inquiring about post-procedural complications. Facilities were instructed to avoid using remaining product. If patients were reported as having complications, their medical records were reviewed to determine if they developed a post-procedural bacterial infection that met case definition.

RESULTS: All three index patient isolates of *E. cloacae* had identical PFGE patterns. Six unopened product vials were tested and all grew *E. cloacae* and *C. freundii*; WGS testing showed that all 9 isolates were highly related to each other. During the onsite assessments at the outpatient clinic, multiple opportunities for improvement were observed and recommendations were provided. Working with 23 health department jurisdictions, contact was made with 61(91%) of the 67 facilities that received the stem cell product of interest. From the 61, 54 (88.5%) reported post-procedural status of a total 321 patients. Five additional patients were identified through case finding and met case definition, bringing the total number of confirmed cases to 8. These 8 cases were identified from 4 (7.4%) different facilities. All cases required hospitalization. In addition to the confirmed cases, four suspect cases were investigated and ruled-out.

CONCLUSIONS: Results of laboratory testing suggest a common source and that these bacterial infections may have occurred due to contamination of the products prior to distribution. Total case count in Texas remains unknown due to optional self-reporting by facilities and patients. Having standard procedures in place for large-scale active case finding aided this investigation. We were able to highlight the importance of large-scale case finding methods during suspected product contamination investigations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	GRETCHEN.RODRIGUEZ@DSHS.TEXAS.GOV
Presenting Author(s)	Gretchen Rodriguez
Institution Affiliation	Texas Department of State Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11224
Abstract Type	Quick
Abstract Title	Collaborative Effort between Regulatory and Epidemiology to Improve Hospital Infection Control Program for Surgical Services

Abstract

BACKGROUND: Historically, the Indiana State Department of Health (ISDH) Health Care Regulation Commission has been able to issue citations; however, the regulatory commission cannot provide educational assistance for improvement. With the help of the regulatory commission, the ISDH Epidemiology Resource Center (ERC) was able to assist on an investigation that resulted in an immediate jeopardy. Immediate jeopardy is defined as actions likely to cause serious harm, injury, impairment or death to an individual.

METHODS: The ISDH Healthcare-Associated Infections (HAI) Epidemiologist received a notification from a hospital infection preventionist (IP) of multiple surgical site infections and improper infection control practices. The IP was facing leadership support challenges; therefore, the HAI Epidemiologist and regulatory commission contact submitted a complaint in order for all pertinent information regarding the complaint to be deemed as high priority. Within three days, an onsite visit was scheduled to review patient records and observe practices in the surgical services and sterile processing department.

RESULTS: The pre-existing relationship between the ISDH ERC and the regulatory commission allowed the HAI Epidemiologist to gain an understanding of the surveying process and complaint submission procedures to demonstrate the urgency of the issue. The regulatory nurse was able to rely on the HAI Epidemiologist for specific knowledge regarding surgical site infection (SSI) classification and issues identified in the sterile processing department. Throughout the process, consistent communication was maintained with the regulatory nurse to ensure understanding of evidence-based best practices.

CONCLUSIONS: Collaboration between regulatory and epidemiology enhanced and improved the investigation of an immediate jeopardy. The HAI Epidemiologist helped the hospital to better understand the citations issued as a result of infection prevention breaches and to identify opportunities for improvement. Ultimately, the hospital was able to make informed decisions based on evidenced-based best practices that led to improved patient safety. This process allowed for continued and future collaboration between regulatory and epidemiology to maximize efforts for overall HAI reduction.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infection Control; Communication; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rcathey@isdh.in.gov
Presenting Author(s)	Rachel Lee Cathey
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11133
Abstract Type	Quick
Abstract Title	Community-Associated Clostridium Difficile Infection and Antibiotic Exposure — Minnesota, 2009–2016

Abstract

BACKGROUND: Community-associated (CA) *Clostridium difficile* infections (CDIs) account for an increasing proportion of CDIs nationally. Prior antibiotic use is a known risk factor for CA-CDI. We sought to identify other risk factors by comparing CA-CDI patients with antibiotic use in the prior 12 weeks to those without antibiotic use.

METHODS: We analyzed Minnesota Department of Health active population- and laboratory-based CDI surveillance data from 2009–2016. A CA-CDI case was defined as a *C. difficile* -positive specimen collected as an outpatient or ≤ 3 days of hospitalization from a person aged ≥ 1 year who resided in 1 of 5 sentinel counties and did not have CDI in the prior 8 weeks or an overnight stay in a healthcare facility in the prior 12 weeks. We limited our analysis to cases with negative laboratory results for other enteric pathogens and with symptoms consistent with CDI. CA-CDI contributing factors were ascertained by reviewing medical records and patient interviews.

RESULTS: Of 2,679 CA-CDI cases, 1,514 (56.5%) were included in the analysis. Antibiotics were not used prior to infection in 749 (49.5%) CA-CDI patients. Compared with patients with prior antibiotic use, patients without antibiotic use were younger (median age: 48.5 years versus 56 years, $P < .001$), more likely male (40.9% versus 35.0%, $P < 0.05$), have preexisting inflammatory bowel disease (IBD) (11.1% versus 5.9%, $P < .001$), take antidiarrheal medications (11.3% versus 7.1%, $P < 0.05$), and had animal exposures (11.5% versus 9.6%, $P < 0.05$). In a multivariate model including these significant variables, being younger ($P < .05$) and having preexisting IBD ($P < .005$) were more likely in CA-CDI patients without prior antibiotic use before CDI.

CONCLUSIONS: After exploring potential exposures, we identified CA-CDI patients without prior antibiotic use were more likely to have preexisting IBD diagnosis. This novel finding warrants further investigation as does consideration of other unexplored risk factors.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Risk Factors; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	okp2@cdc.gov
Presenting Author(s)	Joanne K Taylor
Institution Affiliation	Minnesota Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10588
Abstract Type	Quick
Abstract Title	Dialysis Event Surveillance and Epidemiology in Philadelphia, PA

Abstract

BACKGROUND: Hemodialysis patients are at risk for bloodstream infections (BSIs) and are often prescribed antibiotics for suspected infection. Most hemodialysis-related BSIs are preventable when infection control guidelines are followed. Hemodialysis facilities are required to report dialysis events (DEs) [BSIs, intravenous antimicrobial starts (IVASs), and suspected infections (pus, redness, or increased swelling at vascular access site)] to the National Healthcare Safety Network (NHSN); these events are monitored by the Philadelphia Department of Public Health.

METHODS: We analyzed 42 months of data from NHSN, including DEs and facility characteristics as reported on the 2018 *Outpatient Dialysis Center Practices Survey*. Citywide rates were calculated as the total count of an event over the number of patient-months reported and standardized infection ratios (SIRs) were calculated. Rates were stratified by vascular access type and assessed over time. Analyses were conducted using SAS v.9.4.

RESULTS: A total of 54 facilities were operational in 2018 and completed the survey; all were included in the January 2015-June 2018 event analysis. Most facilities were for-profit (94.3%) and part of a national chain (96.2%). The median number of dialysis stations and patients treated per facility were 21 (IQR=16-24) and 73 (IQR=50-88), respectively. A total of 3,958 DEs were reported, including 937 BSIs, 3,608 IVASs, and 531 suspected infections. Approximately three-quarters of all BSIs (699,74.6%) were related to the access site. The Citywide rate over the study period was 0.67 per 100-patient months for BSI and 2.59 per 100-patient months for IVAS. Of all IVASs, 75.7% included vancomycin. BSI rates in patients with a fistula or graft compared to a central line (CL) were 0.24 and 3.05 per 100 patient-months, respectively ($p<0.0001$). IVAS rates in fistula or graft patients compared to CL patients were 1.56 and 8.26 per 100 patient-months, respectively ($p<0.0001$). The distribution of BSI SIRs was positively skewed with a median of 1.02 (IQR=0.71-1.47). The most commonly identified organism among BSIs was *Staphylococcus aureus* (23.82%).

CONCLUSIONS: Dialysis event rates were significantly higher in CL patients. Prevention efforts should target the reduction of CL usage in an effort to reduce BSIs and antibiotic use. When antibiotics were prescribed, the majority involved vancomycin. While this is likely related to the incidence of *Staphylococcal* infections, prescribing should be closely monitored due to associated nephrotoxic side effects. Future work should explore facility-level data to identify outlier facilities who contribute the highest burden of infection and prescribing; these facilities should be the priority for prevention and intervention efforts.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Surveillance; Healthcare Associated Infections (HAI); Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	phillip.hahn@phila.gov
Presenting Author(s)	Phillip D. Hahn
Institution Affiliation	Philadelphia Department of Public Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	10769
Abstract Type	Quick
Abstract Title	Estimating Time between Central Line-Associated Bloodstream Infection Events

Abstract

BACKGROUND: Acute care hospitals submit central line-associated bloodstream infection (CLABSI) data to the Centers for Disease Control and Prevention's (CDC's) National Healthcare Safety Network (NHSN) in accordance with state and federal requirements, most of which went into effect between 2006 and 2010. The duration and scope of NHSN's CLABSI surveillance coverage enable use of the CLABSI data to evaluate potential value of Time Between Events (TBE) as a complement to the standardized infection ratio (SIR) summary measure. Use of TBE monitoring has yielded benefits for quality measurement when applied to non-healthcare, successive adverse events, but further study is needed to establish whether similar benefits can be achieved when TBE monitoring is applied to CLABSIs or other healthcare-associated infections (HAIs).

METHODS: We calculated TBE for 25,823 CLABSI events reported to NHSN in 2017 for hospital patient care locations, i.e., ICUs and select ward types, reporting ≥ 50 CLABSIs. The Geometric distribution was used to model TBE data for several types of patient care locations and needle plots were used to assess adequate fit. Key features of this modeling are probability limits for TBE and the probability of CLABSI occurring on any given day were estimated from fitted Geometric distributions and these were compared among location types.

RESULTS: Probability estimates of a CLASBI occurring among ICU patients on a given day ranged from $p=0.0377$ for medical ICUs to $p=0.012$ for neurologic ICUs. Among surgical, medical/surgical, and medical wards, the probability was $p=0.0112$, 0.0141 and 0.0141 (Figure 1), respectively. T-chart upper probability limits ranged from 137 days for Medical ICUs (Figure 2) to 437 days for neurologic ICUs and ranged from 372 to 471 among the select wards.

CONCLUSIONS: TBE analysis provides a way to estimate the probability that a CLABSI will occur on any given day, which in turn enables predictions of the likelihood of such rare events. This probability estimate is identical to the prevalence of CLABSI which is useful to assess prevention progress among applicable patient care locations. Implementation of T-charts with lower and upper probability limits could help healthcare staff better track CLABSI TBE and set prevention targets among these patient care locations and be used as an additional national benchmark. Furthermore, mean TBE across patient care locations could also be used for external comparison and help to produce a complimentary metric for performance measurement.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	JREdwards@cdc.gov
Presenting Author(s)	Jonathan R Edwards
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11660
Abstract Type	Quick
Abstract Title	Evaluation of Invasive Methicillin-Resistant Staphylococcus Aureus (MRSA) Reporting from Hospitals in Allegheny County, Pennsylvania – April 2017 through March 2018

Abstract

BACKGROUND: An estimated 72,000 invasive MRSA cases occurred in the United States in 2014. That same year, the Allegheny County Health Department (ACHD) made invasive MRSA a reportable condition. No evaluation of the invasive MRSA reporting system had been conducted since its inception. Our investigation involved three main objectives based on the Centers for Disease Control and Prevention's surveillance system evaluation guidelines: 1) to assess the completeness and timeliness of invasive MRSA reports, 2) to compare hospital reports of MRSA septicemia to hospitalizations involving MRSA septicemia, and 3) to assess perceived barriers to invasive MRSA reporting.

METHODS: To measure data quality, all variables were checked for completeness. Average time from culture to report was used to characterize timeliness. To assess representativeness, the number of reported positive MRSA blood cultures was compared to the number of hospital discharges with a primary or secondary ICD-10 code for MRSA septicemia (A41.02) from April 2017 through December 2017. The Pennsylvania Health Care Cost Containment Council provided hospital discharge data. Phone interviews with hospital infection preventionists (IPs) were conducted to understand the barriers to complete reporting.

RESULTS: ACHD received 144 reports of invasive MRSA from April 2017 through March 2018 for an incidence of 11.8 cases per 100,000 persons. No clusters were identified. Completeness of demographic variables was high (<10% missing), except for ethnicity (49% unknown, 31% missing). Incomplete surveillance variables included reporting facility (46% missing), admitting facility (45% missing), and surgical history (40% unknown). The median number of days between culture and report was 7 (IQR=4-25). There were 167 hospital discharges with an MRSA septicemia diagnosis code and 102 surveillance system reports from April 2017 through December 2017. Of 21 hospitals treating ≥ 1 patient with an MRSA septicemia diagnosis code, 12 (57%) reported cases to ACHD's system. Two hospitals did not discharge any patients with an invasive MRSA diagnosis but reported cases to the system. IPs thought the system was user-friendly but identified finding time and locating the form as reporting barriers. IPs believed that invasive MRSA data are valuable, but they rarely received surveillance feedback.

CONCLUSIONS: Not all hospitals are reporting invasive MRSA cases; providing IPs with consistent surveillance summaries may encourage timely reporting. Other recommendations for system improvement include making reporting facility a required field, interviewing IPs from all non-reporting facilities to understand and address outstanding barriers, and making the report form more accessible on ACHD's website.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Evaluation; Electronic Case Reporting; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	molly.nace@alleghenycounty.us
Presenting Author(s)	Molly E. Nace
Institution Affiliation	Allegheny County Health Department CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11463
Abstract Type	Quick
Abstract Title	External Validation of Massachusetts 2017 Clostridium Difficile Data Reported By Long-Term Care Facilities (LTCFs) through the National Healthcare Safety Network (NHSN)

Abstract

BACKGROUND: Since 2013, the Massachusetts Department of Public Health (MDPH) has received Epidemiology and Laboratory Capacity (ELC) cooperative agreement funding to conduct external validation of acute care hospital (ACH) NHSN data. The purpose of external validation is to assess reporting completeness and accuracy, promote correct application of surveillance definitions and educate on common reporting errors. In collaboration with the New England Healthcentric Advisors QIN/QIO, over 90 LTCFs in Massachusetts have enrolled in NHSN and report *Clostridium difficile* (CDI) Laboratory Identified (LabID) event data. Due to evidence of multidrug-resistant organism and CDI transmission across the continuum of care, MDPH validated CDI LabID event data in both the ACH and LTCF settings.

METHODS: Reporting of CDI data to NHSN using standardized surveillance definitions is required of Massachusetts ACHs and voluntary for Massachusetts LTCFs. The ten LTCFs selected for CDI validation included those with complete NHSN CDI data for the first six months of 2017 and identified as a transferring or receiving facility by one of the validated ACHs. Selected LTCFs provided MDPH with a complete list of positive and negative CDI laboratory results collected in 2017. On-site validations consisted of medical record review of all positive CDI laboratory results. Appropriate NHSN CDI reporting definitions and discrepant validation findings were discussed with facility staff.

RESULTS: Prior to MDPH's validation, only two of the ten selected LTCFs had reported at least one CDI event in NHSN (total of 11 events). Completion of ten LTCF validations resulted in review of 57 records (range: 1-19). Thirty-four CDI events were identified as missed, meaning the facility did not correctly report the positive result as an event in NHSN (range: 1-7, sensitivity=24%, specificity=100%). Only one facility correctly reported zero CDI events. In addition, MDPH identified three discrepant event details among events reported in NHSN, including two discrepant specimen dates and one incorrect resident ID.

CONCLUSIONS: Based on Massachusetts' external validation, many LTCFs are not correctly reporting CDI events in NHSN resulting in an underestimate of the burden of disease in these settings. MDPH created resource materials and conducted an educational webinar to address common misunderstandings in CDI NHSN reporting. These findings also suggest the need for additional and ongoing external validation of data as part of the CDC, CMS, and QIN-QIOs CDI Reporting and Reduction Project. MDPH will continue to conduct external validations of CDI NHSN data among twenty additional LTCFs in 2019.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Surveillance; Data Collection
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	cbrandenburg@massmail.state.ma.us
Presenting Author(s)	Christina Brandenburg
Institution Affiliation	Massachusetts Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11173
Abstract Type	Quick
Abstract Title	KPC-Producing <i>Pseudomonas Aeruginosa</i> Outbreak, Houston, Texas, 2018

Abstract

BACKGROUND: The Texas Department of State Health Services (DSHS) Laboratory is funded to perform mechanism testing on carbapenemase-producing organisms, including *Pseudomonas aeruginosa*, as part of CDC's Antibiotic Resistance Lab Network (ARLN). In June and August 2018 DSHS identified four cases of *Klebsiella pneumoniae* carbapenemase (KPC)-producing carbapenem-resistant *Pseudomonas aeruginosa* (KPC-CRPA) from the Houston region. One of the isolates was non-susceptible to all antibiotics tested. Infections caused by KPC-CRPA are uncommon in the United States. Initial investigations did not identify common exposures among the cases. An additional outbreak investigation was conducted.

METHODS: The outbreak investigation included the patients' healthcare visits in the previous six months. A total of 10 facilities were identified in the healthcare lookback. One of the facilities was a long-term acute care hospital (LTACH) where three of the four patients were admitted to several months prior to the culture collection dates. The other facility was a long-term care facility (LTCF), where two of the patients resided with overlapping stays prior to the positive KPC-CRPA cultures. Both facilities conducted point prevalence screenings (PPS), and the LTACH began performing admission screenings.

RESULTS: The DSHS Laboratory performed PFGE on KPC-CRPA isolates from the index cases, which showed three distinct patterns with 90% relatedness according to the Dice comparison. Infection control assessments at both the LTACH and LTCF identified minor lapses in infection control. Two separate PPS of 36 swabs at the LTCF revealed one positive KPC-*Klebsiella pneumoniae* case. Four separate PPS were performed over a two-month period at the LTACH and 30 swabs were collected; 12 swabs were positive for KPC: 2 for KPC-CRPA, 1 for KPC-*Escherichia coli*, 6 for KPC-*Klebsiella pneumoniae*, and 3 for KPC with no organism identified. Of the two KPC-CRPA identified from PPS at the LTACH, one matched the PFGE pattern of the index cases, and the other strain was a new, highly-related pattern. Out of 9 admission screenings at the LTACH, one was positive for KPC. Best practices in infection control were implemented at the facilities.

CONCLUSIONS: Admission screenings and PPS at the LTACH uncovered ongoing transmission of KPC-CRPA. The facility increased environmental disinfection and performed staff re-education on basic infection control practices. These small but important interventions are believed to be responsible for the decrease in new cases. One newly related case of KPC-CRPA was found in the geographic region from prospective surveillance.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Healthcare Associated Infections (HAI); Infection Control
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Bobbiejean.Garcia@dshs.texas.gov
Presenting Author(s)	Bobbiejean Garcia
Institution Affiliation	Texas Department of State Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10955
Abstract Type	Quick
Abstract Title	Large-Scale Patient Notification Event Following Improperly Reprocessed Surgical Equipment - Colorado, 2018

Abstract

BACKGROUND: In February 2018, the Colorado Department of Public Health and Environment (CDPHE) was notified of infection control breaches related to improperly sterilized surgical equipment at a large metropolitan hospital. CDPHE initiated a disease control investigation to determine if patients who underwent surgery were at risk of acquiring bloodborne pathogens (BBPs) or surgical site infections (SSIs). The risk of disease transmission due to this type of Category B infection control breach was unknown but thought to be low.

METHODS: CDPHE interviewed facility staff from the perioperative (OR) and the sterile processing department (SPD). Facility records including facility occurrence reports, SSI data, immediate use steam sterilization (IUSS) logs and data, OR instrument case reports, and data from a quality improvement project on instrument pre-cleaning/decontamination were collected. Additionally, CDPHE staff conducted infection prevention site visits to observe decontamination and sterilization processes. Finally, CDPHE staff reviewed 2015-2017 data from the National Healthcare Safety Network (NHSN) for SSIs at the facility.

RESULTS: Facility occurrence reports detailed instances of visible bioburden following sterilization on orthopedic and spine surgical instruments from January 1, 2017, to April 2, 2018. The contaminants included bone, blood, cement, black residue, a dead insect and hair. IUSS data from the facility showed IUSS use increased from 2.35% to 4.75% in fiscal year 2017. Interviews with facility staff revealed orthopedic/spine OR staff were not properly wiping down instruments or applying enzymatic cleaner after use, allowing for bioburden to dry on equipment. The SSI standardized infection ratios (SIRs) from 2015-2017 indicated no statistically significant difference between the facility's observed and predicted number of infections using the 2015 national baseline. On March 29, 2018, CDPHE recommended the facility notify orthopedic/spine (including neuro/spine) surgical patients of the possible risk of SSIs and BBPs. Following the initial notification, the facility reported additional issues with a residue on surgical equipment leading to the closure of their ORs and the identification of a second cohort to receive SSI and BBP risk notification. A total of 6,043 patients were notified.

CONCLUSIONS: The investigation details the first patient notification event by CDPHE resulting from a sterilization breach of improperly decontaminated and sterilized surgical equipment. CDPHE was unable to quantify individual patient risk. Determining the appropriate cohort to notify involved complex discussions regarding risk stratification among surgical service lines and exposure periods. The investigation revealed the importance of pre-cleaning surgical instruments at the point of use and following manufacturer's instructions.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email	alana.cilwick@state.co.us
Address(es)	
Presenting Author(s)	Alana Cilwick
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11564
Abstract Type	Quick
Abstract Title	Lessons Learned from Validation of Electronically-Submitted National Healthcare Safety Network (NHSN) Antimicrobial Use (AU) Option Data

Abstract

BACKGROUND: Hospital participation in the Centers for Disease Control and Prevention's (CDC's) National Healthcare Safety Network (NHSN) Antimicrobial Use (AU) surveillance increased exponentially over the last two years, with over 1,100 facilities submitting AU data to NHSN as of December 2018. The NHSN AU Team works closely with hospital participants to identify and mitigate data errors. These data validation activities prompt corrections to erroneous data and serve as guidance for the NHSN AU Team as it develops its technical support. Based on these activities, the NHSN AU Team will provide data validation targets for state and local health departments to establish and extend their roles in AU surveillance and antimicrobial stewardship.

METHODS: The NHSN AU Team analyzed AU data submitted to NHSN between January 1, 2016 and March 31, 2018. The NHSN AU Team identified and categorized data errors with SAS to pinpoint opportunities for targeted outreach and improvement.

RESULTS: The NHSN AU Team notified 474 hospitals with potential data quality issues in antimicrobial days (i.e., numerator data) and days present (i.e., denominator data). The most common numerator errors were:

- More antimicrobial days than the sum of the routes of administration
- Off-label use of certain antimicrobials
- Zero antimicrobial days across all antimicrobials
- Large variance in antimicrobial days from month-to-month
- Equal use of related drugs piperacillin and piperacillin/tazobactam
- Use of antimicrobials discontinued by the manufacturer

The most common denominator errors were:

- Days present less than patient days reported for healthcare-associated infections within a patient care location
- Zero days present when antimicrobial days reported
- Large variance in days present from month to month

CONCLUSIONS: NHSN AU surveillance leverages electronic data capture and reporting by hospital participants, which avoids dependence on manual surveillance processes but requires data validation. The NHSN AU Team's protocols allow hospitals to validate their AU data collection processes and outputs before submitting AU data. These protocols are an important resource for data quality assurance; however, the analysis suggests additional steps to ensure data validity during the AU data submission process. State and local health departments should incorporate data validation that focuses on common errors as they define and develop their roles in AU surveillance and antimicrobial stewardship. Data validation by state and local partners complements CDC's efforts to assure high quality AU data are available for analysis and action at all jurisdictional levels.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Evaluation; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	xga6@cdc.gov
Presenting Author(s)	Laura Blum
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11453
Abstract Type	Quick
Abstract Title	Leveraging Syndromic Surveillance for Automated Notification of Extensively Drug-Resistant Organisms (XDRO) upon Admission to Illinois Hospitals

Abstract

BACKGROUND: Illinois' XDRO Registry maintains a database of patients reported to have XDROs, including highly resistant Enterobacteriaceae and *Pseudomonas aeruginosa*, and *Candida auris*. Since 2015, 67 Illinois hospitals have been connected to its automated alert system, which notifies infection prevention staff when a patient with an XDRO is admitted to their facility. To receive alerts, facilities periodically send a direct feed of inpatient admissions (usually batch uploaded every 15-30 minutes) to Illinois Department of Public Health (IDPH) to be matched against XDRO registry patients. The facility's IT department creates admission files, and through sFTP, interfaces with the registry. This process can be burdensome for local personnel and require technical assistance from XDRO staff. Separately, IDPH established a syndromic surveillance system that requires acute-care hospitals to report emergency department (ED) encounters in near real-time. IDPH expanded syndromic surveillance reporting to include inpatient admissions and patient identifiers, allowing it to be leveraged for automated alerts. Reuse of the existing syndromic surveillance system provides efficiencies in generating automated alerts.

METHODS: In 2018, inpatient admissions from syndromic surveillance at 20 hospitals were matched to XDRO registry patients based on name and birthdate. Matches that generated an alert were recorded in a database. For 12 hospitals already receiving alerts via direct feed, we compared the two methods of generating alerts. Additionally, two facilities manually validated a list of patients who triggered alerts against their hospitals' inpatient records.

RESULTS: From 3/16/2018–8/4/2018, 421 alerts were generated for the 20 test facilities from syndromic surveillance feeds. For 12 sites already receiving alerts, 298 syndromic surveillance alerts were generated vs. 156 direct feed alerts. The direct feed for several of those sites was known to be missing inpatient admissions, including patients admitted through the ED. For the two validation facilities, 82 of 83 (99%) alerts were sent for the correct patients. All 185 Illinois hospitals participate in syndromic surveillance. Of these facilities, 71 included all elements necessary for XDRO alerts in their syndromic surveillance feed and could be connected with minimal time or burden. A pilot with 10 sites is expected to start January 2019.

CONCLUSIONS: Using syndromic surveillance has the potential to rapidly expand XDRO alerting to all Illinois hospitals with more complete admission data and minimal resource investment from their IT departments. In the future, IDPH plans to expand the use of syndromic surveillance reporting to other diseases and public health purposes.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Syndromic Surveillance; Antimicrobial Resistance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	amyfealy@gmail.com
Presenting Author(s)	Amy E. Fealy
Institution Affiliation	Hektoen Institute State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11333
Abstract Type	Quick
Abstract Title	The Impact of Infection Control Assessment and Response (ICAR) Visits on Hospital Infection Rates

Abstract

BACKGROUND: In 2016-17, the Los Angeles County Department of Public Health (LAC DPH) performed ICAR visits in LAC hospitals to assess infection prevention (IP) practices and identify areas for improvement. The objective of this project was to determine the impact of the ICAR visits on healthcare-associated infection rates in participating hospitals.

METHODS: Hospitals were targeted based on current National Healthcare Safety Network (NHSN) data, plus volunteer facilities. Using modified CDC tools, the visits included a review of IP policies, direct observations of practices, and recommendations for improvement. Infection data were obtained via NHSN. Quarterly standardized infection ratios (SIRs) were calculated for all LAC general acute care hospitals for CLABSI and CDI for one year prior to each visit and four quarters following the visit. 2016Q3 was used as time 0 for non-ICAR hospitals as it was the midpoint between the first and last visits. A repeated measures ANOVA was used to compare SIRs of ICAR to non-ICAR hospitals. Analysis were conducted using SAS 9.4. Hospitals unable to generate an SIR in NHSN were excluded. Follow-up calls one year after the visit assessed the effectiveness and changes made following the visit.

RESULTS: Nineteen ICARs were performed from January 2016-February 2017. From follow-up calls, we found all hospitals found the visit beneficial and made recommended changes to their IP program. Overall, county-wide CLABSI and CDI SIRs decreased, with ICAR hospitals showing a more dramatic decrease. For CLABSI, 90% of ICAR hospitals demonstrated a decreased SIR between one quarter before and four after intervention, with an overall average change of -0.57. In comparison, the non-ICAR average change was -0.18. For CDI, 60% decreased their SIR after four quarters, with an overall average change of -0.17; compared to -0.24 for non-ICAR hospitals. Compared to non-ICAR hospitals, ICAR hospitals had a lower average SIR one year post intervention (0.84 vs. 1.17 for CLABSI, 0.94 vs. 1.03 for CDI); however, the ANOVA test showed no statistical significance when comparing average SIRs one year before and one year after intervention between the two groups; CLABSI $p=0.25$, CDI $p=0.28$.

CONCLUSIONS: Overall, CLABSI and CDI rates are decreasing across LAC through combined efforts of public health and individual facilities. The analysis shows that intervention from public health can help to reduce rates faster; however, the change may not be implemented immediately, and continued outreach may be needed to maintain progress.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	shartmann@ph.lacounty.gov
Presenting Author(s)	Stacy Hartmann
Institution Affiliation	Los Angeles County Department of Public Health Local Public Health Agency

Submission Type	Roundtable
ID	10898
Abstract Type	Roundtable
Abstract Title	A New Framework for Patient Notifications of Infection Control Breaches and Outbreak Investigations in Healthcare Settings

Abstract

Key Objectives:

Discuss upcoming updates to CDC's new patient notification framework for healthcare-associated outbreaks; discuss reasons for patient notification; share some commonly encountered scenarios and, as a group, apply the updated framework.

Brief Summary:

Deciding if, when, and how to notify patients about infection control breaches or healthcare-related outbreak investigations can be very challenging. Public health agencies play a critical role in helping assess communication needs under these circumstances. Healthcare providers often have to weigh the potential risks to patients against the perceived risk to the provider's reputation, although it is usually impossible to quantify either. Additionally, the needs of stakeholders, including patients, providers, public health, and the public may not always align. In 2008, CDC published a patient notification framework which focused on bloodborne pathogen exposure risks and defined Category A ("gross error or demonstrated high-risk practice, generally relating to bloodborne pathogen exposure") and Category B (lower likelihood of blood exposure) infection control breaches. We will discuss upcoming updates to this framework, including the expansion of the framework to include bacterial pathogens, notification during an outbreak investigation, and recent research into the benefits of patient notification to protect patients. We will discuss reasons for patient notification, including the need for patient action (e.g., diagnostic testing), the need for public health actions (e.g., case finding, cohorting, product recall), and transparency. We will share some commonly encountered scenarios and, as a group, apply the updated framework. Finally, we will discuss how this revised framework relates to the work of the Council on Outbreak Response: Healthcare-Associated Infections and Antimicrobial-Resistant Pathogens (CORHA).

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Communication; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
Presenting Author Email Address(es)	hzt7@cdc.gov; guu9@cdc.gov
Presenting Author(s)	Ruth Link-Gelles; Kiran Perkins
Institution Affiliation	Centers for Disease Control and Prevention Federal Agency

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	A Tale of Two State Health Departments: Building Robust Capability to Respond to Cases and Outbreaks of Invasive Group a Streptococcus in Long-Term Care Facilities

Abstract

Key Objectives:

- Discuss jurisdictional experiences and lessons learned when responding to cases and outbreaks of invasive Group A streptococcal (GAS) disease in long-term care facilities.
- Share GAS toolkits and resources developed by PA and NC state health department staff.
- Identify strengths and weaknesses of available resources and identify opportunities for improvement or development of additional resources to promote best practices and a robust response to GAS long-term care setting investigations in the absence of published CDC guidelines

Brief Summary:

Group A *Streptococcus* (GAS) infection can result in severe and life-threatening illness, particularly in people aged ≥65 years. Given risk factors inherent to long-term care settings, residents are particularly vulnerable to severe sequelae from GAS infection. Therefore, the CDC recommends that even one case of invasive GAS in a long-term care facility should prompt an epidemiological investigation. Outbreaks in long-term care facilities can result in high morbidity and mortality and might result in a large-scale response involving multiple stakeholders. Epidemiologists from Pennsylvania and North Carolina state health departments will share toolkit resources created to promote a standardized and robust response to invasive GAS in long-term care settings. Resources include investigation algorithms based on draft CDC guidelines; template facility letters; prospective surveillance/symptom identification log; outbreak line list; wound care observation checklist; throat culture collection guidelines; normally sterile site list; antibiotic recommendations for decolonization of carriers; transmission-based precautions for GAS; guidance for restriction of visitors and new admissions during GAS outbreaks; and training webinar slides. During this roundtable, participants will review the toolkits and discuss how their jurisdictions identify and investigate cases or outbreaks of invasive GAS in long-term care settings. Participants will also have an opportunity to provide feedback regarding toolkit strengths and weaknesses, identify additional resource needs, and discuss best practices. Participants will be provided with toolkit resources for implementation in their jurisdictions.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Healthcare-Associated Infections
Consider for Different Presentation?	No
Presenting Author Email Address(es)	james.w.lewis@dhhs.nc.gov; alongenber@pa.gov
Presenting Author(s)	James W Lewis; Allison Longenberger
Institution Affiliation	North Carolina Department of Health and Human Services State Public Health Agency

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Council for Outbreak Response: Healthcare-Associated Infections and Antimicrobial Resistant Pathogens (CORHA) – Progress and Updates

Abstract

Key Objectives:

Participants will hear about the priorities of the Council for Outbreak Response: Healthcare-Associated Infections and Antimicrobial Resistant Pathogens (CORHA), learn about new products developed by CORHA, including work from CORHA's new Workgroup focused on legal and policy considerations related to outbreaks of healthcare-associated infections, and participate in a discussion about future product needs relating to outbreak detection, reporting, investigation, and control.

Brief Summary:

Healthcare-associated infections (HAIs) including antimicrobial-resistant (AR) pathogens cause hundreds of thousands of illnesses and deaths among U.S. patients each year. Despite significant progress, patients are still experiencing preventable harms in the context of outbreaks and other adverse events that stem from delayed recognition of emerging infectious diseases with potential for healthcare transmission, unsafe healthcare practices, contaminated drugs, and medical device risks. Consistent and coordinated approaches are needed to speed up detection of new threats, develop tools to support outbreak investigation, stop outbreaks from spreading, and better inform prevention activities. To address these needs, CDC's Division of Healthcare Quality Promotion (DHQP) funded the Association of State and Territorial Health Officials (ASTHO) and the Council of State and Territorial Epidemiologists (CSTE) to co-lead CORHA. CORHA members include ASTHO, CSTE, CDC, and the National Association of County and City Health Officials (NACCHO), Association for Professionals in Infection Control (APIC), Society for Healthcare Epidemiology of America (SHEA), US Food and Drug Administration (FDA), the Centers for Medicare and Medicaid Services (CMS), and the Association of Public Health Laboratories (APHL). CORHA is a multi-sector collaboration representing the interests of public health and healthcare stakeholders, including healthcare consumers, the medical community, state, local, and territorial public health authorities, professional associations, clinical and public health laboratories, and federal agencies with an interest in HAI and AR prevention and control. Since the 2018 CSTE Annual Conference, CORHA launched a newsletter to highlight CORHA products, outbreak-related news and journal articles, and partner spotlights, developed a series of outbreak detection and response and investigation and control products, and began addressing new topics related to the policy and laboratory aspects of healthcare-associated and antimicrobial resistant organism outbreak response. During this roundtable session, CORHA members will describe newly developed products and discuss new activities— particularly as it relates to developing standards for consistent reporting, notification and public disclosure of HAI outbreaks—with session participants.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Infection Control; Outbreaks
Consider for Different Presentation?	No
Presenting Author Email Address(es)	bzp4@cdc.gov; marion.kainer@tn.gov
Presenting Author(s)	Joseph F Perz; Marion A. Kainer
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Future Development of Applied Public Health Healthcare-Associated Infection/Antibiotic Resistance Workforce: Discussing the Benefits of Certification in Infection Prevention & Control

Abstract

Key Objectives:

Roundtable participants will discuss the importance of public health healthcare-associated infection and antibiotic resistance (HAI/AR) epidemiology staff pursuing professional certification in infection prevention and control (CIC).

Brief Summary:

Historically, the Centers for Disease Control and Prevention (CDC) Epidemiology and Laboratory Capacity (ELC) Cooperative Agreement has focused primarily on surveillance activities. In recent years, an emphasis has been placed on the identification and remediation of gaps and breaches in infection control. The issues identified by public health cross the continuum of care and require evidence-based interventions. A well-trained public health workforce is required to ensure ethical principles are applied in collection, analysis, maintenance, and use of data and information. Obtaining the CIC is a strategy that can assure the level of expertise needed to address the complicated issues identified in healthcare facilities. Certification by the Certification Board of Infection Control and Epidemiology (CBIC) is viewed as a metric of knowledge and assures competency in the field of infection control. Many healthcare facilities require infection preventionists (IPs) to obtain certification; however, it has not been as widely recognized in public health. This round table will provide participants the opportunity to discuss the importance of certification in HAI/AR prevention programs and develop strategies for obtaining CIC. The goal of this roundtable is to facilitate dialogue regarding the importance of certification for the HAI/AR Prevention Programs. Participants will discuss their experience in preparing for the examination and develop strategies to assist the applied public health workforce obtain CIC credentials.

Submission Complete?	Yes
Committee Topic	Infectious Disease Healthcare-Associated Infections
Keywords	Infection Control; Antimicrobial Resistance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
Presenting Author Email Address(es)	dshannon1@isdh.in.gov; danielle.rankin@flhealth.gov
Presenting Author(s)	DJ Shannon; Danielle A. Rankin
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Principles of Successful Collaboration between Public Health Departments' Healthcare Associated Infection (HAI)/Antibiotic Resistance (AR) Programs and State and Local Hospital Partners

Abstract

Key Objectives:

The goals of this session are to identify promising approaches and lessons learned for effective collaboration between public health programs and hospital associations, hospital leadership, chief medical officers, hospital epidemiologists, infection preventionists, and others working in acute care settings. Discussion will focus on the elements of successful collaborations including identifying common goals and priorities, understanding respective roles and obligations, and identifying strategies, challenges, and solutions for maintaining the working relationship as new threats, science, or policy changes emerge.

Brief Summary:

Effective working relationships between public health departments' HAI/AR Programs and state and local hospital or acute care partners are widely considered to be an essential component of an HAI/AR prevention program strategy. State health departments' HAI/AR programs began being funded through CDC in 2009 to promote and support HAI reporting and to publish a state HAI prevention plan. Since HAI reporting becoming mandated through state or other local requirements, as well as via Centers for Medicare (CMS) payment incentive programs, HAI/AR programs and hospitals have had to navigate an evolving relationship that emphasized detection and reporting, but also preventing infections to protect patients. Over the past several years, state and local HAI/AR programs' mission has expanded, especially for infections caused by antibiotic resistant pathogens, to providing significant leadership roles, increasing focus on using data for prevention, and establishing and growing antibiotic stewardship programs in acute care settings. Because of the shared public health and healthcare responsibility to ensure patients receive the highest quality of care, an increasing need exists for public health HAI/AR programs and those individuals working in acute care settings to better understand each other's roles and challenges and to establish common goals and strategies for preventing infections and improving patient outcomes.

Submission Complete?	Yes
Committee Topic	Infectious Disease Healthcare-Associated Infections
Keywords	Collaboration; Antimicrobial Resistance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
Presenting Author Email Address(es)	ekm9@cdc.gov; any9@cdc.gov
Presenting Author(s)	Elizabeth Mothershed; Cecilia Joshi
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Roundtable
ID	11243
Abstract Type	Roundtable
Abstract Title	Roundtable on <i>Candida Auris</i> Surveillance and Control

Abstract

Key Objectives:

- Review current guidance for surveillance for *Candida auris* and public health measures for minimizing transmission.
- Discuss efforts to make *C. auris* reportable in state or local public health jurisdictions.
- Discuss how health departments can partner with healthcare facilities to identify *C. auris* and control its transmission.
- Identify structural barriers to implementing *C. auris* control efforts and possible solutions.

Brief Summary:

Candida auris is an emerging multidrug-resistant yeast that causes invasive infections associated with high mortality. It can spread easily in healthcare settings, causing outbreaks. Since 2016, when CDC first issued a clinical alert regarding *C. auris*, approximately 500 clinical cases have been reported in twelve states. Receipt of healthcare abroad in a country with *C. auris* transmission, being a resident of a high-acuity post-acute care setting, and being colonized with another multidrug-resistant organism (MDRO) are prominent risk factors for *C. auris* infection or colonization. Control of *C. auris* requires good adherence to infection control practices across the continuum of care settings. Institution-level and system-level changes, such as improved staffing ratios and physical layout of patient care areas, may be key factors in limiting transmission. *C. auris* will be nationally notifiable as of January 1, 2019. Many states have already made *C. auris* reportable or are in the process of doing so. It is crucial to support state and local health departments in this effort, as making the condition reportable will aid in earlier detection of and response to cases of *C. auris*, thereby containing its spread. This roundtable session offers an important opportunity to share lessons learned from public health jurisdiction effort to make *C. auris* reportable in their jurisdiction. This roundtable is also an opportunity for state and local health departments to share successes and challenges with *C. auris* surveillance, including efforts to screen patients at high risk for *C. auris*, such as those with recent history of receiving healthcare outside the United States, those colonized with other MDROs (especially carbapenemase-producing organisms), and those with healthcare facility exposure in areas with high prevalence of *C. auris*. Participants will be encouraged to share ideas on how control of other MDROs can help inform *C. auris* control efforts on experiences with implementing control measures, and the role of regulatory agencies and policy in improving compliance with infection control measures in healthcare facilities.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infection Control; Emerging Infections; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
Presenting Author Email Address(es)	ilyn0@cdc.gov; Inv6@cdc.gov
Presenting Author(s)	Brendan R. Jackson; Kaitlin Forsberg
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	An Epidemiologic Profile of Acute and Chronic Hepatitis C Infection and Hepatitis C-Associated Mortality in Saint Louis County, MO

Abstract

BACKGROUND: To better understand the transmission of hepatitis C virus (HCV), the burden of chronic HCV infection, and trends in HCV-associated mortality in Saint Louis County, MO, the Saint Louis County Department of Public Health (DPH) created an epidemiologic profile for HCV infection.

METHODS: We analyzed acute and chronic HCV cases diagnosed among Saint Louis County residents between 2013 and 2017 and HCV-related deaths from 2010 to 2016. In 2016, DPH began investigating reports of HCV infection among people aged 30 years and younger, or reports including evidence of acute infection (e.g., jaundice), to assess behavioral risk factors and classify cases as acute or chronic. We calculated rates per 100,000 population by sub-county region, age group, sex, race, ethnicity, and census tract poverty level. We adjusted mortality rates to the 2000 U.S. population.

RESULTS: In 2017, the acute HCV incidence rate in Saint Louis County was 1.9 cases per 100,000 population, higher than the most recently reported state and national rates. The rate of newly reported chronic HCV infection was 60.2 cases per 100,000 population—a decline of 4.7% from 2016 and a 34.6% decline from the five-year high in 2015. The age-adjusted HCV mortality rate from 2010 to 2016 was 1.4 deaths per 100,000 population. Acute and chronic HCV rates and HCV-associated mortality rates are highest in regions of the county with lower socioeconomic status. For both acute and chronic HCV cases where risk factor data was reported, approximately 75% reported injection drug use. Rates of acute and chronic HCV have increased among younger populations since 2013 and remain higher among men than women. In 2017, black residents had acute and chronic HCV rates 1.5 times and 3.4 times those of whites, respectively. HCV-associated mortality remains highest among persons aged 55 years and older.

CONCLUSIONS: The burden of HCV infection and HCV-related mortality falls disproportionately on Saint Louis County's black residents, men, and people living in very poor census tracts, especially in the county's Inner North region. Acute HCV incidence in Saint Louis County is high, and our reported incidence likely underestimates true incidence due to asymptomatic infections, under-testing, and under-reporting. Surveillance bias inherent to our acute HCV case finding methods may especially underestimate acute HCV incidence in people aged 30 years and older, and an apparent increase in acute infection is likely driven both by a true incidence in transmission related to injection drug use and by increased case finding activity.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Infectious Diseases; Hepatitis; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	atorgerson@stlouisco.com
Presenting Author(s)	Andrew Torgerson
Institution Affiliation	Saint Louis County Department of Public Health Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10720
Abstract Type	Breakout
Abstract Title	Community Outbreak of Hepatitis B, Washington State, 2018

Abstract

BACKGROUND: In August 2018, Spokane Regional Health District (SRHD) observed an increase in cases of acute hepatitis B. Acute hepatitis B outbreaks are rare in Washington State (WA). The WA Department of Health (DOH) was invited to assist with the investigation, including risk factor identification and transmission control.

METHODS: All acute hepatitis B cases with onset dates after December 31, 2017 that spent time in Eastern Washington or the Idaho Panhandle during their exposure period were included. Case investigation included interviews, medical record review, and review of local syringe exchange program use. Contact tracing was performed through interviews, Facebook, jail follow-up, and review of existing sexually transmitted infection program records. When available, case serum specimens were sent to the Centers for Disease Control and Prevention for whole genome sequencing (WGS). SRHD partnered with community organizations to provide outreach and TWINRIX vaccine to adults who inject drugs, have sexual risk, and/or are experiencing homelessness. Text message reminders for subsequent doses and a social media campaign augmented the vaccination effort.

RESULTS: As of December 19, 2018, 14 cases meeting the confirmed outbreak case definition were identified; onset dates ranged from February to September 2018. Nine cases were male, and the median age [range] was 35 [18-67] years. Based on interviews, medical record review, and review of local syringe exchange program use, the following risk factors during the exposure period were identified for persons with information available: 7/14 injection drug use (IDU); 5/12 sexual risk; 4/12 potential healthcare exposures; and 4/11 incarceration. Two cases had both sexual risk and IDU. Two cases with IDU also experienced homelessness. No linkages were identified between potential healthcare exposure sites. WGS of four cases indicated that two specimens had $\leq 0.22\%$ nucleotide variation; a third specimen was closely related. The only identified common risk factor between these three cases was IDU. A fourth case was unrelated by WGS and denied IDU. A total of 193 first doses and 63 second doses of TWINRIX have been administered; 17 persons have received a complete vaccine series.

CONCLUSIONS: This investigation is ongoing. Behavioral risk factors – IDU or sexual risk – were identified in 10 of 14 cases. This investigation highlights the value of combined epidemiological investigation with WGS of hepatitis B virus. Based on this investigation, a targeted vaccination strategy was implemented through collaboration with community partners, use of reminder recall text messages, and educational outreach through social media.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Outbreaks; Risk Factors; Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	mackenzie.fuller@doh.wa.gov
Presenting Author(s)	Mackenzie S Fuller
Institution Affiliation	Washington State Department of Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11063
Abstract Type	Lightning
Abstract Title	Access to Hepatitis C Treatment Providers in Wisconsin Following a Change in State Medicaid Policy

Abstract

BACKGROUND: Rates of hepatitis C virus (HCV) infection have increased in Wisconsin, particularly in rural areas. Treatment with direct-acting antivirals (DAAs) can cure HCV. However, because of their high cost, many state Medicaid programs have restricted which providers can prescribe and which patients can receive DAAs. On July 1, 2017, Wisconsin Medicaid removed restrictions requiring that DAAs be prescribed by specialists in infectious disease or gastroenterology. As a project for the federally-organized HCV/Medicaid Affinity Group, we evaluated whether the number of DAA providers, particularly non-specialists, increased during the 12 months after the policy change. Additionally, we evaluated whether access to DAA providers varied in rural compared to urban areas of Wisconsin.

METHODS: Wisconsin Medicaid prescription claims data were searched to identify the names, medical specialties, and clinic addresses of providers who submitted claims for DAA prescriptions during the 12 months before (Time₁: July 1, 2016-June 30, 2017) and/or the 12 months after (Time₂: July 1, 2017-June 30, 2018) the policy change. We compared the number of providers, by specialty, during Time₁ and Time₂. Additionally, we compared provider locations to HCV prevalence data reported to the Wisconsin Division of Public Health as of 2017. We used ArcGIS to calculate the driving time between the residence address of each prevalent HCV case and the address of the closest provider. Percentages of cases residing within 30 minutes of a provider were calculated and stratified by whether the case resided in a rural or urban zip code.

RESULTS: From Time₁ to Time₂, the number of DAA providers increased by 48% (from 120 to 178). Among the 58 additional providers, 50 (86%) were specialists and 8 (14%) were non-specialists, including 4 family medicine physicians and 3 internal medicine physicians. Specialists accounted for the majority of providers during Time₁ (96%) and Time₂ (93%). The percentage of prevalent HCV cases residing within 30 minutes driving time of a provider was similar during Time₁ (77%) and Time₂ (81%). During Time₂, only 34% of rural cases resided within 30 minutes of a provider compared to 96% of urban cases ($p < 0.001$).

CONCLUSIONS: During the 12 months after the policy change, few non-specialists prescribed DAAs. Additionally, HCV cases residing in rural areas had less access to DAA providers than cases residing in urban areas. Expansion of DAA prescribing to non-specialists may require provider education regarding HCV treatment and current Medicaid policy as well as identification of any institutional barriers.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Geographic Information Systems (GIS); Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ruth.koepke@wisconsin.gov
Presenting Author(s)	Ruth Koepke
Institution Affiliation	Wisconsin Department of Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11379
Abstract Type	Lightning
Abstract Title	Hepatitis C Virus Infection Among Women of Reproductive Age As a Primary Prevention Measure for Neonatal Abstinence Syndrome Infants; Tennessee, 2016

Abstract

BACKGROUND: Tennessee (TN) is home to one of the highest opioid prescribing and hepatitis C virus (HCV) infection rates in the nation and rates are on the rise. Driven by the opioid epidemic, the highest rates of HCV are among people who inject drugs and specifically among people less than 30 years of age, white, and living in rural areas. Given overlapping consequences of the opioid epidemic, we sought to determine the co-occurrence of infants diagnosed with Neonatal Abstinence Syndrome (NAS) and mothers with history of HCV infection.

METHODS: Birth certificate data from 2016 were obtained from the TN Department of Health Birth Statistical File. Maternal information was matched with HCV laboratory data available in the TN NEDSS Based System (NBS) to ascertain maternal HCV history. Mothers were considered to have a history of HCV if maternal HCV infection was denoted on the birth certificate, or if NBS records contained a positive HCV antibody or RNA test result prior to two weeks postpartum. A cohort of infants born in 2016 with an NAS diagnosis was derived from 2016 final and 2017 provisional inpatient and outpatient hospital discharge data using ICD-10 code P96.1 (neonatal withdrawal symptoms from maternal use of drugs of addiction). NAS cases were linked to the maternal HCV surveillance dataset and all analyses were completed using SAS 9.4.

RESULTS: There were 80,755 TN live births in 2016; 1,614 of these infants were born to a mother with a history of HCV infection (20.0 per 1,000 live births) and 1,227 had an NAS diagnosis within one year of birth (15.2 per 1,000 live births). Of infants diagnosed with NAS, 435 (35.5%) were born to a mother with a history of HCV (5.4 per 1,000 live births). The preponderance of these infants resided in Eastern TN (73.8%) and were born to Non-Hispanic white mothers (96.5%), aged 18 to 29 years (65.5%).

CONCLUSIONS: This analysis illustrates a significant overlap between maternal HCV history and subsequent NAS diagnosis of her infant, suggesting that HCV testing among women of childbearing age may serve as a proxy for maternal opioid use and *in-utero* opioid exposure. Therefore, the benefits of HCV testing among women of childbearing age may include linking HCV-positive women to treatment for HCV, as well as to opioid use disorder services.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Maternal and Child Health; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lindsey.sizemore@tn.gov
Presenting Author(s)	Lindsey A. Sizemore
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Lightning
Abstract Title	Hepatitis C Virus Seroconversion Among Health Department Clients: Tennessee, 2016-2018

Abstract

BACKGROUND: In 2016, the TN Department of Health (TDH) piloted hepatitis C virus (HCV) testing in three health departments (HDs) in Eastern Tennessee, with subsequent statewide HD scale-up in 2017. Testing was routine opt-out for STD patients and risk factor (RF) based for others. Risk factors were assessed for all clients tested. Repeat testing was permitted for patients with ongoing RFs. TDH's Public Health Laboratory (PHL) processed all specimens collected in HDs. We sought to quantify the number of HCV seroconversions detected among patients undergoing testing in HDs in TN.

METHODS: Results from HCV testing conducted at TDH's PHL among HD clients tested from June 1, 2016 to December 10, 2018 were aggregated and analyzed using SAS 9.4. Data were matched on a locally defined variable, XID (client last name, client first name, and client DOB) and subsequently sorted by XID, testing date, and test result. Clients with only one test result or with an initial positive Ab were excluded; remaining clients were then examined to determine if they met our definition of HCV seroconversion (initial negative HCV Ab test result followed by a positive HCV Ab result), as well as the elapsed time period between the two tests.

RESULTS: During the evaluation period, 4,575 people within our cohort had 2 or more HCV Ab tests conducted at different points in time, with 1.6% (n=74) seroconverting. Additionally, 3,033 people had at least 2 tests occurring within 12 months, with 1.6% (n=48) seroconverting and meeting CSTE's definition of confirmed acute HCV infection. Of clients with confirmed acute HCV, 60.4% (n=29) were tested in Eastern TN; 58.3% (n=28) were female; 75.0% (n=36) were white; and the median age at seroconversion was 27 years (17-61). Reported RFs changed from the time of first negative to first positive Ab test: 45.5% to 57.8% for history of injection drug use, 40.9% to 51.1% for non-professional tattoo, 52.3% to 62.2% for incarceration, and 57.8% to 62.2% for intranasal drug use.

CONCLUSIONS: Our findings demonstrate the importance of repeat HCV testing among clients with RFs and the utility of capturing HCV Ab negative test results for the detection of acute HCV cases that would otherwise go unreported. These 48 cases represent about one-third of currently reported confirmed acute HCV cases in TN each year. The identification of additional acute HCV cases provides valuable opportunities for case investigation, partner services, and linkage to prevention and treatment services.

Submission Complete?	Yes
Committee Topic	Infectious Disease Hepatitis
Keywords	Hepatitis; Infectious Diseases; Health Care
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lindsey.sizemore@tn.gov
Presenting Author(s)	Lindsey A. Sizemore
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11727
Abstract Type	Lightning
Abstract Title	Increase in Hepatitis C Testing at Facilities Serving High Risk Clients in Allegheny County, PA

Abstract

BACKGROUND: Hepatitis C is a liver disease caused by infection with the bloodborne hepatitis C virus (HCV). Allegheny County launched an HCV elimination initiative in 2018, with increasing testing and linkage to care and treatment as primary goals. To assess access to HCV testing and better understand testing barriers in Allegheny County, the Allegheny County Health Department (ACHD) conducts sentinel surveillance of HCV testing at community organizations serving individuals at high risk for HCV infection.

METHODS: Facilities participating in the sentinel surveillance system include federally qualified and neighborhood health centers, organizations providing HIV services, drug and alcohol treatment facilities, homeless service programs, corrections, and syringe service programs. The ACHD annual survey captures data on the number of 1) HCV screening tests completed, 2) the number of positive HCV screening tests, 3) the number of HCV confirmatory tests completed, 4) the number of positive confirmatory tests, 5) the number of referrals to care, and 6) the number of clients treated. Data are analyzed in Excel and Epi Info.

RESULTS: Of 82 organizations contacted, 78 (95%) provided HCV testing data for both 2016 and 2017. In 2016, 9 (12%) facilities reported conducting HCV screening compared to 21 (27%) in 2017. Between 2016 and 2017, the volume of HCV screening tests increased (2,502 in 2016 vs. 15,447 in 2017), but the percent positive remained similar (14% in 2016 vs 13% in 2017). In 2016, 6 (8%) facilities offered confirmatory testing for individuals with positive HCV screening tests while 8 (10%) facilities offered confirmatory testing in 2017. Between 2016 and 2017, the volume of confirmatory tests increased (149 in 2016 vs 1,993 in 2017); the positivity also increased (60% in 2016 vs 66% in 2017). Lack of resources and the inability to bill for services were reportedly the main barriers to HCV testing.

CONCLUSIONS: The number of facilities conducting any HCV testing increased between 2016 and 2017, but the total number of facilities screening remained low. Many facilities serving clients at high risk for HCV infection do not currently offer HCV testing. To reduce the burden of HCV and its sequelae, health department staff must work with key partners to increase testing of persons at risk and ensure that individuals with active infection are linked to care and treatment. Sentinel surveillance is useful for monitoring progress towards HCV elimination and identifying organizations in need of testing services.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Infectious Diseases; Surveillance; Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email	jennifer.fiddner@alleghenycounty.us
Address(es)	
Presenting Author(s)	Jennifer Fiddner
Institution Affiliation	Allegheny County Health Department Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11152
Abstract Type	Lightning
Abstract Title	Increasing Completeness and Timeliness of Reporting in an Acute Hepatitis A Outbreak

Abstract

BACKGROUND: Prior to 2017, the incidence of acute hepatitis A (HAV) in Kentucky was at or near the national average annually: the majority of cases were associated with travel to endemic areas. An HAV outbreak was declared in November 2017, when Kentucky saw a sharp increase in the number of HAV cases not associated with travel. Kentucky requires that cases of acute HAV be reported within 24 hours (902 KAR 2:020). Prompt reporting allows public health to implement control measures more effectively, such as removal from high-risk occupations and administration of post-exposure prophylaxis (PEP) to close contacts. Due to the historically low incidence, local health department (LHD) staff were unaccustomed with the investigation and reporting process for acute HAV infections, resulting in delayed reporting and decreased opportunities to prevent further transmission.

METHODS: Reportable disease staff at KDPH worked to develop guidance documents for distribution to LHD staff, which were shared electronically and placed on KDPH's website. As delays in reporting HAV cases continued, individual emails and phone calls to jurisdictions were implemented but proved to be too time-consuming given rapidly rising case counts. A quick Plan-Do-Study-Act (PDSA) cycle identified the need for further improvement with technical assistance. An "outstanding case" document was created to notify LHD staff of outstanding cases in their jurisdiction. The document identified what actions needed to be completed in order to approve the case and was electronically shared amongst counties with outstanding cases.

RESULTS: At the time of implementation of the outstanding case list, there were 50 outstanding cases. Within 2 days of county notification, outstanding cases decreased to 27. Prior to a second notification, outstanding cases totaled 35, decreasing to 20 after notification.

CONCLUSIONS: As case counts increased across more counties in Kentucky, outstanding cases continued to be an issue. However, recurring distribution of the outstanding case list yielded similar results, allowing cases to be confirmed in a timelier manner and PEP offered to more individuals. Improved communication between KDPH and investigators in LHDs allowed for swift improvement of HAV reporting, setting a standard for communication and rapid response in future outbreaks. The outstanding list has been beneficial as a reminder to LHD staff, who typically work on multiple tasks daily. Although delayed reporting continues to occur on occasion, routine notification of these cases has resulted in fewer missed opportunities for PEP.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Communication; Hepatitis; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Amanda.Hunt@ky.gov
Presenting Author(s)	Amanda Hunt
Institution Affiliation	Kentucky Department for Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11236
Abstract Type	Lightning
Abstract Title	Negative Impacts of Surveillance Definition Change on Kentucky's Ongoing Hepatitis A Virus Outbreak

Abstract

BACKGROUND: Kentucky declared an acute hepatitis A virus (HAV) outbreak in November 2017. Kentucky's outbreak definition incorporates positive HAV-sequencing results, risk factor information, and the CSTE 2012 surveillance case definition. Recently, CSTE voted to adopt a revised definition effective January 2019. Key differences between surveillance definitions include minimum bilirubin levels if jaundice is unknown, minimum serum alanine aminotransferase (ALT) levels, nucleic acid amplification test (NAAT) for HAV RNA positive, and absence of more likely diagnoses. This project identified how changing surveillance definition during an ongoing outbreak affects the number of cases identified and investigated.

METHODS: Data collected for previous outbreak-associated cases were reviewed to determine whether case status would change using the 2019 definition. If jaundice was not reported, cases with ALT levels under 200 IU/L were excluded. Cases with bilirubin levels of at least 3.0 mg/dL were included. ALT levels were evaluated before bilirubin levels since they are not consistently reported. More likely diagnoses were not considered. Although HAV sequencing information was available for some case specimens, this could not be evaluated for all cases due to a significant delay in receiving results for all specimens. Data from August 1, 2017 through December 29, 2018 (end of 2018 MMWR week 52) were used.

RESULTS: Of 3421 outbreak-associated cases, 3381 met 2012 surveillance and outbreak definition criteria. Non-surveillance cases include 40 individuals with positive HAV sequencing, which would be included under 2019 criteria. Using 2019 criteria for jaundice, bilirubin levels, and ALT levels, 166 cases were excluded (N=3255), a 4.9% decrease. Jaundice was unknown for 365 cases. ALT information was unknown for 69 cases. Bilirubin information was available for 582 cases, 448 of which met bilirubin level criteria. Five cases that would have been excluded worked in high-risk settings.

CONCLUSIONS: This project highlights the importance of considering milder forms of illness during a large, ongoing outbreak. With limited resources, it is difficult for local investigators to prioritize case investigations when illnesses do not meet surveillance definition but meet outbreak definition. Revising the outbreak definition to incorporate changes in the 2019 surveillance case definition would exclude several cases, even those positive for HAV by sequencing. Cases excluded using 2019 criteria would not have been investigated, leading to an underestimation of HAV cases and decreased ability to provide education and implement control measures prevent further transmission among non-risk populations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Surveillance; Hepatitis; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jennifer.khoury@ky.gov
Presenting Author(s)	Jennifer Khoury
Institution Affiliation	Kentucky Department for Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10932
Abstract Type	Poster
Abstract Title	An Evaluation of Hepatitis C Surveillance — Harris County, TX, 2010-2018

Abstract

BACKGROUND: Chronic Hepatitis C virus (HCV) infects an estimated 4.1 million persons in the US (Hofmeister et al., 2018). In 2016, nearly 3,000 cases of acute HCV were reported, with estimates that the actual total exceeds 40,000 (CDC, 2018). HCV burden grows each year and screening has increased as recommendations have changed (CDC, 2018; USPSTF, 2013). This increase, along with evolving treatment options, changes in case definition, and implementation of electronic laboratory reports (ELRs), all contribute to the increase in Hepatitis C reports received by Harris County Public Health (HCPH). As a result of these changes, we identified the need to evaluate, update, and improve our HCV surveillance system.

METHODS: The purpose of this evaluation was to understand timeliness, simplicity, flexibility, data quality, and usefulness within HCPH's current HCV surveillance system. We utilized *Updated Guidelines for Evaluating Public Health Surveillance Systems* (MMWR, 2001) to evaluate all Hepatitis C reports received from January 1, 2010 through October 31, 2018. Data were pulled from our Insight database and imported to STATA 14.2 for cleaning and analysis. Results were used to identify strengths and weaknesses within HCPH's current surveillance system and formulate recommendations for improvement.

RESULTS: For the specified time period, we investigated 765 reports. Over half (51.6%) were referred to other jurisdictions, while the remaining 370 belonged to HCPH. We observed variability in the number of annual reports, ranging from four in 2011 to 177 through October 2018. We also noted a sharp increase in reports beginning in 2017. This recent influx requires greater resource utilization, while the total number of acute cases, which are reportable in Texas, has not exceeded five in any given year. Most demographic data were complete, except for missing data on race (5.8%), ethnicity (9.7%), or both fields (29.6%). The average time from report receipt to completion was 17.9 days and the median was eight days.

CONCLUSIONS: This evaluation shows that although HCV reports have increased over time, the number of acute HCV cases identified have remained relatively stable, a finding which warrants further study to understand the reasons for the variance. We identified timeliness and completeness of certain variables, including race and ethnicity, as areas for improvement. Action is required to more accurately capture cases and streamline report completion. Results from this evaluation will be applied to future projects to improve our HCV surveillance system, including increasing sensitivity, using HCV ELRs.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Surveillance; Evaluation
Consider for Different Presentation?	Yes
Presenting Author Email	melanie.kowalski@phs.hctx.net
Address(es)	
Presenting Author(s)	Melanie Kowalski
Institution	Harris County Public Health
Affiliation	CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11398
Abstract Type	Poster
Abstract Title	Assessing Hepatitis B Case Categorization through Positive IgM Anti-Hbc Results in Jefferson County, Kentucky

Abstract

BACKGROUND: IgM antibody to hepatitis B core antigen (IgM anti-HBc) is considered an important diagnostic marker of acute hepatitis B and distinguisher between chronic infection. In addition to clinical symptoms and abnormal liver function tests, the acute hepatitis B case definition conditionally requires a positive IgM anti-HBc test if done. All 2016-2017 IgM anti-HBc lab reports received were assessed how many were associated with an acute confirmed infection. Lacking a probable case definition, we evaluated remaining positive labs to discern which criteria failed to meet the confirmed case definition.

METHODS: Lab reports and confirmed acute cases were extracted from Kentucky's National Electronic Disease Surveillance System (NEDSS) for years 2016-2017. All IgM anti-HBc results were categorized as positive, negative, or undetermined. Each category of lab results associated with an acute case was determined. Positive IgM anti-HBc results not connected with a case were investigated to find which criteria did not meet case definition (positive HBsAg result, symptomatic, elevated liver enzymes or jaundiced, and previous history of infection).

RESULTS: Among 3822 IgM anti-HBc associated lab reports for years 2016-2017, 6 indeterminate results and 2 orphaned records were excluded from further investigation. All 46 acute Hepatitis B cases have an associated positive IgM anti-HBc lab result. Amid the remaining 124 (72.3%) positive labs were not associated with an acute case, 2 (1.6%) were misclassified, 22 (17.7%) positive results lacked at least one unknown or unrecorded criterion to classify, 68 (54.8%) reported no clinical signs or symptoms, 31 (25%) had negative HBsAg testing, 38 (30.6%) had no HBsAg recorded, 36 (29%) had normal liver function tests, 61 (49.2%) lacked liver function testing or noted jaundice.

CONCLUSIONS: Classification of acute hepatitis B requires several criteria from different categories, and incomplete reporting is a major challenge of passive surveillance. A modified electronic surveillance system with improvement of how information is entered and stored in a standardized process will lead to more accurate results. Though a positive IgM anti-HBc result is often regarded as an important marker, less than a third of positive lab results were seen to be acute cases; this warrants the importance of a complete evaluation of other criteria and receiving accurate information from providers.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Surveillance; Hepatitis; NNDSS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	fatima.ali@louisvilleky.gov
Presenting Author(s)	Fatima Ali
Institution Affiliation	Louisville Metro Department of Public Health and Wellness Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10910
Abstract Type	Poster
Abstract Title	Development of a Best Practices Hepatitis C Virus Testing Algorithm

Abstract

BACKGROUND: About 71 million people are infected with chronic hepatitis C virus (HCV); almost 400,000 die annually from its complications. CDC recommends targeted screening (August 2012) and streamlined testing (May 2013): a reactive HCV antibody (Ab) test should be followed by confirmatory HCV RNA viral load (HCVL). After input from key clinical providers, critical laboratory personnel, and administration, Lifespan labs instituted a novel testing protocol that adheres to this national guideline and optimizes patient testing.

METHODS: Prior testing involved HCV Ab screening; with reactive results requiring the clinician to call the patient back for a second blood draw for confirmation of active disease using a RNA test. • Internal medicine and Pathology jointly approached the Medical Executive Committee (October 2015) to approve an automatic reflex from a positive Ab to a confirmatory RNA test. This allowed two blood specimens to be drawn at one time.

- The Laboratory Information (LI) department created an algorithm automatically initiating this reflex testing.
- To ensure patient specimens remained stable for RNA detection, use of plasma preparation tubes were instituted.
- The protocol went live in March 2016 with a qualitative RNA test (Hologic).

Further optimization in July 2017 included validating a quantitative HCVL test (Roche Diagnostics) and the qualitative test was eliminated.

RESULTS: With implementation of reflex testing, patient samples more than doubled; processing and technical labor increased. From July to December 2017, 12,727 HCV Ab tests were performed; of those, 508 were positive (3.9%) and reflexed to the HCVL (44% were confirmed active disease). 200 of these active patients were randomly selected and evaluated to assess how automatic reflex changed test ordering. More true positive HCV patients were identified; yet 30% had multiple Ab tests performed unnecessarily. Based on this repetitive testing, we worked with the LI department and laboratory leadership to formulate an appropriate auto-cancel algorithm.

CONCLUSIONS: Patients tested through Lifespan get HCV Ab screening and a baseline HCVL from one phlebotomy visit. This optimizes follow-up for treatment of HCV and value of reflex testing on patient outcomes. Because of the high percentage of repeat Ab testing, we utilized the electronic medical record to auto-reject duplicate requests in those with active HCV. Future investigation of the reduction of this superfluous testing will be warranted to determine the impact on both laboratory costs and patient care.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Cost-Effectiveness; Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	sara.geffert@lifespan.org
Presenting Author(s)	Sara Geffert
Institution Affiliation	Warren Alpert Medical School at Brown University / Rhode Island Hospital / Lifespan Academic Institution

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	11002
Abstract Title	Poster
	Epidemiologic and Clinical Differences between Treated and Untreated Hepatitis C Patients in Rhode Island

Abstract

BACKGROUND: The majority of Hepatitis C virus (HCV) testing in Rhode Island (RI) occurs at Lifespan laboratories, providing an opportunity for comprehensive review of HCV screening and treatment practices. The objective of this study is to identify clinical and socioeconomic factors associated with patients who were treated for HCV vs those who were not.

METHODS: 2028 quantitative Hep C viral loads (HCVL) were performed between 7/1/2017 and 12/31/2017 at Lifespan laboratories. Duplicates were removed, leaving 1544 unique patients. Patients with negative Hep C antibody/negative HCVL were excluded. Screening and treatment locations, gender, age, intravenous drug abuse (IVDA), alcohol abuse, presence of cirrhosis, Fibrosis-4 score, human immunodeficiency virus (HIV) co-infection, and insurance were extracted from medical records of 200 randomly selected confirmed Hep C infected patients. Statistically significant differences between the treated/non-treated were calculated using single tailed fisher exact test and odds ratios.

RESULTS: Of 200 patients reviewed, 64% (127/200) had undetectable HCVs: 15% spontaneously cleared, 69% had sustained virologic response (SVR), and 8% were treated but had a 12-week SVR pending. 40% of patients were treated at gastroenterology (GI), and 30% at infectious disease (ID) clinics. 36.5% (73/200) of patients had detectable HCVs: 92% were untreated, 4% failed treatment, and 4% were treated then re-infected. No statistically significant differences were found in gender, IVDA, alcohol abuse, and HIV co-infection between the treated and untreated groups. Patients were more likely to be treated if born between 1945 and 1965 (OR 2.5, 95 CI 1.3-4.8, $p = .004$), had a Fib4 score of 1.45-3.25 (OR, 95 CI 1.1-3.9, $p = .02$), compensated cirrhosis (OR 6.1, 95 CI 2.2-16.6, $p < .001$), or initially screened at an ID clinic (OR 2.6, 95 CI 0.9-6.9, $p = .03$). Patients were less likely to be treated if born after 1965 (OR 0.5, 95 CI 0.2-0.9, $p = .02$), and screened while an inpatient (OR 0.16, 95 CI .04-.6, $p = .003$).

CONCLUSIONS: A HCV screening/treatment training program for RI primary care providers would be helpful to increase treatment of those screened at IM, FM, and GI clinics. The program should focus on those born after 1965; with the opioid epidemic afflicting younger patients those born after 1965 are at an increasing risk of acquiring HCV. And, this year RI passed legislation extending Medicare coverage for treatment of all Fib4 scores/ fibrosis stages so treatment efforts should also focus on Medicare patients with Fib4 scores <1.45 .

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Hepatitis
Consider for Different Presentation?	Hepatitis; Infectious Diseases; Screening
Presenting Author Email Address(es)	Yes
Presenting Author(s)	yousaf.anna@gmail.com
Institution Affiliation	Anna Yousaf
	Warren Alpert Medical School at Brown University
	Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11554
Abstract Type	Poster
Abstract Title	Epidemiological Study of Eight West Virginia Counties Involved in Statewide Hepatitis A Outbreak, March-December 2018

Abstract

BACKGROUND: Hepatitis A is a communicable disease transmitted by the fecal-oral route or by consumption of contaminated food or water. It is caused by the hepatitis A virus and can inflame and damage the liver and is typically an acute infection. West Virginia has seen a recent increase in the number of hepatitis A cases since March 2018. In the whole state of West Virginia, there have been 2,089 confirmed cases as of October 19, 2018, 634 of which were in Boone, Cabell, Jackson, Lincoln, Logan, Mason, Mingo, and Wayne counties.

METHODS: I am conducting a retrospective observational study to look at the prevalence and incidence of hepatitis A cases in these eight counties and compare these values from before and during the outbreak. I will also determine associated risk factors, including concurrent hepatitis B infection, hepatitis C infection, or both hepatitis B and C infection, homelessness, IV drug use, non-IV drug use, and recent incarceration using relative risk, increased risk, and odds ratio. The population of this study will include cases of hepatitis A collected by the regional epidemiologist at Cabell Huntington Health Department during the non-outbreak and outbreak periods in these eight counties. Confirmed hepatitis A cases will be identified using the case definition determined by the CDC and the Cabell Huntington Health Department records will be studied for demographic characteristics, possible exposures and risk factors, signs and symptoms, infectious periods, and other relevant information. The data will be collected from equivalent non-outbreak and outbreak time periods. Identifiable information will be removed from the data to maintain patient confidentiality. Data analysis will be done using SAS software and using the CDC's program Epi Info™ to generate statistics and visual aids.

RESULTS: Preliminary evaluations indicate a possible link with IV drug use and co-infection with hepatitis C. This will be further investigated along with other associated risk factors as reported cases within the window are investigated and completed.

CONCLUSIONS: This project will show the spread of hepatitis A in these eight West Virginia counties, and will identify the populations most at-risk for developing Hepatitis A. My findings will help the health department and other health organizations focus their resources, especially testing and vaccination, to control the spread of hepatitis A.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Epidemiology; Risk Factors
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nerhood1@marshall.edu
Presenting Author(s)	Kayleigh J Nerhood
Institution Affiliation	Marshall University Student

Submission Type	Breakout/Quick/Lightning/Poster
ID	11682
Abstract Type	Poster
Abstract Title	Estimation of Hepatitis C Prevalence in Allegheny County, PA

Abstract

BACKGROUND: Infection with hepatitis C virus (HCV) can cause severe liver disease if not diagnosed and treated. The Allegheny County Health Department (ACHD) is collaborating with partner agencies to increase HCV testing and treatment. To help determine resources needed, ACHD estimated the number of county residents exposed to HCV (antibody positive) and the number currently infected (RNA positive) using the methodology published by Hofmeister et al.

METHODS: The number of HCV-positive noninstitutionalized adults ≥ 18 years was estimated using the National Health and Nutrition Examination Survey (NHANES) HCV prevalence estimates for 2013-2016 (1.5% HCV antibody positive and 0.9% RNA positive). The number of HCV-positive persons in populations excluded from NHANES was estimated using HCV antibody/RNA prevalence estimates derived by Hofmeister et al for the homeless (14.7%/10.8%), the incarcerated (16.1%/10.7%), nursing home residents (1.3%/0.5%), and active military personnel (1.0%/0.5%). The population size for these groups in Allegheny County was estimated based on local surveys (nursing homes, homeless), county jail and state prison census (incarcerated), and a proportion of the statewide active military census. Estimates of HCV prevalence were compared with the number of HCV cases reported to ACHD.

RESULTS: Of noninstitutionalized adults (≥ 18 years) in Allegheny County, we estimated that 14,674 (1.5%) are HCV antibody positive and 8,806 (0.9%) are RNA positive. HCV-antibody positive estimates for excluded groups include 168 homeless, 915 incarcerated, 88 nursing home residents, and 6 active duty military personnel for a total of 15,373 HCV antibody positive persons in the county. Similarly, adding 124 homeless, 608 incarcerated, 34 nursing home residents, and 3 military personnel yields a total of 9,575 HCV RNA positive persons. By comparison, in 2006-2017, 18,885 persons were reported to ACHD as HCV antibody positive and 13,021 as HCV RNA positive.

CONCLUSIONS: The estimates of HCV-positive persons in Allegheny County are lower than the number of persons already reported. Estimates may be too low if 1) NHANES underestimates prevalence in the general population, 2) the county's population is at higher risk than the nation as a whole, e.g. includes a higher percentage of substance users, 3) the prevalence in the county's excluded groups is higher than Hofmeister's values or 4) local surveys underestimate size of the excluded populations. Reports received by ACHD in the past exceed the number of current residents already diagnosed due to migration, death, or other factors. Alternative methods of estimating current prevalence are needed to better assess burden and target resources.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Local Epidemiology; Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Kristen.Mertz@AlleghenyCounty.US
Presenting Author(s)	Kristen Mertz
Institution Affiliation	Allegheny County Health Department Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11555
Abstract Type	Poster
Abstract Title	Hepatitis C Cause of Death in North Carolina, 2017

Abstract

BACKGROUND: It is estimated that there are 150,000 individuals in North Carolina infected with hepatitis C (HCV). Despite the growing burden of disease, little is known about cause(s) of death for individuals with HCV. HCV electronic laboratory records became reportable by law in North Carolina in October of 2016. Currently, North Carolina collects limited risk data for chronic HCV. Utilizing two years of HCV reporting data, we matched and analyzed ICD-10 codes from death certificates to assess the cause(s) of death for individuals with acute and chronic HCV.

METHODS: We used the Centers for Disease Control and Prevention (CDC) Link Plus cancer registry linkage program to match case records to death certificates and identify cause(s) of death in individuals diagnosed with HCV in the state of North Carolina in the year 2017. Individuals were matched based on their first and last name, date of birth, social security number, and race/ethnicity. SAS 9.4 (Cary, NC) programming was utilized to merge death records from Link Plus with HCV cases in our North Carolina Electronic Disease Surveillance System (NC EDSS).

RESULTS: In total, laboratory test results for 19,773 North Carolina residents with HCV were received in 2017. Among these, we identified 567 persons with matching death certificates. Each death certificate contained between one and eleven ICD-10 codes defining their cause(s) of death. The average age at death was 54.6 years (range, 20-91 years). The majority of people with HCV case records were men (11,700/19,773, 59%), and the overall case-fatality rate was higher among men (365/567, 68%). However, women had a higher case-fatality rate in the 25-29 (18/29, 62%) and 40-44 (12/20, 60%) age groups. Further investigation revealed a higher proportion of deaths among women ages 20-34 in the category of "accidental poisoning and exposure to drugs" (19/30, 63%), compared to 41% of male deaths in the same age group (23/56). Men had the highest overall proportion of deaths due to "Neoplasms" (77/365, 21%) compared to 13.7% for women (25/182).

CONCLUSIONS: Matching death certificate data to HCV case data in NC EDSS allows us to determine the cause(s) of death and other comorbidities in individuals diagnosed with HCV. The ongoing effect of the opioid epidemic can be seen in the proportion of drug exposure in the deaths of HCV recorded individuals. Efforts to increase access to treatment could decrease death rates in this group.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	melodie.bianchini@dhhs.nc.gov
Presenting Author(s)	Melodie Bianchini
Institution Affiliation	North Carolina Department of Health and Human Services State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	Hepatitis C Screening and Treatment in the Vermont Medicaid Population

Abstract

BACKGROUND: In 2018, Vermont joined 9 other states in partnering with the U.S. Department of Health and Human Services Hepatitis C (HCV) Medicaid Affinity Group. The Group's goal is to increase the number of Medicaid enrollees living with HCV who are treated and cured. The Vermont Department of Health and Department of Vermont Health Access (DVHA), Vermont's Medicaid agency, collaborated on several strategies including improving testing, referral and treatment for Medicaid enrollees, and enhancing provider knowledge and reducing stigma around HCV. The Group developed outcome measures to identify needs and monitor progress toward goals.

METHODS: Administrative billing claims, from DVHA, were pulled for January 2015-June 2018. Five outcome measures: HCV screening, confirmation of diagnosis, chronic HCV prevalence, treatment of chronic HCV, and post-treatment care, were calculated in SAS 9.3. Measures used ICD-9-CM and ICD-10-CM codes to identify patients diagnosed with HCV. Procedure codes identified claims associated with an antibody or RNA screening test. National Drug Codes for direct acting anti-HCV agents (DAA) identified people receiving treatment. Data also were stratified by individuals who inject drugs, using diagnosis and procedure codes, and baby-boomers (born 1945-1965). Measures were calculated for two reporting periods; calendar year 2017 and July 2017-June 2018.

RESULTS: In 2017, 7,528 enrollees or 5.0% of the Medicaid eligible population ages 18 years and over were screened for HCV using an RNA and/or an antibody test. The rate remained the same (4.9%) for the July-June reporting period. In 2017, the rate for baby-boomers was 4.8% and the preliminary rate for individuals who inject drugs was 88.7%. Approximately 92.3% (n=263) of enrollees who received an antibody test had their results confirmed with an RNA test. The prevalence rate for chronic HCV was 1.6%. In 2017, approximately 12.1% of enrollees ages 18 years and over with an HCV test and chronic HCV diagnosis were treated with DAAs. Additionally, DVHA saw a steep increase in individuals being treated with DAAs in the beginning of 2018.

CONCLUSIONS: There is room for improvement in screening and treatment of HCV, but Vermont is making progress. Providers are screening the majority of identified individuals who inject drugs, but the low screening rate among baby-boomers warrants further investigation. In 2018, Vermont removed all fibrosis and sobriety restrictions for receiving treatment. This change in treatment policy expanded DAA access for Medicaid enrollees. The impact of these changes was evident in the data, but continued surveillance is necessary to track the trends in treatment.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Outcome Measures; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	anita.wade@partner.vermont.gov
Presenting Author(s)	Anita Wade
Institution Affiliation	Vermont Department of Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	10945
Abstract Type	Poster
Abstract Title	Identification of Sustained Virologic Response Among Individuals with Hepatitis C Virus Infection — Chicago, Illinois

Abstract

BACKGROUND: Hepatitis C treatment is not routinely collected in surveillance, creating difficulty in calculating proportion of persons with hepatitis C achieving sustained virologic response (SVR), (i.e., cure). However, a laboratory algorithm for this purpose has been proposed using negative hepatitis C virus (HCV) RNA tests to identify those in treatment (1 negative RNA test) and those with SVR (2 negative RNA tests). A public health collaborative, the Hepatitis C Community Alliance to Test and Treat (HepCCATT), has created a novel hepatitis C registry containing both laboratory and pharmacy data. We used this registry to compare SVR percentages derived from the laboratory algorithm with those from a treatment algorithm.

METHODS: The registry comprises data from electronic surveillance, pharmacy chains (n = 2), and clinics (n = 11) in Chicago. We calculated SVR status for 2,754 persons tested at these clinics with positive HCV antibody testing or any HCV RNA testing during September 30, 2013–September 30, 2018. SVR was calculated using 2 algorithms, including ≥ 1 positive RNA followed by ≥ 2 negative RNA tests without further positive values (laboratory algorithm); secondly, evidence of treatment and a negative posttreatment RNA (treatment algorithm).

RESULTS: Both algorithms yielded similar SVR percentages (laboratory: 6.7% [184/2,754]; treatment: 7.5% [206/2,754]). Among 324 unique persons identified as having SVR, 66 (20.4%) were identified by both methods, 118 (36.4%) by laboratory algorithm only, and 140 (43.2%) by treatment algorithm only.

CONCLUSIONS: Inclusion of pharmacy data identified SVR among people who would not be identified using routinely collected surveillance data. SVR identified by the laboratory algorithm alone might result from missing treatment data or spontaneous resolution of infection. Enrollment of additional pharmacy chains to the registry are planned; future studies should determine if treatment data from additional pharmacies validate more instances of SVR identified by the laboratory algorithm. To better estimate SVR, public health jurisdictions could consider incorporating pharmacy data into standard hepatitis C surveillance.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Outcome Measures; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	megan.patel@illinois.gov
Presenting Author(s)	Megan Toth Patel
Institution Affiliation	Illinois Department of Public Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	National Surveillance for Hepatitis Among Sexual Minority Populations

Abstract

BACKGROUND: Cases of hepatitis B and C reported to the CDC rarely contain information regarding sexual identity, but national population surveys may serve as a valuable source of surveillance data. The purpose of this research is to determine if stable estimates of hepatitis can be obtained from the National Health Interview Survey (NHIS) and a collective estimate of hepatitis B and C from the National Survey on Drug Use and Health (NSDUH) for sexual minority populations.

METHODS: Data from 2015-2017 were pooled to increase the sample size for self-reported estimates of lifetime hepatitis from NHIS and lifetime hepatitis B or C from NSDUH for men and women who identified as straight, gay/lesbian, or bisexual. NHIS was used to estimate hepatitis screening in these populations and NSDUH was used to estimate lifetime injection drug use (IDU). Analyses accounted for each survey's sampling design and applied National Center for Health Statistics (NCHS) standards for display of proportions.

RESULTS: Higher proportions of gay men reported hepatitis in both NHIS (9.3%) and NSDUH (6.5%) compared to straight men (2.7% and 1.6%, respectively). Estimates for bisexual men were unstable for NHIS, and estimated at 3.4% for NSDUH. Screening for both hepatitis B and hepatitis C was highest among gay men, and lifetime IDU was highest among bisexual men. For women, hepatitis prevalence could be estimated for all groups in both NHIS and NSDUH. In NSDUH, hepatitis was more common in bisexual women (2.0%) compared to straight women (1.0%); however, in NHIS, hepatitis prevalence did not vary significantly for women who identified as straight, lesbian/gay, and bisexual. Lifetime IDU was higher for women identifying as bisexual (4.4%) compared to straight women (1.0%).

CONCLUSIONS: NSDUH produced stable estimates of lifetime hepatitis B/C for all sexual minority groups, and NHIS produced stable estimates of lifetime hepatitis for all groups except bisexual men. The higher prevalence of screening among gay men may explain in part the higher proportion reporting hepatitis compared to bisexual men, bisexual women, and gay/lesbian women. Results from NSDUH show that women who identify as bisexual are at higher risk for hepatitis B and C compared to straight women—findings that are consistent with IDU estimates but not replicated in NHIS.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Minority Health; Behavioral Health; Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	gfg8@cdc.gov
Presenting Author(s)	Greta Kilmer
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11007
Abstract Type	Poster
Abstract Title	Tennessee's 2017 Hepatitis C Virus Continuum of Cure

Abstract

BACKGROUND: Hepatitis C virus (HCV) is the most common bloodborne pathogen in the U.S. and accounts for more deaths than all other communicable diseases combined. HCV can be cured with 2-3 months of treatment; however, only about half of people living with HCV are diagnosed, and far fewer access treatment. We utilized HCV surveillance data to develop a statewide HCV continuum of cure (CoC), quantifying access to HCV diagnostics and rates of viral clearance and subsequent infection.

METHODS: We defined our cohort as clients with an acute or newly reported chronic HCV NBS investigation start date between July 1, 2015-December 31, 2016, and thought to be alive and living in TN as of December 31, 2017. TN vital statistics all-cause death data (2015-2017) was used to exclude deceased clients, and most recent state of residence in NBS was used to determine residence. "Diagnosed" clients had a positive HCV Ab or RNA; confirmatory status was based on first HCV RNA on/after diagnosis, stratified as "cleared", "unknown", or "confirmed" based on the RNA results; "cured" clients were "confirmed" clients who had at least one negative HCV RNA following confirmatory RNA; clients with "subsequent infection" were among "cleared" and "cured" clients whose most recent RNA was positive. Laboratory information within NBS through December 20, 2018 was utilized to build the CoC. All data was aggregated and analyzed using SAS 9.4.

RESULTS: From July 2015 to December 2016, 26,659 clients were diagnosed with acute or newly reported chronic HCV in TN, of whom 1,561 died and 46 moved out of state by the end of 2017. Among the 25,052 "diagnosed" clients, 2.4% (n=613) had lab evidence of "cleared", 49.2% (n=12,319) "unknown", and 48.4% (n=12,120) "confirmed" HCV status. Among "confirmed" clients, 13.4% (n=1,622) were "cured"; and among "cleared" and "cured" clients, 6.9% (n=155) developed subsequent infection (14.7% and 4.0%, respectively).

CONCLUSIONS: The development of an HCV CoC provides a unique opportunity to characterize a jurisdiction's HCV epidemic, monitor progress toward elimination goals, and identify and quantify areas of potential intervention (such as confirmatory testing and linkage to prevention and treatment services). The HCV CoC framework and analysis presented here demonstrates the feasibility and utility of producing a jurisdiction-wide CoC predicated solely on surveillance laboratory data. Limitations include the potential for incomplete data reporting (particularly of negative HCV RNA results) as well as the inability to discern between persistent versus re-infection among clients deemed to have "subsequent infection."

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Surveillance; Epidemiologic Methods
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lindsey.sizemore@tn.gov
Presenting Author(s)	Lindsey A. Sizemore
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	Trends in Hepatitis C Testing in Los Angeles County, 2013-2018

Abstract

BACKGROUND: Following hepatitis C virus (HCV) acquisition, approximately 70% of persons will develop chronic infection. Chronic HCV infection can result in cirrhosis, liver cancer, and death. Many persons with chronic HCV infection are asymptomatic so identification of infected persons depends on screening at-risk populations. Guidelines recommend HCV testing for persons with risk factors for HCV infection and, as of 2012, one-time testing for all persons born between 1945 and 1965 (birth-cohort screening). Safe and highly-effective second-generation HCV antiviral drugs were introduced in 2013. We describe trends in and characteristics of persons tested for HCV in Los Angeles County (LAC) during 2013–2018.

METHODS: In LAC, chronic HCV surveillance occurs through mandated electronic laboratory reporting of positive HCV tests (antibody, polymerase chain reaction [PCR], genotype). Additionally, certain laboratories voluntarily report negative HCV PCR results. Reports from 2013-2018 were deduplicated at the test level by test type, result, and date. A probabilistic record linkage program, Link Plus, was used to deduplicate cases that had been reported multiple times. Frequencies by test type, year, and demographics were generated.

RESULTS: During 2013–2018, 291,872 HCV test results were reported for 102,620 unique persons in LAC. The number of reported HCV antibody tests increased from 12,059 in 2013 to 23,556 in 2018. Among persons with a positive HCV antibody test, 46,753 (63%) were male, 42,719 (57%) were in the birth-cohort, and 38,273 (51%) had an associated PCR/genotype result. In 2013, 2,912 (28%) of persons with positive HCV antibody tests had an associated PCR test result compared with 9,056 (48%) in 2018. In 2013, 877 (6%) of persons had PCR results that were negative or below the limit of detection, compared with 6,167 (22%) in 2018.

CONCLUSIONS: The number of positive HCV antibody tests reported from 2013 to 2018 potentially represents increased screening for HCV. The majority of screening tests occurred in the birth-cohort. A greater than expected proportion of persons with a positive antibody test lacked a corresponding positive PCR test, indicating that many are not receiving appropriate follow-up confirmatory testing. The number of persons with undetectable PCR results increased during the study period, which could be related to an increase in the number of persons receiving HCV treatment.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	mhaddix@ph.lacounty.gov
Presenting Author(s)	Meredith Haddix
Institution Affiliation	Los Angeles County Department of Public Health Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11312
Abstract Type	Quick
Abstract Title	CDC Division of Viral Hepatitis Support of NNDSS Modernization Initiative (NMI)

Abstract

BACKGROUND: Cases of viral hepatitis are voluntarily reported to CDC by state and territorial health departments via CDC's National Notifiable Disease Surveillance System (NNDSS). Most jurisdictions collect case data using a formatted questionnaire and report those data using the National Electronic Telecommunications System for Surveillance (NETSS) that has been receiving electronic data since 1990. About 20 jurisdictions are currently transmitting or preparing to transmit production generic and hepatitis specific surveillance data using a more current and extensive case report form via the NNDSS Master Message. Most of these systems are using the NEDDSS Base System to collect data.

METHODS: The Division of Viral Hepatitis (DVH) continues to collaborate with the Center for Surveillance, Epidemiology, and Laboratory Services and CSTE (DSTDP) at CDC to develop HL7 message mapping guides for Acute Hepatitis A, B and C, Perinatal Hepatitis B, and Chronic Hepatitis B and C. DVH continues to work with CSELS and other CDC programs to standardize and harmonize both the data elements that are collected and HL7 messages. DVH works with states to answer questions related to the viral hepatitis data collection and hepatitis HL7 message. DVH also conduct data quality assurance by validating data collected using the hepatitis HL7 message and collecting and responding to comments from states regarding the utility of the current viral hepatitis collection form.

RESULTS: In addition to working with states to implement the hepatitis specific HL7 message, CDC and DVH have also rolled out the new HL7 message guides for perinatal hepatitis C. This presentation will provide current statistics on data quality, describe the HL7 message and processes, and provide an overview of the perinatal hepatitis C message.

CONCLUSIONS: DVH has worked diligently to translate our current data collection methods into a standardized and harmonized format that will make data collection easier for States and data management and reporting easier for CDC.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; NNDSS; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	bbk3@cdc.gov
Presenting Author(s)	Benjamin A Kupronis
Institution Affiliation	Centers for Disease Control and Prevention Federal Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11072
Abstract Type	Quick
Abstract Title	Hepatitis C Care Cascade Among Medicaid-Enrolled Women of Childbearing Age, Wisconsin, 2015-2018

Abstract

BACKGROUND: Recent increases in hepatitis C virus (HCV) infections among women of childbearing age are concerning because infants born to women with HCV can become infected perinatally. The curative treatment for HCV, direct-acting antiviral (DAA) medication, is not approved for use in pregnant women and there is no intervention to prevent infection of the infant. Therefore, to prevent perinatal HCV transmission, women need to move through the steps of the HCV “care cascade”, including screening for HCV infection, confirmation of the diagnosis, and treatment with DAAs, before becoming pregnant. As a project for the federally-organized HCV/Medicaid Affinity Group, we evaluated the HCV care cascade among women of childbearing age enrolled in Wisconsin Medicaid. Additionally, we evaluated whether more women received DAA treatment after Wisconsin Medicaid policy changed in 2017, allowing patients with any level of liver damage to receive DAAs.

METHODS: Using Wisconsin Medicaid enrollment and claims data, we identified a cohort of women age 15-44 years who were continuously Medicaid-eligible for ≥12 months during 2015-2018. We extracted information regarding claims for HCV antibody testing, HCV RNA testing, and DAA treatment. These data were linked, by the woman’s name and birth date, to HCV surveillance data to identify any positive HCV antibody or RNA results. We defined the steps of the care cascade as (1) screening: ≥1 claim for HCV antibody testing, (2) confirmatory testing: ≥1 claim for RNA testing, (3) treatment initiation: ≥1 claim for DAA treatment.

RESULTS: Of the 305,315 women in the cohort, 27,452 (9%) were screened for HCV. Of these women, 886 (3%) had positive HCV antibody results indicating the need for confirmatory testing. Of the 886 antibody-positive women, 693 (78%) received RNA confirmatory testing. Of these 693 women, 544 (78%) had positive RNA results confirming the diagnosis. Of the 544 women with confirmed HCV, 90 (17%) initiated treatment. When stratified by the year of first antibody-positive result, the percentage of women with confirmed HCV who initiated treatment increased from 13% among women first antibody-positive in 2015 to 23% among women first antibody-positive in 2017.

CONCLUSIONS: By linking Medicaid claims and surveillance data, we established a method for evaluating the HCV care cascade among Medicaid-eligible women of childbearing age in Wisconsin. The percentage of newly-diagnosed women treated with DAAs increased after the Medicaid policy change, but remained low. To improve the identification and treatment of women with HCV, provider education is needed regarding HCV testing, treatment, and current Medicaid policy.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ruth.koepke@wisconsin.gov
Presenting Author(s)	Ruth Koepke
Institution Affiliation	Wisconsin Department of Health Services State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Increase in Hepatitis A Virus Infections- Florida, 2018

Abstract

BACKGROUND: In 2018, the Florida Department of Health saw an increase in reported cases of hepatitis A virus (HAV). The 560 cases were a 268% increase over the 5-year average of 152 cases and several jurisdictions experienced outbreaks of HAV among persons who are homeless or use injection or non-injection drugs. Descriptive epidemiology was performed to better understand the risk factors of HAV cases and initiate targeted vaccination for at-risk populations.

METHODS: An outbreak case was defined as any confirmed case of hepatitis A that was classified as acquired in Florida (entire exposure period was spent in the state), acquired in Florida or another state/country (cases spent some portion of their exposure period outside of the state), or unknown. Serum specimens were sent to the Bureau of Public Health Laboratories in Tampa (BPHL Tampa) for molecular typing and results were confirmed by the Centers for Disease Control and Prevention (CDC) Division of Viral Hepatitis.

RESULTS: Between December 31, 2017-December 29, 2018, 560 cases of hepatitis A were reported in Florida with 535 meeting outbreak case definition and included in the analysis. 423 cases (76%) were hospitalized and 2 deaths (0.4%) were reported. While cases were reported throughout much of the state, the Tampa Bay and Central Florida areas were primarily affected. The median age was 38 years (range 2-88 years). 353 (63%) cases were male and 405 (76%) identified as non-Hispanic white. The most commonly reported risk factor was drug use in 265 (47%) cases. Fewer cases occurred among persons who were homeless (n=70/13%) or men who have sex with men (MSM) (n=60/11%). The CDC confirmed the genotypes of the 28 samples submitted for sequencing: 21 belong to genotype 1A, and 7 belong to genotype 1B. The 1A strains are similar to strains circulating in Europe and the United States among MSM and not the strains circulating in other states experiencing HAV outbreaks among persons who are homeless or drug users.

CONCLUSIONS: Florida experienced a significant increase in cases of HAV in 2018, primarily among men who use drugs. Results of the genotyping indicate this increase is likely unrelated to other concurrent outbreaks in the United States. In response, county health departments developed targeted vaccination efforts to at risk groups. Additionally, a health advisory and press release were issued by the state surgeon general, and notifications sent to healthcare providers. The situation is ongoing and the vaccination efforts are continuing.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Epidemiology; Hepatitis; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	andrea.leapley@flhealth.gov
Presenting Author(s)	Andrea Leapley
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Perinatal Hepatitis C Incidence and Epidemiology of Hepatitis-C Infected Mothers in Michigan, 2012-2016

Abstract

BACKGROUND: Over the last decade there has been an increase in the incidence of Hepatitis C Virus (HCV) associated with the rise of the opioid epidemic. New annual diagnoses in persons aged 18-29 have doubled in Michigan between 2012 and 2016. Females have been equally impacted by this trend and HCV infection in a pregnant woman poses a risk of vertical transmission. A 2014 CDC study estimated the rate of HCV infection at 2.6-5.0 per 1,000 live births in Michigan. Our study looked to measure the known HCV prevalence among women who gave birth and compare the epidemiological characteristics of women known to be infected with HCV versus those who were not. We also sought to measure the number of predicted perinatal HCV infections that have been identified.

METHODS: A de-duplicated dataset of all female HCV patients referred from 2012-2016 was extracted from the Michigan Disease Surveillance System (MDSS). This list was matched to vital statistics birth records based on the mother's name and date of birth using LinkPlus. Variables from the birth record were collected and stratified by HCV status.

RESULTS: Between 2012 and 2016 there were 567,485 live births in Michigan for which 3,926 were from women reported to MDSS with HCV (6.92 per 1,000 live births). Factors significantly associated with HCV infection among women who gave birth included being 20-29 years of age, Caucasian, being a Medicaid beneficiary, and reporting smoking during pregnancy. Women reported for HCV who gave birth were less likely to have completed 8 prenatal care visits, possess a college degree and were less likely to be married compared to women who gave birth that were not known to be infected with HCV. Given a 5-15% rate of vertical HCV transmission we estimated 196-589 perinatal HCV infections. From 2012-2016, there were a total of 26 perinatal cases reported to the MDSS.

CONCLUSIONS: HCV infection rates among pregnant women in Michigan surpassed that of a recent national estimate. Our rate is also an underestimate as HCV infection is often underdiagnosed. Only 4-13% of the predicted number of perinatal HCV infections have been reported to the MDSS, suggesting that HCV testing among newborns is low. Understanding the risk factors associated with HCV infection among pregnant women can help providers prioritize who to screen for HCV. The low rate of perinatal HCV identification suggests efforts to increase clinical knowledge of HCV testing of infants is warranted.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Epidemiology; Hepatitis; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	OswaldM@michigan.gov
Presenting Author(s)	Marjorie E. Oswald
Institution Affiliation	Michigan Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11635
Abstract Type	Quick
Abstract Title	Responses to Hepatitis A in Local County Jails--Indiana, 2018

Abstract

BACKGROUND: Acute hepatitis A infection is caused by the hepatitis A virus. The virus is transmitted via fecal-oral routes, commonly through contaminated food or water, as well as from person to person. The morbidity of hepatitis A in Indiana in 2017 was 0.31 per 100,000. On December 28, 2017, a case of hepatitis A was identified by a local health department in the county's jail (Jail A) and reported to the Indiana State Department of Health (ISDH). On January 10, 2018, a case of hepatitis A was identified in a neighboring county jail (Jail B).

METHODS: The ISDH assessed infection control practices in both jails and reviewed evidence-based best practices with the local health departments and jail staff. The ISDH sent a questionnaire to be used for all ill jail inmates to record case information, requested active surveillance for additional ill individuals, and sent disinfection and isolation recommendations. The ISDH obtained a line list and positive lab results for all suspect cases linked to the original case in Jail A. The number of exposed inmates requiring post-exposure prophylaxis (PEP) was identified in both jails and PEP was administered. An outbreak case was defined using the 2012 Center for Disease Control and Prevention (CDC)-Council of State and Territorial Epidemiologists' (CSTE) definition of acute hepatitis A infection, as well as an epidemiological link to the original case or to an outbreak ongoing in Jefferson County, Kentucky.

RESULTS: Two index cases of hepatitis A was identified in Jail A, followed by five secondary confirmed and suspect cases. Assessment findings indicated that Jail A did not follow all of the best practices for responding to hepatitis A in a jail setting. One confirmed case was identified in Jail B, with no secondary cases. In this instance, the jail staff followed the best practices and were proactive in their response to exposure in the jail.

CONCLUSIONS: The differences between the two local jail responses was reviewed to determine how best to assist local health departments and jails for future situations of infectious illness in this setting. A best practice document for hepatitis A in jail settings was created to ensure future outbreak responses follow the best protocol. Subsequent hepatitis A cases in other local Indiana jails have followed best practices and have not experienced hepatitis A outbreaks within the jail itself. Vaccination of inmates in local jails was identified as a priority for prevention of hepatitis A in Indiana.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Underserved Populations; Hepatitis; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	NStone2@isdh.IN.gov
Presenting Author(s)	Nicole Stone
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11264
Abstract Type	Quick
Abstract Title	Use of a Control Bank to Facilitate Recruitment of Controls during a National Outbreak Investigation of Hepatitis A in Canada

Abstract

BACKGROUND: In June 2018 a national outbreak investigation was initiated to investigate a cluster of hepatitis A (HAV) cases in five provinces across Canada.

METHODS: A case was defined as a resident or visitor to Canada with lab-confirmed HAV genotype 1A, one of two genetically related RNA fingerprints, and with illness onset on or after October 1, 2017. A retrospective matched case-control study was conducted to identify the likely source of the outbreak. Three healthy controls, with no previous HAV infection or vaccination against HAV, were recruited for each case and matched based on geography, age group, and sex, using a previously established control bank. When the control bank was exhausted, controls were selected through random landline and cell phone call lists. Food exposures in the case control study were selected based on case exposure information and a literature review of potential sources of HAV. The exposure period was 15-50 days prior to symptom onset for cases, and 15-50 days prior to interview date for controls. McNemar's odd ratios for matched pairs were calculated to provide an estimate of risk associated with exposure and contraction of HAV.

RESULTS: Eighteen cases in five provinces were identified with onset dates from October 31, 2017 to May 24, 2018. Case ages ranged from 3 to 69 years (median age = 40) and 50% were male. Nine cases were hospitalized and no deaths were reported. Results from the case control study pointed to shrimp/prawns (OR: 15.75, $p=0.01$) and blackberries (OR: 7.21, $p=0.02$) as food items of interest. Seventy-two percent of controls were recruited through the control bank, and required on average 25.5 calls per control. In contrast, use of a random listed landline sample required an average of 741.9 calls per control, and a random cell phone sample required an average of 331.7 calls per control.

CONCLUSIONS: Analysis of the case-control data was useful in identifying two foods of interest in the investigation, but limited product specificity from cases and an absence of any product leftovers prevented a food safety investigation. The previously established control bank proved to be a more efficient method for control recruitment than random call lists; however, matching on demographic variables extended the time needed to find eligible controls through all recruitment methods. Other methods of control recruitment, such as online surveys, may prove beneficial for increasing the timeliness and reducing costs of case control studies during an outbreak investigation.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Hepatitis
Keywords	Foodborne Disease; Outbreaks; Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email	tanis.kershaw@canada.ca
Address(es)	
Presenting Author(s)	Tanis Kershaw
Institution	Public Health Agency of Canada
Affiliation	International Health Agency

Submission Type ID	Roundtable
Abstract Type	10601
Abstract Title	Roundtable
	Examination of the Hepatitis C Care Cascade and Its Impact on Data Reporting and Health Equity

Abstract

Key Objectives:

- Discuss the current epidemiology and outlook of the hepatitis C Virus (HCV) in the United States.
- Assess qualitative and quantitative data from a large network of community health centers demonstrating gaps in the current HCV care cascade model, specifically safety-net patients deemed “lost to follow-up”, or who do not receive treatment.
- Identify recommendations to improve the HCV care cascade allowing for greater understanding around patients “lost to follow-up” or who did not receive treatment and influences on public health surveillance, data reporting, access to care, policy, and health equity.

Brief Summary:

Background: Hepatitis C (HCV) is the leading cause of liver cancer in the United States. Relatively new treatments for HCV can lead to a sustained virologic response (SVR), preventing morbidity, mortality, and further transmission. Current HCV summary data is adapted from the HIV cascade and includes positivity, treatment, and SVR rates, but the cascade lacks nuance for those considered “lost to follow-up” (LTFU). **Methods:** This mixed methods study combines electronic health record (EHR) data with chart audits to quantitatively analyze HCV disease progression, treatment, and cure. All data comes from a large community health center (CHC) network from 2015-2016; chart audits were conducted on a probability sample of HCV patients deemed LTFU to discover reasons for lack of treatment. De-identified case studies and results from qualitative interviews with CHC providers will also be discussed. **Results:** In a preliminary review of 35 chart audits, nearly all patients determined to be LTFU have discussed treatment options with their primary care provider. Chart audits revealed that patients who were considered LTFU were often referred to a specialist outside of the CHC network for treatment, living with severe comorbidities, be a current substance user, and/or were denied treatment coverage by Medicaid. This project is ongoing and data analysis will be completed and available by June 2018. **Conclusion:** HCV data reported in the format of the HIV cascade lacks nuance and detail around transitions of care and social determinants of health that may impact patients’ treatment and overall health. Recommendations to update the current HCV care cascade may improve the understanding of patients identified as LTFU or who did not receive treatment, providing information impacting public health surveillance, data reporting, access to care, and Medicaid payment policy. This understanding may be vital in guiding both social and medical interventions.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Hepatitis
Consider for Different Presentation?	Barriers to Care; Electronic Health Records; Surveillance
Presenting Author Email Address(es)	No
Presenting Author(s)	stilmon@peds.bsd.uchicago.edu
Institution Affiliation	Sandra Tilmon
	University of Chicago Medicine
	Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11019
Abstract Type	Breakout
Abstract Title	Aidsvu and Hepvu: Using Data Visualize to Understand the HIV and Hepatitis C Epidemics

Abstract

BACKGROUND: AIDSVu and HepVu.org are free, publicly available websites that visualize the HIV and Hepatitis C epidemics through highly interactive and simple maps and infographics to give users easy access to this information for program planning, policy development, and resource allocation. AIDSVu provides data visualizations of HIV prevalence and new diagnoses in the United States at state- and county-levels, as well as at the ZIP Code-level for cities most highly impacted by HIV. HepVu maps state Hepatitis C prevalence estimates, mortality data, and opioid indicators (soon to come). These websites can be used to understand how HIV and Hepatitis C affect communities and to help guide prevention efforts.

METHODS: AIDSVu and HepVu data are updated every year to visualize the most current and useful data. In 2018, AIDSVu launched the first-ever state-level interactive maps on PrEP users and rates of PrEP use, in addition to updated maps on HIV prevalence, new diagnoses and mortality. In January 2019, HepVu will be launching data and interactive maps on 2013-2016 Hepatitis C estimates along with three new opioid indicators to help visualize the opioid epidemic and its relationship to the Hepatitis C epidemic.

RESULTS: The data on AIDSVu and HepVu can be viewed at the overall level, or stratified by certain demographic filters, like age and sex. PrEP usage and HIV new diagnoses can be seen over time, showing geographical trends, by accessing the individual maps by year, from 2012-2017 for PrEP and 2008-2016 for new diagnoses. Additionally, five social determinants of health can be displayed side-by-side with the maps. Provider overlays may be added on top of the maps to show service locations, such as HIV testing sites and PrEP services. Majority of the data and maps can be downloaded for use in analyses and presentations.

CONCLUSIONS: All of the information on AIDSVu and HepVu can be leveraged by public health officials, policymakers, researchers, and community leaders to understand the levels of HIV, PrEP use, Hepatitis C, and opioids (soon to come) in their community. For example, public health professionals at the state or local government levels can analyze the PrEP use data to determine which sub-populations of people have lower PrEP uptake, and inform how resources should be allocated for the next year. Researchers can also look at new HIV diagnoses across the years to see what counties in their state are improving and what counties need improved education and access.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	HIV/AIDS; Hepatitis; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	epemblem@emory.edu
Presenting Author(s)	Elizabeth S Pembleton
Institution Affiliation	Emory University, Rollins School of Public Health Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11789
Abstract Type	Breakout
Abstract Title	Barriers and Challenges to Implementing and Evaluating State Level Molecular HIV Clusters in Florida

Abstract

BACKGROUND: Partner elicitation and contact tracing by Disease Intervention Specialists (DIS) are foundational tools used to interrupt transmission of disease within a community by identifying, contacting and linking persons at risk for HIV to prevention and care services. In the absence of partner contact information and other epidemiological data, transmission networks may not accurately reflect the transmission of HIV. Molecular HIV Surveillance (MHS) data from point-of-care nucleotide genotype sequencing can identify links between individuals when partner elicitation data is lacking, by linking and comparing those with similar HIV genetic sequences to identify recent and rapid transmission within molecularly-linked clusters (genetic distance threshold of 0.5% or less). With the second highest rates of new HIV diagnoses in 2017 (22.9 per 100,00), 1.9 times the national rate, Florida has implemented MHS activities to identify and respond to the HIV epidemic.

METHODS: MHS case definitions and response activities were developed for HIV transmission networks. A protocol outlining roles and responsibilities of state and county health department (CHD) staff was developed. DIS would investigate or re-interview individuals in rapidly growing (RG) clusters (5 or more new HIV diagnoses within the last 12 months) who are not in care or not virally suppressed (>200 copies/mL). A database integrating state-level HIV and STD surveillance system data was constructed to disseminate and collect information for cluster response.

RESULTS: As of January 2019, there were 11 RG clusters of 290 individuals in Florida (ranging from 9–65 members). Most molecularly-linked individuals in RG clusters were male (97.6%), Hispanic (51.4%), and men who have sex with men (MSM) (89.3%); injection drug use (IDU) and MSM/IDU risk was present for 0.7% and 2.4% respectively. Of the 1,663 partners claimed by molecularly-linked individuals, 81.9% were anonymous. DIS re-interview would be required for 77 (26.8%) molecularly-linked and 308 epidemiologically-linked (sex or needle sharing) persons. Persons for re-interview/investigation are predominately located in Miami-Dade, Broward, and Orange counties.

CONCLUSIONS: Through MHS, RG clusters with many epidemiologically-linked and anonymous partners were identified. Protocol-defined interventions and evaluation for these networks requires substantial DIS involvement and is difficult due to the high morbidity DIS must content with and large numbers of anonymous partners. There is a need to tailor cluster response around predominate risk factors while considering the feasibility and potential outcomes of individual-level investigation. Community-based interventions should be considered to reach members of networks that would be otherwise unidentifiable.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	HIV/AIDS; Prevention; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	shana.geary@flhealth.gov
Presenting Author(s)	Shana M Geary
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11830
Abstract Type	Breakout
Abstract Title	Beyond Linkage to Care: Utilizing Surveillance Data to Promote Continual HIV Care Utilization and Viral Suppression Maintenance in Louisiana

Abstract

BACKGROUND: Studies show that viral suppression achievement and maintenance, through continual utilization of HIV care and treatment, prevents the occurrence of AIDS-related events and inhibits HIV transmission to sexual partners. Despite these benefits, only 73% of persons living with HIV (PLWH) in the US with a known HIV diagnosis received HIV care in 2015 and only 60% had exhibited viral suppression. In September 2013, the Louisiana Department of Health initiated a data-to-care program, Louisiana Links, which utilizes HIV surveillance and other data to identify PLWH that are presently not engaged in HIV medical care and facilitate (re)linkage to HIV care and supportive services. Data suggests that data-to-care programs may temporarily help clients (re)link to care and achieve viral suppression, but it is unclear if these benefits are sustained after clients are discharged. In this study, we will compare rates of HIV care engagement and viral suppression within the first year post-enrollment to those at 2-5 years post enrollment.

METHODS: Clients were enrolled from September 29, 2013 – September 30, 2016. Clients had a minimum of 2 years and a maximum of 5 years of follow-up time post-enrollment by September 29, 2018. Results from HIV laboratory tests conducted from September 2013 – September 2018 were obtained from Louisiana Department of Health’s HIV registry.

RESULTS: 542 clients had 2-5 years of follow-up time by September 29, 2018. Of these, 87% were black, 55% were male and 35% were MSM. The median amount of follow-up time was 3.6 years. Within one year of enrollment, 94% (n=507) of enrolled clients were (re)linked to HIV care and 61% (n=333) achieved viral suppression after enrollment. As of September 30, 2018, 77% (n=415) were engaged in care and 55% (n=297) exhibited viral suppression.

CONCLUSIONS: Within one year after enrollment, clients had an initial rate of care engagement (94%) which was higher than the state average in 2017 (75%). After 2-5 years of follow-up, this rate fell to 77%. Clients experienced a viral suppression rate that was similar to the state average in 2017 (62%) within one year after enrollment; however, this rate decreased to 55% after 2-5 years of follow-up. In response to these results, Louisiana Department of Health is expanding the scope of their data-to-care efforts to include a focus on long-term lab monitoring and follow-up for discharged clients and working with partner agencies to find and implement permanent solutions for addressing structural barriers to HIV care and treatment.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Surveillance; Barriers to Care; HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	antoine.brantley@la.gov
Presenting Author(s)	Antoine Brantley
Institution Affiliation	Louisiana Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11514
Abstract Type	Breakout
Abstract Title	Sexual Transmission of <i>Shigella</i> in the Portland Oregon Metropolitan Area 2008-2018: Case Case Analyses of Related Pathogens and Classic STIs

Abstract

BACKGROUND: *Shigella* is a bacterial pathogen that causes severe and often bloody diarrhea, fever, and sepsis. Infections are spread via the fecal-oral route and humans are the sole reservoir. Sex-dependent fecal-oral transmission is a known *Shigella* risk factor especially among men who have sex with men (MSM) and sexual networks have enabled the emergence and dissemination of drug resistant *Shigella*. However, the risk of shigellosis during sexual activity among heterosexual men and women is poorly defined. Similarly, limited data exist on the role of sexual transmission for other closely related bacterial pathogens. We hypothesized that sex-dependent fecal-oral transmission mirrors sexual transmission among other sexually transmitted infections (STIs) and this represents a unique epidemiological niche for *Shigella* compared to other fecal-oral bacterial pathogens.

METHODS: To investigate the burden of illness due to sexual activity for *Shigella* relative to: *Salmonella*, Shiga Toxigenic *E. coli* (STEC), and *Campylobacter* we analyzed data from domestically acquired, “at risk” (>14 years), sporadic cases from July 2008-July 2018. Using STI diagnoses as a proxy for high risk sexual behavior we performed a broad case-case analysis comparing the odds of having an STI diagnosis among representative fecal-oral pathogens as well as traditional STIs including *Chlamydia*, *Gonorrhea*, *Syphilis*, and HIV. Multiple logistic regression analyses were performed to model the odds of having an STI diagnosis between diseases.

RESULTS: Since 2008, the Portland Metropolitan Area had 343 cases of *Shigella*. 76% were male and 23% were female. 51% of *Shigella* cases had an STI diagnosis including 63% of males and 16% of females. After stratifying by sex and adjusting for confounding factors including age, county, race, and year, we found that cases of *Shigella* were significantly more likely to have an STI diagnosis compared to all other fecal-oral pathogens (males adjusted Odds ratio [OR] 15.9-24.7 $p<0.01$; females OR 2.4-4.0 $p<0.02$). Conversely, male *Shigella* cases had similar odds of having an STI diagnosis compared to the STIs (OR 0.8-2.3 $p>0.1$), and 92% of cases with an STI were MSM.

CONCLUSIONS: Our evidence strongly suggests that the majority of domestically acquired *Shigella* infections were acquired sexually, predominantly among MSM. However, we found no evidence that other fecal-oral bacterial pathogens are consistently transmitted sexually. Given the overlap of *Shigella* with other STIs, we recommend foremost consideration of domestically acquired *Shigella* infections as being sexually acquired. Shigellosis cases, especially MSM, should be tested for other STIs and provided fecal-oral sexual health education.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Enteric Infectious Diseases; Epidemiology; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	russell.barlow@multco.us
Presenting Author(s)	Russell Barlow
Institution Affiliation	Multnomah County Health Department Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10851
Abstract Type	Breakout
Abstract Title	The Rise and Spread of Female Syphilis Cases in Florida, 2012-2017

Abstract

BACKGROUND: From 2012 through 2017, reported cases of female syphilis increased 67% (n=910 in 2012 to n=1519 in 2017) and congenital syphilis cases increased 138% (n=39 in 2012 to n=93 in 2017). We sought to geospatially assess the increase within Florida, specifically, if a subset of Florida's counties were responsible for the female syphilis increase, or if the proliferation was pervasive statewide, and how stable any resulting patterns were.

METHODS: We analyzed reported congenital syphilis cases and all cases of syphilis, all stages, among females, from 2012 to 2017, in Florida. Outbreak counties were defined as those with a 25% increase in female cases for a given year than the previous five-year average, consistent with Florida's outbreak definition. We excluded any counties that had fewer than 10 cases in the year being examined. Counties meeting the outbreak definition were mapped using ArcMap to visualize the location and spread of the outbreak counties.

RESULTS: In 2012, four out of Florida's 67 counties were experiencing outbreak conditions for reported female syphilis cases, this number increased to 18 counties by 2017. In 2012, the four outbreak counties were distantly spaced across the state. By 2017, the outbreak counties were dispersed throughout the central region of the state and became more contiguous, with few outliers outside this area. The proportion of the state's female syphilis cases made up by these counties has changed temporally. The lowest year was 2013, when the outbreak counties comprised 9% of the state's total cases, and the highest year was 2016, with 65% of the state's cases coming from the defined outbreak counties. The 2017 outbreak counties also experienced a 386% increase in congenital syphilis cases since 2012.

CONCLUSIONS: Most of Florida's counties were not experiencing outbreak conditions of female syphilis in the examined years. However, counties meeting the outbreak definition account for a large proportion of the statewide increase in female syphilis. Visualization efforts, via maps, revealed an expanding and more contiguous pattern of counties meeting the outbreak definition for female syphilis cases spreading within the central area of the state. Developing tools for timely Identification and evidence-based responses to outbreaks are needed. Geospatial visualization techniques could aid in focusing limited intervention resources to high-risk jurisdictions. These counties were also experiencing significant increases in congenital syphilis cases and focusing efforts on female syphilis case reduction could also aid in decreasing congenital syphilis cases in the state of Florida.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Maternal and Child Health; Outbreaks; Geographic Information Systems (GIS)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	victoria.pearson@flhealth.gov
Presenting Author(s)	Victoria M Pearson
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11859
Abstract Type	Breakout
Abstract Title	Utilizing Electronic Lab Reporting of Non-Positive Laboratory Results to Assess the Impact of Extragenital Testing on Statewide Chlamydia and Gonorrhea Rates

Abstract

BACKGROUND: Extragenital testing for gonorrhea and chlamydia benefits persons who engage in receptive anal intercourse and oral sex by detecting infections that urogenital testing alone misses. CDC recommends that sexually active men who have sex with men (MSM) receive extragenital screening annually. The level of statewide adherence to this recommendation is unknown. The Utah Department of Health (UDOH) collects non-positive laboratory results electronically for both chlamydia and gonorrhea. These results are stored in EpiTrax, Utah's NEDSS-based surveillance system.

METHODS: Diagnostic laboratory results were analyzed for all cases of chlamydia and gonorrhea reported in 2017. Laboratory results were limited to those collected on the date of diagnosis. Specimen source and laboratory test result were utilized to determine the frequency that chlamydia and gonorrhea cases were provided extragenital screening and the impact of this screening on statewide rates of reported disease. Results were stratified by sex.

RESULTS: In 2017, there were 10,134 cases of chlamydia and 2,541 cases of gonorrhea reported in Utah. A total of 16,342 diagnostic laboratory test results were reported to UDOH and appended to these cases in EpiTrax (11,069 chlamydia results and 3,254 gonorrhea results); 77.1% of these test results were reported via electronic lab reporting. The source of the specimen was reported for 76.3% of these test results. Only one diagnostic laboratory result was reported for the vast majority of cases (92.7% of chlamydia cases and 80.0% of gonorrhea cases). Multi-site testing (testing for infection at multiple anatomic sites) was reported more frequently in male cases than female cases, 10.9% and 0.6% respectively. Three site testing (urogenital, pharyngeal, and rectal) was reported for 221 male chlamydia cases (6.3%) and 177 male gonorrhea cases (10.6%). Two site testing was reported for 97 male chlamydia cases (2.8%) and 70 male gonorrhea cases (4.2%). In males with no reported urogenital infections, there were 117 rectal infections, 90 pharyngeal infections, and 45 rectal and pharyngeal infections. Therefore, extragenital testing alone was responsible for diagnosing 9.9% of male gonorrhea cases in 2017.

CONCLUSIONS: Extragenital screening for chlamydia and gonorrhea detects more infections than urogenital screening alone. The electronic reporting of non-positive laboratory results permits statewide analysis of trends in extragenital screening. Further efforts to improve the quality of reported specimen source are merited.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Sexually Transmitted Diseases; Electronic Laboratory Reporting (ELR)
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	swhite1@utah.gov
Presenting Author(s)	Scott White
Institution Affiliation	Utah Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Zika Virus Disease and HIV/AIDS

Abstract

BACKGROUND: During the 2016 Zika virus outbreak, the Florida Department of Health in Miami-Dade County was frequently approached by concerned healthcare providers regarding co-infections of Zika virus (ZIKV) and human immunodeficiency virus (HIV). At the time of the outbreak, it was unknown whether patients with HIV/AIDS were more likely to experience severe clinical outcomes during their ZIKV infection. This study is unique as it is the first report examining clinical outcomes of HIV and Zika virus disease (ZD) co-infections. The purpose of this study was to examine clinical symptoms associated with Zika virus (ZIKV) infection and HIV co-infection among Miami-Dade County residents with confirmed ZIKV disease in 2016.

METHODS: Analysis of pre-existing epidemiological and laboratory data collected during the 2016 Zika virus outbreak by the Florida Department of Health in Miami-Dade County. Descriptive statistics were calculated to examine differences in age group, gender, symptoms, distribution of symptoms, GBS diagnosis, hematology, healthcare visits, hospitalization, and transmission type by HIV status. Among HIV positive ZIKV disease cases, CD4 counts and HIV viral loads were examined. Odds ratios were calculated between demographics, pregnancy, symptomology, prolonged viremia, cycle threshold values, and HIV status.

RESULTS: During the 2016 ZIKV outbreak in Miami-Dade County, HIV/ZD cases accounted for nine (1.9%) of all confirmed ZD cases (n=474). The median age of HIV/ZD co-infected cases was 48 (range 24 -71); there were no co-infections among pediatric ZD cases. Among the 4 (44.44%) female co-infected case patients, none were pregnant at the time ZIKV infection. HIV status was not found to be associated with age, gender, race/ethnicity, symptom severity, development of Guillian-Barre Syndrome, thrombocytopenia, lymphocytopenia, neutropenia, or anemia.

CONCLUSIONS: Individuals with virally suppressed HIV infection may be less likely to have severe complications associated with ZIKV infection. Five (55.56%) HIV/ZD case patients reported only two of the four main symptoms; whereas, the majority of all ZD cases reported three of the four main symptoms. HIV/ZD patients may present similarly to ZD patients outcomes.

Submission Complete?	Yes
Committee Topic	Infectious Disease HIV & STD
Keywords	Infectious Diseases; Vectorborne Disease; HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Isabel.Griffin@flhealth.gov
Presenting Author(s)	Isabel Griffin
Institution Affiliation	Florida Department of Health in Miami-Dade County Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Lightning
Abstract Title	Disparities in Drug Overdose Deaths Among Persons Living with HIV and the General Population in Louisiana

Abstract

BACKGROUND: The sharp increase of premature deaths due to drug overdose (OD) has been a concerning public health trend in recent years. Evidence suggests significant disparities in drug use among people living with HIV (PLWH) as compared to the general population. An examination of OD mortality trends was conducted to assess the impact of drug use among PLWH in Louisiana.

METHODS: A retrospective analysis of OD deaths between August 2012-December 2016 was conducted among adults ≥ 18 years in Louisiana with a valid cause of death. OD deaths were identified using International Classification of Diseases, Tenth Revision (ICD-10) underlying cause of death codes: X40-X44, X60-X64, X85, Y10-Y14. Deaths among PLWH were ascertained through the enhanced HIV/AIDS Reporting System (eHARS). Deaths in the general population were identified through the Louisiana Vital Records Registry. Standardized mortality ratios (SMR) were calculated using U.S. Census data to provide an age-adjusted comparison of OD deaths among PLWH and the Louisiana general population.

RESULTS: During the study time period there were 1,804 deaths among PLWH, of which, 68 (3.8%) were OD deaths. The crude OD death rate for PLWH (8.4 per 10,000 pys; 95% CI 6.6, 10.6) was significantly higher than the OD death rate for the Louisiana general population (2.3 per 10,000 pys; 95% CI 2.2, 2.4). The median age of death among PWLH who died by OD was 45 years (Interquartile range: 37-53). On average, individuals died from an OD 12 years ($SD \pm 7.7$) after their HIV diagnosis; 55.9% were White; 77.9% were male; 51.5% had injection drug use as a reported HIV transmission risk. Within the year prior to their OD death, 49 (72.1%) individuals had ≥ 1 viral load tests, and 24 (35.3%) individuals were virally suppressed (< 200 copies/mL) at their last viral load. OD deaths among PLWH were triple that of the Louisiana general population after adjusting for differences in age structure (SMR: 3.0; 95% CI 2.3, 3.7).

CONCLUSIONS: Drug overdose death rates among PLWH are significantly higher than the Louisiana general population. The results are likely an underestimate as OD deaths are frequently under-reported due to lengthy investigations and incomplete data on death certificates. The findings highlight the need for integrated HIV and substance use services to improve engagement in HIV care and overall health outcomes for PLWH.

Submission Complete?	Yes
Committee Topic	Infectious Disease HIV & STD
Keywords	Health Disparities; Substance Use; HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lauren.ostrenga@la.gov
Presenting Author(s)	Lauren Ostrenga
Institution Affiliation	Louisiana Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11650
Abstract Type	Lightning
Abstract Title	HIV and Women in North Carolina: Small Rates, but Higher Proportion of Late HIV Diagnoses

Abstract

BACKGROUND: Early diagnosis of HIV results in better health outcomes. In North Carolina (NC), new HIV diagnoses are most frequent among young men, and women are not a high priority for targeted testing compared to men, which may result in later diagnosis for women. This analysis evaluates whether HIV is diagnosed at a similar stage of disease for men and women in NC, and whether other health outcomes are affected if diagnosis occurs at different stages.

METHODS: All newly diagnosed HIV in NC from 2008 through 2017 reported to the enhanced HIV/AIDS Reporting System (eHARS) were included. We compared demographics and the proportion of late HIV diagnoses (HIV and AIDS diagnosis within six months) between women and men. Retention in care (virally suppressed or two care visits at least 90 days apart one-year post-diagnosis), and viral suppression (most recent VL <200 copies/ml one-year post-diagnosis) were assessed using data from NC Engagement in Care Database for HIV Outreach (NC ECHO), which contains laboratory test, drug dispense, and Medicaid claims data. Death records were obtained from the NC State Center for Health Statistics and were matched to HIV case data to examine death rates between early and late diagnoses. Chi-square analyses were used to assess statistical significance.

RESULTS: A total of 14,225 people were newly diagnosed in NC between 2008 and 2017 (3,170 women and 11,055 men). HIV diagnosis rates among men have decreased (36.1 per 100,000 population in 2008 to 25.4 in 2017), as have rates among women (11.6 in 2008 to 5.7 in 2017). Women were more likely to be diagnosed over the age of 40 and non-White/Caucasian ($p<0.0001$). The proportion of late HIV diagnoses among men has decreased (27% in 2008 to 20% in 2017), while the proportion among women has slightly increased (24% in 2008 to 26% in 2017). The proportion of individuals who were retained in care and achieved viral suppression was similar for women and men, regardless of the stage of diagnosis. While death rates have decreased among men diagnosed late (1.2 in 2012 to 1.0 in 2017), rates among women diagnosed late have remained stable (0.3 in 2012 to 0.4 in 2017).

CONCLUSIONS: While other outcomes are similar, women are more likely to be diagnosed late, and the death rate among women diagnosed late has remained stable. Additional outreach, targeted testing, and prevention activities may decrease late diagnoses of HIV among women.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Epidemiology; HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nicole.d.adams@dhhs.nc.gov
Presenting Author(s)	Nicole Dzialowy Adams
Institution Affiliation	North Carolina Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11529
Abstract Type	Lightning
Abstract Title	Using Risk Factors to Predict Participation in Partner Services Interviews

Abstract

BACKGROUND: Syphilis has been on the rise nationally and in Louisiana, with a 37% increase in early syphilis (P&S syphilis and early non-primary non-secondary syphilis) in Louisiana from 2014 to 2017. Disease intervention specialists (DIS) are tasked with interrupting disease transmission and stand on the front line of STD prevention efforts. Between 2014 and 2017, the percentage of early syphilis cases without a DIS Partner Services interview in Louisiana doubled, from 8.3% to 16.6%. In order to evaluate and improve Partner Services activities, it is important to identify groups less likely to be successfully interviewed.

METHODS: A risk factor analysis was conducted to determine if client attributes can identify individuals less likely to receive a DIS Partner Services interview. Logistic regression of attributes of persons with early syphilis with and without DIS Partner Services interviews from 2014 to 2017 was performed. Variables of interest included sex at birth, race/ethnicity, age group, public health region, urban or rural residence, patient treatment status, HIV status at diagnosis, and sex of sex partner. In Louisiana, when an individual is not interviewed, sex of sex partner is collected from other sources such as prior interviews, HIV records, and electronic health records, allowing the assessment of this variable despite the lack of an interview record.

RESULTS: Analyses revealed that males were 1.2 times more likely to be missing an interview than females (CI=1.11-1.34). Non-Hispanic Whites were 1.3 times more likely to not be interviewed (CI=1.19-1.46) than non-Hispanic Blacks. How likely an individual was to be interviewed varied by public health regions in the state ($p<0.0001$). Gay and bisexual men (GBM) were 3.86 times less likely to be interviewed (CI=3.44-4.35). Persons who were untreated for their infections were 2.16 times less likely to have an interview (CI=1.94-2.42). With each five year increase in age, persons were 1.18 times less likely to be interviewed (CI=1.16-1.20).

CONCLUSIONS: Risk factor and demographic analysis were a valuable resource when evaluating Partner Services outcomes. More efforts are needed to reach GBM because they were least likely to receive a DIS Partner Services interview. Variation in completeness by public health region may indicate a need for increased staffing in those areas, calling for new workload analyses. Sex positivity trainings have been implemented in Louisiana for DIS since 2018. Finally, future plans include expanding Client Satisfaction Surveys to persons who declined an interview to identify weaknesses and preferred methods of partner notification.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Disease Prevention; Sexually Transmitted Diseases; Evaluation
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	catherine.desmarais@la.gov
Presenting Author(s)	Catherine Desmarais
Institution Affiliation	Louisiana Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	10858
Abstract Title	Poster
	Association of Chlamydia or N. Gonorrhea Infection Rates per County in People Ages 15-24 Years in Alabama and Race, Gender, and Socio-Economic Variables (2014-2015)

Abstract

BACKGROUND: Sexually Transmitted Diseases (STDs) continue to be an important Public Health issue. Young adults carry a significant amount of STD burden, representing over half of new cases in the US, despite making up only 1/4 of the sexually active American population. Our objective was to assess the correlation between STD infection rates (per 100,000 population) per county in people 15-24 years old from Alabama, with gender, race, and socioeconomic variables.

METHODS: Rates of *Chlamydia* and *N. gonorrhea* for 2014 and 2015 were calculated from data on the Alabama Department of Public Health's website. All other variables were collected from the US Census Bureau or the Alabama Department of Education. Correlations and multivariate analysis (GEE model) between rates of *Chlamydia* or *N. gonorrhea* and all variables were calculated using a statistical software (SAS).

RESULTS: In the multivariate model, variables statistically significantly associated with *Chlamydia* infection rate were: % Black or African American, % female, urban/rural, % high school graduation, median household income, and year ($p < 0.1$). Multivariate model of *N. gonorrhea* infection rate per county in the 15-24 years age group showed a statistically significantly association with % Black or African American, urban/rural, % high school graduation, and year ($p < 0.1$).

CONCLUSIONS: Our analysis showed slightly different final multivariate models for *Chlamydia* or *N. gonorrhea* infection rates based on statistical significance. However, for both *Chlamydia* or *N. gonorrhea* infection rates per county in people age 15-24 years in Alabama (2014-2015), % Black or African American was the single most significant variable in the multivariate analysis ($p < 0.0001$).

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	HIV & STD
Consider for Different Presentation?	Children and Adolescents; HIV/AIDS; Social Determinants
Presenting Author Email Address(es)	Yes
Presenting Author(s)	analuna@uab.edu
Institution Affiliation	Ana L Oliveira
	University of Alabama at Birmingham
	Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11506
Abstract Type	Poster
Abstract Title	Early Initiation of HIV Care in Georgia, 2014-2017: Prevalence and Association with Longer Term Viral Suppression

Abstract

BACKGROUND: With the recognition that persons with HIV whose viral load (VL) is undetectable do not transmit HIV, there has been an increased emphasis on reducing time from diagnosis to viral suppression (VS). We sought to describe the proportion of persons achieving VS within 3 months of diagnosis in Georgia between 2014 and 2017, and assess the association between VS within 3 months of diagnosis and 2 years later.

METHODS: We analyzed VL test results for persons diagnosed with HIV during 2014-2017 from Georgia's eHARS surveillance database to calculate the proportion virally suppressed within 3 months of diagnosis for each year of diagnosis and to assess disparities by demographic characteristics. We used Poisson regression to examine the relationship between achieving VS within 3 months of diagnosis in 2015 and VS in 2017 (last VL in 2017 <200 copies/ml), controlling for sex, age group, race/ethnicity, transmission category, and location.

RESULTS: The proportion of persons who achieved VS within 3 months of diagnosis increased markedly: 21.3% in 2014, 22.0% in 2015, 26.7% in 2016, and 32.7% in 2017. The relative increase in viral suppression at 3 months during this time period varied across groups. Between 2014 and 2017, the prevalence ratio for Whites versus Blacks decreased from 1.8 to 1.3, the prevalence ratio for Whites versus Hispanics decreased from 1.5 to 1.0, and the prevalence ratio for persons 40 years and older versus persons 20-29 decreased from 2.1 to 1.2. In contrast, the prevalence ratio for men who have sex with men versus persons who inject drugs increased from 1.1 to 1.4, and the prevalence ratio for persons in metro Atlanta versus the rest of the state remained unchanged at 1.3 and 1.4. Among persons diagnosed in 2015 who achieved VS within 3 months, 70% were virally suppressed in 2017, compared with 48% of those who did not achieve VS within 3 months. After controlling for sex, age group, race/ethnicity, transmission category, and location, persons who were virally suppressed within 3 months were significantly more likely to be virally suppressed in 2017 (RR 1.42, 95% CI 1.30-1.55).

CONCLUSIONS: The proportion of persons achieving VS within 3 months of diagnosis has increased substantially in Georgia, indicating that efforts to initiate antiretroviral therapy earlier have been effective. Ongoing monitoring of the association between early suppression and longer term suppression will help assess the impact of those changes.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	HIV/AIDS; Surveillance; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	wendy.wen@dph.ga.gov
Presenting Author(s)	Wendy Wen
Institution Affiliation	Georgia Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11634
Abstract Type	Poster
Abstract Title	Evaluating Chlamydia and Gonorrhea Positivity Among Risk Groups in a State-Funded Testing Program, Indiana, 2018

Abstract

BACKGROUND: The Indiana State Department of Health (ISDH) Laboratory analyzes laboratory tests for clinics funded through the STD Prevention Program's Chlamydia and Gonorrhea Screening Program (CT/GC Program). Patient testing fees are covered through this program provided that they meet at least one of nine established risk criteria. Electronic laboratory reports (ELRs) submitted by the ISDH Lab include the risk group, or reason for test. Participating clinics are encouraged to recruit patients according to these risks. This study examined positivity rates within each risk group.

METHODS: ELRs submitted by the ISDH Lab between January 1 and November 30, 2018, were extracted from the Data Repository and Exchange (DREX). Equivocal or invalid test results and submissions from sites not participating in the CT/GC Program were excluded. Chlamydia and gonorrhea test results were analyzed together for this study. Records were recoded to categorize each given risk group individually. Odds ratios were calculated using SAS 9.4.

RESULTS: During the study period, 30,600 valid laboratory results for chlamydia and gonorrhea were reported by the ISDH Lab (11.2% positivity overall). The most frequent risk groups reported included priority age (less than 25 years) (45.9%; 8.1% positivity), symptomatic of an STD (31.6%; 12.7% positivity), and contact to a known case (11.7%; 23.1% positivity). Priority age patients were 0.6 times less likely to test positive than patients whose age was not considered a risk factor. Patients meeting the symptomatic risk criteria were 1.3 times more likely to test positive than those who did not indicate being symptomatic. Contacts to a person previously diagnosed with an STD were 2.9 times more likely to test positive compared to those who were not contacts.

CONCLUSIONS: State testing programs should evaluate positivity rates by risk category to effectively reach populations in need of services. In Indiana, priority age patients were the largest share of submitted tests but less likely to test positive compared to those over 25, suggesting they may be seeking testing at rates higher than needed. The 23.1% positivity of contacts to prior cases may demonstrate the importance of Disease Intervention Specialist services in facilitating testing and treatment of partners or the success of patient-referred partners. This analysis may be used by CT/GC Program participants to prioritize outreach initiatives for risk groups. Future studies could evaluate differences in positivity by demographics, infection, and clinic site type.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Sexually Transmitted Diseases; Risk Factors
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	aross2@isdh.in.gov
Presenting Author(s)	Amara D Ross
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10681
Abstract Type	Poster
Abstract Title	Gonorrhea Control in Alaska: Lessons from the Yukon-Kuskokwim Region

Abstract

BACKGROUND: During 2008–2011, Alaska experienced a gonorrhea outbreak that disproportionately impacted the Yukon-Kuskokwim (YK) region. During 2009–2011, the YK region had the highest rate of gonorrhea infection in the state. In response to this outbreak, health care providers at the Yukon Kuskokwim Health Corporation (YKHC) tribal health organization implemented several changes to reduce gonorrhea infection rates.

METHODS: Gonorrhea case data were obtained from the Alaska Section of Epidemiology’s Patient Reporting Investigation Surveillance Manager (PRISM) database, and crude rates were examined for Alaska and the YK region. Several informal interviews were conducted with YKHC’s Obstetrics/Gynecology specialist who helped develop new procedures for testing, treating, tracking, and reporting gonorrhea and chlamydia cases in YK.

RESULTS: Gonorrhea rates in YK declined in correlation with changes in practice. In response to a 2008–2011 outbreak, and after reading an Alaska Epidemiology Bulletin on expedited partner therapy (EPT), a YKHC clinician assembled local stakeholders to develop a strategy to provide easy access to chlamydia and gonorrhea treatment for patients and their sexual partners. EPT is the clinical practice of treating the sex partners of patients diagnosed with gonorrhea and chlamydia without their examination. Key elements of this strategy included:

- Assembling a team of clinical champions to develop and implement a clear policy of how sexually transmitted infections (STIs) would be treated.
- Collaborating with pharmacy staff to ensure that pre-mixed medications and educational materials were available for patients and their sexual contacts in village clinics, emergency rooms, outpatient clinics, etc.
- Expanding access to STI medication in rural areas of YK by training Community Health Aides/ Practitioners to work under standing orders for EPT and ensure that medications are available at their clinics.
- Hiring an STI case manager to report to public health, interview patients, trace patient sexual contacts, provide medication for patients and partners, and order extragenital testing and additional medication, if indicated.
- Developing a reporting form on patient diagnosis and prescriptions (including EPT) that health care providers forwarded to the STI case manager.

CONCLUSIONS: Although still above the statewide rate, the incidence of gonorrhea in the YK region declined from 1,316 cases per 100,000 population in 2010 to a low of 390 cases per 100,000 population in 2015. The activities performed by YKHC outlined in this report may have contributed to this decline, and this epidemiologic and qualitative study may be useful to other regions investigating infections disease transmission.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Disease Prevention; Rural Health; American Indians / Alaska Natives
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	katie.cueva@alaska.gov
Presenting Author(s)	Katie Cueva
Institution Affiliation	Alaska Department of Health and Social Services CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11435
Abstract Type	Poster
Abstract Title	Impact of an Electronic Medical Record Best Practice Alert on Expedited Partner Therapy for Chlamydia Infection and Reinfection

Abstract

BACKGROUND: Patients with *Chlamydia trachomatis* infections are at high risk for reinfection if their sex partners are not treated. Expedited partner therapy (EPT) allows providers to prescribe treatment to sex partners of patients diagnosed with chlamydia without examining the partner. In October 2014, Atrius Health implemented an electronic best practice alert (BPA) to encourage providers to prescribe EPT. We sought to describe patient characteristics associated with EPT provision, and to assess the impact of the BPA on EPT provision and chlamydial reinfection.

METHODS: We included patients aged ≥ 15 years with ≥ 1 positive chlamydia laboratory test between January 2013 and August 2018. Data were collected using the Electronic medical record Support for Public Health surveillance platform (esphealth.org). We used log-binomial regression with generalized estimating equation methods to identify patient characteristics associated with EPT provision. We performed interrupted time series analyses to identify changes in level and slope corresponding to the BPA release in October 2014 for the following monthly outcomes: 1) chlamydia cases with EPT provided; 2) chlamydia cases with test of reinfection in 12 months; 3) chlamydia reinfection in 12 months.

RESULTS: Between January 2013 and August 2018 there were 6,639 laboratory-confirmed chlamydia diagnoses. EPT was provided to 1,411 (21%). Patients who received EPT were more likely to be female (prevalence ratio (PR) 1.77, 95% CI 1.47, 2.13), and to have a history of ≥ 2 chlamydia tests (PR 1.19, 95% CI 1.01, 1.39) or diagnoses in the two years preceding their current diagnosis (PR 1.44, 95% CI 1.05, 1.99). EPT prescription frequency increased each month from 15% of chlamydia cases in January 2013 to 24% in October 2014 (slope=0.003, $p=0.03$). The frequency of EPT prescriptions decreased after introducing the BPA, to 16% of chlamydia cases in August 2018 (slope=-0.005, $p<0.01$). On average, 65% of chlamydia cases received a test of reinfection and 11% were re-infected; there were no changes in these percentages after the BPA was implemented. Among chlamydia cases that did and did not receive EPT, the percentages that were re-infected did not change after the BPA was implemented.

CONCLUSIONS: EPT provision declined after introducing a BPA to facilitate EPT prescribing. Reasons for the decrease are unclear and may be independent of the BPA. BPAs in electronic medical record systems may not be effective at sustaining awareness of EPT and decreasing chlamydial reinfection. Periodic trainings or other approaches may be more successful at increasing EPT provision among clinicians.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Epidemiology; Sexually Transmitted Diseases; Electronic Health Records
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	sarah_willis@harvardpilgrim.org
Presenting Author(s)	Sarah J Willis
Institution Affiliation	Harvard Pilgrim Health Care Institute and Harvard Medical School Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11256
Abstract Type	Poster
Abstract Title	Risk Factor Analysis and Changes for Non-Congenital Syphilis Cases Residing in Jefferson County, Kentucky, for 2013 to 2017

Abstract

BACKGROUND: In August 2018, the Centers for Disease Control and Prevention reported dramatic and sustained increase in sexually transmitted diseases (STDs) in recent years, including syphilis. In Kentucky, syphilis cases are investigated by STD Prevention and Control Program - patient follow up and interviews are conducted by STD staff at a local health department, such as Louisville Metro Public Health and Wellness (LMPHW), while data are managed by Kentucky Department for Public Health (KDPH). LMPHW set out to determine whether Jefferson county is experiencing a similar trend to what was observed nationally and explored the possibility of any significant changes in characteristics among reported non-congenital syphilis cases investigated from 2013 to 2017.

METHODS: KDPH provided syphilis data of Jefferson County residents. Data analysis includes all syphilis diagnoses, except congenital syphilis. Prevalence rates were calculated using the year-specific population estimates from the Kentucky State Data Center for Jefferson county, Kentucky. The investigation questionnaire includes questions about sexual history and behaviors, drug use behaviors, and other risk factors for the 12 months prior to diagnosis. Regardless of reason, not interviewed cases were excluded from risk factor analysis. For analysis purposes, responses were simplified to “reported”, consisting of only “yes” answers, or “not reported”, consisting of the remaining choices or lack thereof. Responses were analyzed for both individual risk factor questions, and clustered versions of similar questions such as having high risk sexual partners, high risk sexual acts, substance use, and incarceration while controlling for gender and race. Cases were categorized as being reported in 2013 to 2015 (Y1315), and 2016 to 2017 (Y1617). Fisher’s Exact Test was performed to test for differences in responses between Y1315 and Y1617 reported cases among interviewed cases.

RESULTS: From 2013 to 2017, KDPH interviewed 986 (77%) out of 1281 reported non-congenital syphilis cases. In 2016 we observed the largest increase in unadjusted prevalence rates at 9.6 per 100,000. No significant differences in age was observed between the Y1315 and Y1617 cases. Between the two case groups, significant differences ($\alpha \leq 0.05$) were observed in white males for drug use, sex with males and females, and in black males for sex with females.

CONCLUSIONS: The risk factor analysis suggests that certain behaviors among certain groups of people may have changed since 2015. Thus, interventions can be targeted towards those individual groups to better reduce the incidence of non-congenital syphilis in Jefferson county.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Risk Factors; Sexually Transmitted Diseases; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rui.zhao@louisvilleky.gov
Presenting Author(s)	Rui Zhao
Institution Affiliation	Louisville Metro Department of Public Health and Wellness Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	An Evaluation of Postpartum HIV Viral Load Rebound in Mothers in Pennsylvania, 2007-2016

Abstract

BACKGROUND: HIV positive mothers have added responsibility of raising their newborn babies as well as caring for themselves. The arrival of a newborn can result in shifts in priorities. The purpose of the study was to evaluate whether there is postpartum HIV viral load (VL) rebound in mothers who had demonstrated VL suppression within 30 days before delivery. **METHODS:** Data was compiled from the Enhanced HIV/AIDS Reporting System to formulate a study cohort of mothers who showed a suppressed VL (less than 50 copies/ml) within one month of delivery for births occurring between 1/1/2007 and 12/31/2016. The study cohort had at least three reported VL tests in the first post-partum year. Additionally, data on demographically similar non-mothers were obtained as a control group. A computer algorithm randomly selected non-mothers by iteratively matching attributes of each mother in the study group by location, age, age at diagnosis, and risk category. A randomly selected suppressed VL was chosen for each non-mother to act as a comparative starting point. Selected VL occurred at a point that left a minimum of 12 months follow-up period. Non-mothers were evaluated for the next 12 months for rebound/non-rebound. **RESULTS:** There were 126 mothers who met the criteria for study, and of those 31 (24.6%) showed a VL rebound within the first 3 months postpartum, with a true rebound probability of 17.1% to 32.1%, based on a 95% confidence interval (CI). Within 6 months, 45 (35.7%) showed a rebound, with a true rebound probability of 27.3% to 44.1%. Within 12 months, 62 (49.2%) showed a rebound, with a true rebound probability of 40.5% to 57.9%. For 145 non-mothers, 18 (12.4%) showed a VL rebound within the first 3 months, with a true rebound probability of 7.1% to 17.8%, based on a 95% CI. Within 6 months, 39 (26.9%) showed a rebound, with a true rebound probability of 19.7% to 34.1%. Within 12 months, 69 (47.6%) showed a rebound, with a true rebound probability of 39.5% to 55.7%. **CONCLUSIONS:** A quarter of mothers who had suppressed VL 30 days prior to delivery experienced VL rebound within 3 months postpartum, compared to only 12.4% for the control group 3 months after a suppressed VL, which is significantly different at 95% confidence level. This evaluation confirms findings in similar observational studies. Ensuring continuity of medical care from antepartum period to postpartum period may lead to continued VL suppression for new mothers.

Submission Complete?	Yes
Committee Topic	Infectious Disease HIV & STD
Keywords	Evaluation; Maternal and Child Health; HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	c-shkepner@pa.gov
Presenting Author(s)	Shawn Kepner
Institution Affiliation	Pennsylvania Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11014
Abstract Type	Quick
Abstract Title	Cases of <i>Neisseria Gonorrhoeae</i> with High-Level Azithromycin Resistance Detected in Indiana, Strengthening U.S. Response to Resistant Gonorrhea (SURRG), 2017-2018

Abstract

BACKGROUND: Gonorrhea is the second most commonly-reported notifiable disease in the United States, and reported rates continue to steadily increase. Antibiotic resistance in *Neisseria gonorrhoeae* (Ng) continues to be documented across the globe. National surveillance data show Ng azithromycin (AZI) susceptibility has been declining in the United States, but high-level azithromycin-resistance (HL AZI-R) remains rare. Several HL AZI-R Ng isolates have been identified in Indiana. This study describes a cluster of HL AZI-R cases and the resulting public health response.

METHODS: Indiana, through participation in the national surveillance system Gonococcal Isolate Surveillance Project (GISP), and Strengthening U.S. Response to Resistant Gonorrhea (SURRG), a Centers for Disease Control and Prevention (CDC)-supported multisite program to bolster local capacity to rapidly detect and respond to Ng with reduced antibiotic susceptibility, collected genital and extra-genital samples from men and women attending a sexually transmitted disease (STD) clinic and two non-STD clinics for Ng culturing. Local antimicrobial susceptibility testing (AST) via Etest was performed on all 674 Ng isolates collected from September 2017 to September 2018 (an estimated 12% of total morbidity in the jurisdiction). Reduced AZI susceptibility was defined as MICs $\geq 2.0 \mu\text{g/mL}$; HL AZI-R was defined as MICs $\geq 256 \mu\text{g/mL}$. Disease Intervention Specialists (DIS) conducted investigations on all patients with reduced susceptibility of any level and offered testing and treatment to partners.

RESULTS: Of the 674 isolates, 54 (8.0%) demonstrated reduced AZI susceptibility, of which 14 (2.1%) demonstrated HL AZI-R (11 urethral, two pharyngeal, one rectal). All isolates were susceptible to ceftriaxone (MIC $\leq 0.125 \mu\text{g/mL}$) and were adequately treated with ceftriaxone 250mg and azithromycin 1g. The 14 HL AZI-R isolates were obtained from 12 men, two with both urethral and pharyngeal infections. Of the 12 men, nine were white, eight were men who have sex with men/bisexual, and six reported anonymous partners. Nine patients completed a test-of-cure; all were negative. The 12 men claimed 36 sex partners during the two months prior to infection. DIS elicited enough information to initiate 11 partners for follow-up, and six tested positive for Ng. Only two cases were epidemiologically-linked.

CONCLUSIONS: During a 13 month period, Indiana identified twelve men with HL AZI-R Ng in Indiana. The continued detection of these infections and lack of epidemiological-linkage between the patients and their partners suggest sustained local transmission. Intensified surveillance, expanded AST, and elicitation of local sexual networks may provide future opportunities to curtail local spread of this concerning strain.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Capacity / Capacity Building; Sexually Transmitted Diseases; Antimicrobial Resistance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	juholderman@isdh.in.gov
Presenting Author(s)	Justin Holderman
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Chlamydia Among Males Aged 15-24 Years in the United States in 2016: How Much Is Actually out There?

Abstract

BACKGROUND: Most *Chlamydia trachomatis* (CT) infections are asymptomatic and prevention efforts in the United States focus on routine screening and treatment of females to prevent adverse reproductive sequelae. Understanding the burden of CT infections in males may help inform prevention and control efforts. We describe the epidemiology of CT in young males in the United States and provide estimates of the extent to which infections in males may go undiagnosed.

METHODS: Data from national case reporting and the National Health and Nutrition Examination Survey (NHANES) were used to estimate the number of reported CT cases and the number of prevalent CT infections among males aged 15-24 years in 2016. The number of prevalent CT infections was calculated by multiplying weighted NHANES prevalence estimates by the average of the American Community Survey population estimates during 2015–2016. Assuming that all undiagnosed cases are not reported, undiagnosed infections were estimated by calculating the number of CT cases reported as a percent of prevalent CT infections. Estimates were calculated overall and by race/ethnicity.

RESULTS: In 2016, 272,524 CT cases were reported among all 15-24 year old males; 92,249 cases were among Black, non-Hispanics, 59,006 among White, non-Hispanics, and 31,292 among Hispanics. Based on NHANES, the population-based CT prevalence among all young males was 2.7%, equating to an estimated 583,113 prevalent CT infections, suggesting that over half (53%) of infections among young males may go undiagnosed. Estimated CT prevalence was highest among Black non-Hispanic young males, at 12.0%, equating to an estimated 360,346 prevalent infections with an estimated 74% of infections undiagnosed. CT prevalence estimates for White non-Hispanic and Hispanic young males are lower than for Black non-Hispanic males in NHANES although small sample sizes resulted in unstable estimates; however, the difference between case reports and prevalent infections suggests that 36% of infections among White non-Hispanics and 64% among Hispanics went undiagnosed.

CONCLUSIONS: A comparison of national case report and prevalence estimates suggests that CT infections are common in young males and a large percent of prevalent CT infections may go undiagnosed in this population. The estimated percent undiagnosed differed by race/ethnicity, with a higher proportion of infections undiagnosed among racial minorities compared to Non-Hispanic Whites. Observed racial differences may be due to differences in access to quality sexual health care. Additional research is needed to determine how undiagnosed infections in males affect CT prevention and control efforts in women.

Submission Complete?	Yes
Committee Topic	Infectious Disease HIV & STD
Keywords	Infectious Diseases; Sexually Transmitted Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ltq1@cdc.gov
Presenting Author(s)	Kristen Kreisel
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Demographics and Risk Factors of Men Who Have Sex with Men (MSM) with Syphilis in Florida, 2017

Abstract

BACKGROUND: Florida reported 8,859 cases of syphilis in 2017, with most cases being in men (n=7317). Most of the cases in men are in individuals who self-report as an MSM (n=5,297). In 2017, 4,969 MSM with syphilis were interviewed by disease intervention specialists and asked about risk factors. We sought to elucidate if there were any characteristics shared among the interviewed MSM, and if the risks differed between those currently living with HIV/AIDS and those not coinfecting.

METHODS: The demographics and self-reported risk factors of MSM with syphilis were extracted from Florida's sexually transmitted disease surveillance database for 2017 and analyzed. Differences between the demographics and risk factors of the individuals currently infected with HIV at the time of their syphilis diagnosis were compared, using X² tests, to MSM with syphilis who are not currently coinfecting with HIV.

RESULTS: The highest self-reported risk factor for MSM coinfecting with HIV and syphilis was a prior STD history, with 63% (n=1,928) of individuals disclosing at least one previous STD in their lives, compared to 41% (n=789) of non-coinfecting MSM (odds ratio 2.4, confidence limits 2.1 – 2.7, p<0.001). Those already infected with HIV were also more likely to report HIV+ partners in their interviews (33% vs 15%; odds ratio 2.8, confidence limits 2.4 – 3.2). Conversely, the highest self-reported risk factor for MSM not coinfecting with HIV was anonymous sex partners, with 61% (n=1,168) of individuals disclosing this risk factor compared to 46% (n=1,401) of coinfecting MSM (odds ratio 1.9, confidence limits 1.7 – 2.1, p<0.001). White Hispanic (32% vs 28%) or black (30% vs. 19%) MSM were at an increased likelihood to be coinfecting with HIV and syphilis (p<0.005 for both comparisons). Conversely, white non-Hispanic MSM were more likely to be infected with syphilis only (32% vs. 28%; p<0.001).

CONCLUSIONS: Given the high percentage of MSM with syphilis, but not HIV, reporting anonymous sex partners, additional HIV prevention tactics, including pre-exposure prophylaxis (PrEP), are warranted for MSM who present with STDs. White Hispanic and black MSM are at an increased risk of having HIV and syphilis. As white non-Hispanics do not share this risk, common causes of health inequity may be contributing factors. Prior STD history is a common coinfection predeterminant; as such, educational and other public health efforts focused on HIV prevention tactics in the MSM community are critical when an MSM individual test positive for syphilis.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	HIV/AIDS; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	victoria.pearson@flhealth.gov
Presenting Author(s)	Victoria M Pearson
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11655
Abstract Type	Quick
Abstract Title	Frequent Gonorrhea Infections and Subsequent Early Syphilis Diagnoses in Louisiana: An Opportunity for Intervention

Abstract

BACKGROUND: Since 2012, gonorrhea diagnoses in the US have increased 66% and early syphilis diagnoses have more than doubled. During this same period, Louisiana has ranked in the top three nationally for its gonorrhea and syphilis diagnosis rates. While both diseases are easily treatable, the prevalence of antimicrobial-resistant gonorrhea has increased, and the sequelae of untreated syphilis can be serious, including congenital syphilis in the children of infected pregnant women. Optimal STD control requires timely testing and treatment of infected persons to reduce the period of infectivity and subsequent disease transmission. Gonorrhea and syphilis are also markers for high-risk sexual behavior and for subsequent STDs and HIV. In this study, we assess the risk of early syphilis infection after frequent repeat gonorrhea infection (FRGI) in persons living in Louisiana.

METHODS: Surveillance data from Louisiana Department of Health's STD registry were used to compile gonorrhea and early syphilis diagnoses occurring in Louisiana between 2012 and 2017. Persons were classified as having FRGIs if they had two or more gonorrhea diagnoses within an 18-month period, forming a retrospective cohort of individuals with FRGIs. Descriptive statistics and survival analyses using variables regularly collected during surveillance activities were performed to determine likelihood of a syphilis infection following an FRGI classification.

RESULTS: From 2012 through 2017, 5,459 persons were FRGI classified. FRGI classified persons were 54% female, 86% non-Hispanic Black, and had a mean age of 23. The number of gonorrhea infections among FRGI classified persons ranged from 2 to 11. Males were more likely to have an early syphilis diagnosis following FRGIs (HR=1.24). Non-Hispanic Whites were more likely to have an early syphilis diagnosis following FRGIs (HR=1.32), and with each year increase in age, a person was more likely to have an early syphilis diagnosis (HR=1.04) after FRGIs.

CONCLUSIONS: Males, non-Hispanic Whites, and older individuals with multiple gonorrhea infections within an 18 month period were more likely to experience a subsequent early syphilis infection than other populations with FRGIs in Louisiana despite a greater proportion of females and non-Hispanic Blacks bring FRGI classified. Because both gonorrhea and syphilis infection are indicators of unprotected sexual contact and facilitate the transmission of HIV, screening for HIV is suggested in persons with FRGIs. Providers should be made aware of the association between FRGIs and subsequent syphilis infection so they can monitor patients with FRGIs more closely and perform regular syphilis screening.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Co-Morbidity; Risk Assessment; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	catherine.desmarais@la.gov
Presenting Author(s)	Catherine Desmarais
Institution Affiliation	Louisiana Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11835
Abstract Type	Quick
Abstract Title	From Free to Fees: Evaluating the Local Health Impact of a Public Health STI Clinic Policy Change

Abstract

BACKGROUND: In July 2017, due to a statewide policy change, public health sexually transmitted infection (STI) clinics in Fairfax County, Virginia switched from providing no cost, walk-in services, to operating as an appointment-based clinic with sliding-scale fees. Nationally, the shift towards a revenue generating public health structure is common given reductions in funding for public health services and expanded opportunities for third-party billing. Sustainably funding STI clinics for underserved populations is a public health essential; however, evaluations detailing the local impact from these types of policy changes are lacking. We aim to evaluate changes in STI epidemiology temporally associated with this policy shift in Fairfax Health District (FHD).

METHODS: We analyzed FHD STI public health clinic visit data and laboratory-confirmed STI diagnoses for chlamydia, gonorrhea, HIV, and syphilis among FHD residents. For confirmed cases, we classified the provider site as an FHD clinic, other public health clinic, or private sector site. Data were compared for the six months before and after the policy change, excluding July 2017 as a transition period. Differences were assessed using Chi-squared, Fisher's exact, t-test, and interrupted time series analysis, as appropriate. Statistical significance was defined by a p-value of <0.05.

RESULTS: Compared with the baseline period, we saw a 55% decrease in the number of patients seen at FHD clinics during the six months after the policy change (from August 2017 to January 2018). At FHD clinics, we identified a 41% decrease in chlamydia diagnoses (from 181 to 107, $p < 0.001$); numbers of gonorrhea, HIV and syphilis diagnoses before and after the change were similar. The proportion of tests from FHD clinics positive for chlamydia and gonorrhea increased significantly (from 9.9% to 12.9%, and 1.1% to 3.3%, respectively). Increases occurred in the number of STI diagnoses at other public and private sector sites, such that total confirmed diagnoses increased for all STIs in the six months after the policy change. Policy impacts on location of diagnosis and proportion of positive tests varied significantly by age, race and sex.

CONCLUSIONS: We found a significant shift in chlamydia diagnoses among Fairfax County residents from FHD clinics to other public and private sector sites following imposition of appointment-based clinics with fees. Increased yield of positive tests suggests a reduction in the worried-well population seeking care at FHD clinics. Although these results suggest the policy change has not increased the risk of undetected STI, further surveillance is needed to understand long-term impacts.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Evaluation; Local Epidemiology; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	benjamin.klekamp@fairfaxcounty.gov
Presenting Author(s)	Benjamin G Klekamp
Institution Affiliation	Fairfax County Health Department Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11545
Abstract Type	Quick
Abstract Title	Improving HIV Data Quality Using ELR Demographics

Abstract

BACKGROUND: As part of routine HIV surveillance practices, persons living with HIV are reported into the enhanced HIV AIDS Reporting System (eHARS) which is managed at Louisiana's STD/HIV Program. Date of birth (DOB) is a mandatory variable for all cases of HIV reported to the Centers for Disease Control and Prevention (CDC). Both intrastate and interstate case deduplication efforts rely heavily on DOB; if recorded incorrectly, true matches are left undocumented. Through Louisiana's electronic lab reporting (ELR) system, DOB is reported in conjunction with laboratory results. Using ELR data to identify discordant DOB in eHARS is a simple, cost effective, quality control method to enhance database management and reduce case duplication.

METHODS: Using SAS 9.3, all laboratory results with a valid DOB were compiled by unique person and DOB. The most frequently reported DOB per person was tabulated, including the number of laboratory results in which it appeared. This dataset was then matched against the current DOB in eHARS to identify discordant results (N=829). To maximize impact, persons with the highest frequencies of discordant DOB via ELR were prioritized. Frequency quartiles were established and follow-up was conducted on quartiles one through three, defined as greater than or equal to 13 laboratory results with discordant DOB present (N=614). Among these individuals, additional verification was conducted using Accurant LexisNexis before DOB was updated in eHARS. Finally, for individuals with a corrected DOB, a CDC Soundex match was conducted for out of state indications for deduplication.

RESULTS: For quartiles one through three, the majority of cases had an incorrect DOB previously recorded in eHARS and the true DOB was received via ELR. 480 profiles (78.2%) in eHARS were updated with the corrected DOB and four persons were subsequently deduplicated. After CDC soundex matching, 170 unique persons returned 270 potential out of state matches not previously identified. To date, 61 cases have been deduplicated from calls with other jurisdictions. Furthermore, while validating DOB with Accurant, 46 Social Security Numbers (SSN) were corrected and seven were collected on individuals with a missing or incomplete SSN.

CONCLUSIONS: In instances where DOB is discordant between eHARS and ELR data, the DOB from the ELR was more likely to be accurate. Utilizing these data as a tool for quality control is a simple and cost-effective strategy. Improving DOB accuracy enhances internal data quality used for reporting and the ability to deduplicate records on a national level.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Information Databases; Electronic Laboratory Reporting (ELR); HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Molly.Votaw@LA.gov
Presenting Author(s)	Molly Votaw
Institution Affiliation	Louisiana Department of Health and Hospitals Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11877
Abstract Type	Quick
Abstract Title	Monitoring Viral Suppression among Medicaid Enrollees Living with HIV: Results from Four Years of Medicaid/Surveillance Data Linkage

Abstract

BACKGROUND: In Louisiana, approximately 58% of people living with HIV (PLWH) are enrolled in Medicaid. The number of enrolled PLWH increased significantly with Medicaid expansion in July 2016. The Office of Public Health HIV Surveillance Program (OPH) and Medicaid Program have shared data for the past four years in order to monitor outcomes among PLWH, especially as PLWH transitioned to Medicaid post-expansion. All Medicaid managed care organizations (MCOs) are required to monitor and report HIV viral load suppression on a quarterly basis using data provided by OPH.

METHODS: For the MCO viral load suppression measure, Medicaid submits a file of persons enrolled in Medicaid who have an HIV diagnosis and at least one medical visit during the measurement year. These data are linked to HIV surveillance data to determine whether the person's last viral load was less than 200 copies/mL (i.e., virally suppressed). Data have been linked 13 times since 2014 and are now being exchanged every quarter. During the period of Medicaid expansion (July 2016- January 2017) data were linked monthly to monitor the transition of clients from Ryan White services to Medicaid, including monitoring viral load suppression.

RESULTS: In 2014 among all MCOs combined, 71% of persons enrolled in Medicaid with an HIV diagnosis were virally suppressed; viral suppression was 71% in 2015, 75% in 2016, 77% in 2017, and 77% in September 2018. Of the 3,684 persons receiving Ryan White services who transitioned to Medicaid between July 2016 and January 2017, viral suppression increased from 84% pre-transition to 88% 2 years post-transition.

CONCLUSIONS: Linking Medicaid data and HIV surveillance data has enabled OPH and the MCOs to better monitor HIV-related outcomes among Medicaid enrollees. OPH was able to monitor Ryan White clients who transitioned to Medicaid to ensure there were no gaps in services. MCOs can use the data to improve their outreach and services for enrollees who are living with HIV who are not virally suppressed. Data will continue to be linked and analyzed to identify subgroups of PLWH who need additional intervention to improve outcomes.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Data Sharing; HIV/AIDS; Outcome Measures
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Debbie.Wendell@LA.GOV
Presenting Author(s)	Debbie Wendell
Institution Affiliation	Louisiana Department of Health and Hospitals State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	New HIV Infections Among People Who Inject Drugs — Northeast Massachusetts, 2015–2018

Abstract

BACKGROUND: In mid-2016 Massachusetts Department of Public Health (MDPH) identified an increase in HIV diagnoses among people who inject drugs (PWID) in northeastern Massachusetts, an area with high rates of fatal opioid overdoses. MDPH initiated an investigation to characterize the outbreak and recommend control measures.

METHODS: Cases were defined as HIV diagnoses during January 2015–May 2018 in PWID who received medical care, resided, or injected drugs in the Cities of Lawrence or Lowell; or who were a named injecting or sex partner, or were molecularly linked by HIV nucleotide sequences at a genetic distance of $\leq 1.5\%$ to a case meeting temporal and geographic criteria. Case interviews identified needle-sharing and sexual contacts. Stakeholders provided information on local services. A purposeful sample of 34 PWID gave qualitative interviews.

RESULTS: Of 122 people identified as cases, 71 (58%) were male; 89 (73%) were aged 20–39 years at diagnosis; 80 (66%) were white, and 101 (85%) reported injection drug use. Thirty-one cases (25%) had only molecular links to other cases. Three molecular clusters of ≥ 5 cases were identified. Median CD4 count at diagnosis was 556 cells/ μL (range 1–1470 cells/ μL). Stakeholders reported fentanyl use and frequent homelessness and incarceration among PWID. Syringe service program (SSP) accessibility was higher in Lawrence than Lowell. All PWID interviewed expressed a desire not to share syringes and acknowledged that sharing injection equipment occurs; 7 reported injecting >10 times/day, and 7/13 females reported exchange sex.

CONCLUSIONS: Molecular analysis aided case identification and indicates several introductions of HIV into this population with recent rapid transmission alongside detection of longstanding infections. Fentanyl use alters risk behaviors including increasing injection frequency. In 2016, Lawrence established a state-funded SSP; a privately funded SSP opened in Lowell in 2018. MDPH has expanded local field epidemiology to link individuals to care.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	HIV & STD
Consider for Different Presentation?	Substance Use; HIV/AIDS
Presenting Author Email Address(es)	No
Presenting Author(s)	calpren@bphc.org
Institution Affiliation	Charles Alpren
	Centers for Disease Control and Prevention
	EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	10849
Abstract Type	Quick
Abstract Title	Progress Towards Implementation of 2018 CSTE Revised Syphilis Case Definition

Abstract

BACKGROUND: Syphilis, a sexually transmitted disease (STD), can lead to severe complications if untreated, including blindness and deafness. In January 2018, a revised CSTE case definition for syphilis went into effect and included definitions for new variables to capture important clinical manifestations of syphilis. To facilitate transfer of these new variables when providing case notifications to CDC, the record layout for notifiable STDs was concurrently revised. We reviewed syphilis case reports sent to CDC to identify progress in implementing this aspect of case definition change.

METHODS: We reviewed case reports of syphilis, all stages (excluding congenital syphilis), sent to CDC in 2018 (as of 12/13/2018). For each new clinical manifestation variable (late clinical, otic, and ocular manifestations), we reviewed the value reported (1=Yes, verified; 2=Yes, likely; 3=Yes, possible, 4=No, 9=Unknown, or Missing). We identified states that had reported at least one syphilis case with a non-9, non-missing value and estimated the prevalence of clinical manifestations in these states.

RESULTS: As of 12/13/2018, 90,689 syphilis cases (all stages) were reported in the United States for 2018; all states and the District of Columbia reported at least one case of syphilis. Only fourteen (27%) states reported at least one case with a non-9, non-missing value for late clinical, otic, or ocular manifestations variables. In these states, 13,333 cases were reported. Overall, the majority of these cases (78%) were coded as missing or unknown for the clinical manifestation variables. Among the cases with a non-missing or unknown value, the prevalence of late clinical manifestations (verified, likely, or possible) was 2.0% (58/2,871), of ocular manifestations was 2.8% (80/2,883), and of otic manifestations was 1.1% (31/2,881).

CONCLUSIONS: Only about a quarter of states have begun sending information to CDC on clinical manifestations identified in the current CSTE syphilis case definition. Based on data from a limited number of states, prevalence of reported complications is low. Documenting clinical consequences of syphilis is important to inform patient management, as well as to monitor trends in sequelae. Barriers to implementation of the revised case definition may be related to difficulties modifying surveillance information systems.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Sexually Transmitted Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	igf0@cdc.gov
Presenting Author(s)	Elizabeth Torrone
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Sexual Risk Behaviors Associated with HIV Testing Among Sexually Active High School Females in the U.S. By Race/Ethnicity – Youth Risk Behavior Survey, 2015-2017

Abstract

BACKGROUND: Nearly 1,000 young women aged 13-24 received an HIV diagnosis in 2016, two-thirds of which were among black/African American women. Most new diagnoses among young women were attributable to heterosexual contact. CDC recommends “at least once in a lifetime” HIV screening for everyone aged 13-64, and annually for high-risk individuals. Between 2005 and 2013, less than 1/3 of sexually experienced high school females had ever been tested for HIV. Our objective was to examine the association between sexual risk behaviors and HIV testing among sexually active high school females by race/ethnicity.

METHODS: Using 2015 and 2017 Youth Risk Behavior Survey data, we analyzed data from 4,097 sexually active high school females. We calculated prevalence estimates and 95% confidence intervals [CIs] of sexual risk behaviors (first had sex before age 13, ever been forced to have sex, had 4 or more lifetime sexual partners, did not use a condom during last sex, and used alcohol or drugs before last sex) and ever had an HIV test. We used logistic regression to calculate prevalence odds ratios and 95% CIs for the association between each sexual risk behavior and HIV testing adjusted for high school grade. All analyses were stratified by race/ethnicity (non-Hispanic white [NHW], non-Hispanic black/African American [NHB], Hispanic or Latina [Hispanic]). We used non-overlapping CIs as a conservative test of significance at the 0.05 alpha level to determine differences in prevalence across racial/ethnic groups.

RESULTS: NHB females reported the highest prevalence of having had an HIV test (34.4%) compared with NHW (20.2%) and Hispanic (20.3%) females. A higher proportion of NHB reported first sex before age 13 than did NHW (7.7% vs 3.2%). Prevalence of other sexual risk behaviors were similar across racial/ethnic groups. Among NHW and Hispanic females, all sexual risk behaviors were positively associated with HIV testing except alcohol or drug use before last sex among Hispanics. Among NHB females, only having 4 or more lifetime sexual partners was positively associated with HIV testing.

CONCLUSIONS: The prevalence of ever having been tested for HIV among sexually active NHW, NHB, and Hispanic high school females was lower in 2015 and 2017 than is recommended by CDC, indicating a need for more “once in a lifetime” HIV testing in all groups. Additionally, more annual testing and sexual health education to reduce sexual risk behaviors may be warranted for all females with high risk behaviors.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Minority Health; Children and Adolescents; HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	fdx7@cdc.gov
Presenting Author(s)	Alissa Cyrus
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10575
Abstract Type	Quick
Abstract Title	Sleuthing for Risks: Drug Use and Exchanging Sex for Drugs or Money Among Mothers of Congenital Syphilis (CS) Babies

Abstract

BACKGROUND: Gathering risk information, specifically drug use and exchanging of sex for money/goods, for pregnant females with syphilis is critical to both provide the best support for obtaining treatment, and to make informed procedural shifts to reduce syphilis within our communities. We assessed whether the number of CS mothers with self-reported risk factors in our database is accurate or under-reported when supplemented with other surveillance tools.

METHODS: Self-reported risk factors of the mothers of CS babies (n=81) were extracted from Florida's sexually transmitted disease surveillance database for 2017 and analyzed for disclosure of drug use, including marijuana, or prostitution. Case review was performed to identify any mentions of drug use or exchanges of sex for drugs or money not contained in self-reported risk factors. Accurint® searches were completed on all the mothers of CS infants to view any related criminal charges. Differences between the number of CS mothers reporting these risk factors, versus the total number reporting it, plus those with criminal records of the behavior, were analyzed using χ^2 tests.

RESULTS: Extraction of risk factors related to drug use and exchange sex from the surveillance database indicated 15% (n=12) of CS mothers used drugs and 10% received money or drugs for sex (9% for both). Case review identified an additional 12% (n=10) of mothers that may be using drugs and no additional mothers reporting sex exchanges. Accurint® criminal records were found for 52% (n=42) of the mothers. Drug and/or prostitution charges were identified for 22% (n=18) of the mothers (drug: 20%, n=16; prostitution: 11%, n=9). Adding case review and Accurint® searches yielded significantly more mothers using drugs (32%), compared to those only self-reporting these risk factors (14%) (risk ratio 2.7, confidence limits 1.2 – 4.0). Conversely, although we found additional mothers with histories of prostitution (15%), this increase was not significantly higher than the self-reported risk factors alone (10%) (risk ratio 1.5, confidence limits 0.6 – 3.5).

CONCLUSIONS: Drug use among mothers of CS infants is likely higher than our surveillance database indicates. Further, criminal databases can be a useful tool in identifying addition mothers where drug use was likely, but either the mother was never located for interviewing, the interviewer never asked, or the women were reluctant to disclose drug use. Training techniques to help the interviewer establish trust with the clients, and to reinforce the need to ask these questions, could aid in improving response rates to sensitive questions.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Substance Abuse; Maternal and Child Health; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	victoria.pearson@flhealth.gov
Presenting Author(s)	Victoria M Pearson
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11079
Abstract Type	Quick
Abstract Title	Violence Victimization, Suicide Attempt, and HIV Testing Vary By Nhas HIV Risk Profile Among Sexual Minority Male High School Students

Abstract

BACKGROUND: An aim of the National HIV/AIDS Strategy (NHAS) was a reduction in the percentage of adolescent sexual minority males (SMM) who have engaged in HIV risk behaviors by at least 10% from the 2015 national baseline of 35.2%, which was achieved in 2017. Adolescent SMMs are at increased risk for several concerning experiences, including violence and suicidality compared to their heterosexual peers. Information is limited on health behavior differences by NHAS HIV risk behaviors. This study aimed to compare violence victimization (VV), attempted suicide and HIV testing status among SMM students who have and have not engaged in HIV risk behaviors.

METHODS: The 2015 and 2017 cycles of the national Youth Risk Behavior Survey, a nationally representative, cross-sectional survey conducted among students in grades 9-12 were combined and, analyses were restricted to male students who engaged in sexual contact with males only or with both males and females (SMM) (n=484). NHAS HIV risk behaviors were defined as engaging in at least one of the following: (1) had sexual intercourse during the past three months with 3+ persons, (2) had sexual intercourse during the past three months and did not use a condom during last sexual intercourse, or (3) ever injected any illegal drug. SMM were then dichotomized into 2 groups -- NHAS HIV risk behaviors vs no NHAS risk behaviors. Descriptive analyses compared demographic characteristics, six VV indicators, attempted suicide, and HIV testing by NHAS HIV risk profile. Logistic regression analyses estimated prevalence ratios (PRs) and 95% confidence intervals (CIs) for associations between NHAS HIV risk profile and health behavioral outcomes.

RESULTS: SMM students were more likely to have engaged in NHAS HIV risk behaviors if they missed school because they felt unsafe (PR=1.87;95% CI:1.34-2.81), had been threatened/injured by a weapon on school property (1.83;1.22-2.76), experienced sexual dating violence (2.00;1.39-2.88), experienced physical dating violence (2.76;1.88-4.06), attempted suicide (1.75;1.19-2.58), and had ever been tested for HIV (1.56;1.10-2.22).

CONCLUSIONS: SMM students who engage in NHAS HIV risk behaviors experience higher rates of VV and suicidal behaviors compared to SMM students who do not engage in such behaviors. SMM at higher risk for HIV may benefit from interventions that address a variety of risk domains. Opportunities for prevention may include increasing protective factors for adolescent SMM (e.g., safe and supportive environments), access to mental health services in schools, as well integrating different behavior domains into evidence-based health education programs.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Violence; Suicide / Self-Inflicted Harm; HIV/AIDS
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	hhc9@cdc.gov
Presenting Author(s)	Heather Clayton
Institution Affiliation	Centers for Disease Control and Prevention CDC

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Special/Vulnerable Populations; Infection Control; Respiratory Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Namitha.Reddy@doh.nj.gov
Presenting Author(s)	Namitha Reddy
Institution Affiliation	New Jersey Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11454
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Outbreaks; Respiratory Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lisa.mchugh@doh.nj.gov
Presenting Author(s)	Lisa A McHugh
Institution Affiliation	New Jersey Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11701
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Indicators; Influenza Surveillance; Epidemiologic Methods
Consider for Different Presentation?	Yes
Presenting Author Email	balbanese@tchd.org
Address(es)	
Presenting Author(s)	Bernadette Albanese
Institution	Tri-County Health Department
Affiliation	Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11254
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Local Epidemiology; Outbreaks; Influenza / Pandemic Influenza
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Julie.Payne@kentcountymi.gov
Presenting Author(s)	Julie Payne
Institution Affiliation	Kent County Health Department Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11129
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza Surveillance; Respiratory Diseases; Influenza / Pandemic Influenza
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	zmo2@cdc.gov
Presenting Author(s)	Matthew Biggerstaff
Institution Affiliation	Centers for Disease Control and Prevention CDC

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	Influenza Surveillance; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	skyler.brennan@dph.ga.gov
Presenting Author(s)	Skyler Brennan
Institution Affiliation	Georgia Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10744
Abstract Type	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(N3N2) 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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza / Pandemic Influenza; Influenza Surveillance; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	shari.barlow@fammed.wisc.edu
Presenting Author(s)	Shari Barlow
Institution Affiliation	University of Wisconsin School of Medicine and Public Health Academic Institution

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Healthcare Associated Infections (HAI); Influenza / Pandemic Influenza; Influenza Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kyoo.shim@dallascounty.org
Presenting Author(s)	Kyoo Shim
Institution Affiliation	Dallas County Department of Health and Human Services Local Public Health Agency

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Infectious Diseases; Outbreaks; Respiratory Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	sarah.shrum@state.nm.us
Presenting Author(s)	Sarah Shrum Davis
Institution Affiliation	New Mexico Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
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
Keywords	Influenza / Pandemic Influenza; Influenza Surveillance; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Osaro.mgbere@houstontx.gov
Presenting Author(s)	Osaro Mgbere
Institution Affiliation	Houston Health Department Local Public Health Agency

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza Surveillance; Epidemiologic Methods
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	idg3@cdc.gov
Presenting Author(s)	Alissa Carey O'Halloran
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11503
Abstract Type	Poster
Abstract Title	Outbreak of <i>Kingella Kingae</i> Infections in a North Dakota Child Care Facility

Abstract

BACKGROUND: *Kingella kingae* is a member of the *Neisseriaceae* family that colonizes the upper respiratory tract of humans. Rarely, colonized bacteria can enter the bloodstream and cause serious invasive infections. Outbreaks of severe *K. kingae* infections among children ages 6 to 36 months have been associated with child care facilities. In December 2017, the North Dakota Department of Health (NDDoH) was notified of a possible outbreak of *K. kingae* infections among children in a child care facility. Two children who attend child care at the facility had been recently diagnosed with bone and joint infections. *K. kingae* was isolated from a clinical specimen collected from one of the children.

METHODS: The NDDoH recommended that all children who attended child care at the same facility as the two cases receive chemoprophylaxis with rifampin and amoxicillin. Parents or guardians of the children were advised to consult with their child's primary healthcare provider for appropriate antimicrobial prophylaxis. Child care providers were advised to thoroughly clean and disinfect all toys and surfaces in the facility and encourage good hand hygiene. Two epidemiologists from the NDDoH and the director of the local public health unit met with parents and guardians at the child care facility to address questions and concerns. A Health Advisory regarding the *K. kingae* outbreak was sent to all healthcare providers in the state via the North Dakota Health Alert Network (HAN). Parents or guardians of children who attended child care at the facility were asked to participate in a voluntary online survey to gather data on compliance with prophylaxis recommendations.

RESULTS: Survey responses were received for 45 (49%) of the 91 children at the childcare facility. Thirty-five (78%) of the 45 survey respondents reported completing the chemoprophylaxis as recommended. No additional cases have been reported.

CONCLUSIONS: One possible limitation to the reported data is that parents or guardians who were compliant with recommendations were more likely to respond to a survey. Limited guidance exists on the public health response to *K. kingae* infection outbreaks in child care facilities. Additional research on transmission routes of *K. kingae* and infection control measures is warranted.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Infectious Diseases; Children and Adolescents
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lcronquist@nd.gov
Presenting Author(s)	Laura Cronquist
Institution Affiliation	North Dakota Department of Health State Public Health Agency

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Epidemiology; Infectious Diseases; Respiratory Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	gik8@cdc.gov
Presenting Author(s)	Mila M. Prill
Institution Affiliation	Centers for Disease Control and Prevention CDC

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	Hospital Data; Influenza Surveillance; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	sboktor@pa.gov
Presenting Author(s)	Sameh W. Boktor
Institution Affiliation	Pennsylvania Department of Health State Public Health Agency

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza / Pandemic Influenza; Minority Health; Tribal Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	matthewd@uihi.org
Presenting Author(s)	Matthew Doxey
Institution Affiliation	Urban Indian Health Institute Non-profit

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(unknown subtype) (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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza / Pandemic Influenza; Respiratory Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	sor1@cdc.gov
Presenting Author(s)	Sarah Reagan-Steiner
Institution Affiliation	Centers for Disease Control and Prevention CDC

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Infectious Diseases; Influenza / Pandemic Influenza; Disease Prevention
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	yaoakpalu@gmail.com
Presenting Author(s)	Yao Akpalu
Institution Affiliation	Brazos County Health Department Local Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Infectious Diseases; Respiratory Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	cperez5@health.nyc.gov
Presenting Author(s)	Carley Perez
Institution Affiliation	New York City Department of Health and Mental Hygiene CDC/CSTE Fellow

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	Influenza Surveillance; Information Systems; Communication
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kmccaffrey@utah.gov
Presenting Author(s)	Keegan McCaffrey
Institution Affiliation	Utah Department of Health State Public Health Agency

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	Syndromic Surveillance; Influenza Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	meagan.burns@state.ma.us
Presenting Author(s)	Meagan Burns
Institution Affiliation	Massachusetts Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11411
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	NPF6@CDC.gov
Presenting Author(s)	Bryanna L Cikesh
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Rural Health; Infectious Diseases; Respiratory Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	sarah.labuda@arkansas.gov
Presenting Author(s)	Sarah M Labuda
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	10583
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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza / Pandemic Influenza; Disease Prevention; Infection Control
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	yaoakpalu@gmail.com
Presenting Author(s)	Yao Akpalu
Institution Affiliation	Brazos County Health Department Local Public Health Agency

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Influenza / Pandemic Influenza; Influenza Surveillance
Consider for Different Presentation?	No
Presenting Author Email Address(es)	acp4@cdc.gov; lsb1@cdc.gov
Presenting Author(s)	Alicia Budd; Lynnette Brammer
Institution Affiliation	Centers for Disease Control and Prevention CDC

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?	Respiratory Diseases; Influenza Surveillance; Surveillance
Presenting Author Email Address(es)	No
Presenting Author(s)	Heather.Rubino@flhealth.gov; audrey.kunkes@dph.ga.gov
Institution Affiliation	Heather Rubino; Audrey Kunkes
	Florida Department of Health
	State Public Health Agency

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	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Collaboration; Outbreaks; Respiratory Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	lisa.mchugh@doh.nj.gov
Presenting Author(s)	Lisa A McHugh
Institution Affiliation	New Jersey Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10905
Abstract Type	Breakout
Abstract Title	Acute Hepatitis A Infection Among Previously Vaccinated People Living with HIV: Implications for Postexposure Prophylaxis — Tennessee, 2017–2018

Abstract

BACKGROUND:

Partial vaccination, or one dose of hepatitis A virus (HAV) vaccine, effectively protects the general population against HAV infection for approximately 10 years. However, people living with HIV (PLWH) might not develop the same level of immunity after vaccination as immunocompetent people. Post exposure prophylaxis (PEP) with a dose of HAV vaccine and immune globulin (IG) is only recommended for PLWH who have not been vaccinated. The Tennessee Department of Health (TDH) sought to define the extent to which PLWH developed HAV infection during an HAV outbreak despite having received HAV vaccination.

METHODS: Confirmed HAV cases reported to TDH during an ongoing HAV outbreak during December 1, 2017–September 20, 2018 were reviewed for HIV coinfection. Data gathered from case report forms, surveillance databases, and medical records were used to evaluate HIV status and HAV vaccination history.

RESULTS:

Among 249 reported cases of HAV infection, 11 (4%) were in PLWH. Six (55%) of 11 coinfecting patients had received a partial or complete vaccination series before acute HAV infection. Two patients completed monovalent HAV vaccination before infection onset. A third patient had previously received a single dose of monovalent HAV vaccine and a post exposure prophylaxis dose of monovalent vaccine and immune globulin (IG), but developed infection 6 days later. Three patients were partially vaccinated with the combined hepatitis A and B vaccine.

CONCLUSIONS:

Previous vaccination may not reliably provide protection among PLWH. CDC guidelines recommend IG as post exposure prophylaxis for unvaccinated people who are immunocompromised. In response to these findings, TDH changed its outbreak PEP guidelines to recommend consideration of IG administration to all PLWH with high-risk HAV exposure (e.g., household member or sexual contact of a person with HAV) regardless of prior vaccination history or immune status.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Hepatitis; HIV/AIDS; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	mpn4@cdc.gov
Presenting Author(s)	Julia Brennan
Institution Affiliation	Tennessee Department of Health EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	11735
Abstract Type	Breakout
Abstract Title	Assessing the Effects and Enforcement of a Mandatory Hepatitis A Vaccination Ordinance for Food Handlers in Saint Louis County, MO

Abstract

BACKGROUND: In 1999, in response to multiple hepatitis A virus (HAV) outbreaks involving transmission by foodservice workers in the 1990s, Saint Louis County passed an ordinance (effective June 2000) mandating HAV vaccination for all county food handlers. Saint Louis County, Missouri's most populous county, is a commercial hub for the eastern part of the state. In the context of recent widespread and costly HAV outbreaks elsewhere in the country, we sought to examine the effectiveness of Saint Louis County's vaccination ordinance in preventing HAV outbreaks in Saint Louis County and the Saint Louis region, foodservice establishments' compliance with the ordinance, and the effort required to enforce it.

METHODS: We analyzed reported HAV cases from 1999 to 2017 among residents of Missouri's Eastern District (Saint Louis County plus eleven surrounding jurisdictions). We also analyzed food service establishment inspection data collected by the Saint Louis County Department of Public Health (DPH) Division of Environmental Services.

RESULTS: Fifteen cases of HAV infection were reported among food handlers in Missouri's Eastern District in 1999 and 5 cases in 2000. Between 2001 (the first full year since the vaccination ordinance was implemented) and 2017, five cases were reported among food handlers. Of these, three worked for establishments outside of Saint Louis County; workplaces were not documented for the other two. The Eastern District has not experienced a hepatitis A outbreak since 2000. Enforcement of the vaccination ordinance requires considerable oversight. Violations of the ordinance were cited in 1,751 (18.7%) of the 9,377 inspection records analyzed. A majority of these violations (n=1,321; 75.4%) were documented during routine inspections, considerably fewer (n=323; 18.4%) were documented during first follow-up inspections, and still fewer (n=93; 5.3%) were documented during second or third follow-up inspections. The inspection and violation data did not distinguish between violations resulting from unvaccinated workers and those resulting merely from deficient record-keeping.

CONCLUSIONS: Enforcing Saint Louis County's vaccination ordinance requires significant effort, but that enforcement is effective. The number of establishments found to be out of compliance decreases by at least 70% with each round of follow-up inspections. Nationally, recent HAV outbreaks have led to considerable morbidity and mortality, and response efforts have cost tens of millions of public dollars and strained vaccine supplies. While homelessness and injection drug use have driven these outbreaks, food handlers remain an important potential source of HAV transmission. Thus, mandatory food handler vaccination policies remain a viable opportunity for local jurisdictions' outbreak prevention efforts.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Enteric Infectious Diseases; Hepatitis; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	atorgerson@stlouisco.com
Presenting Author(s)	Andrew Torgerson
Institution Affiliation	Saint Louis County Department of Public Health Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10959
Abstract Type	Breakout
Abstract Title	Epidemiology of Measles, Mumps, and Rubella (MMR), Miami-Dade County, Florida 2008 – 2018

Abstract

BACKGROUND: In recent years, outbreaks of vaccine-preventable diseases among vaccinated populations have become increasingly common. The purpose of this report was to examine the epidemiology of measles, mumps, and rubella to determine whether outbreaks occurred among vaccinated populations within Miami-Dade County (MDC).

METHODS: Confirmed, probable, and suspect cases reported to the Florida Department of Health in MDC between January 1, 2008 and November 1, 2018 were obtained from Merlin, the Florida Department of Health surveillance system. Variables of interest included age (years), gender, race/ethnicity, pregnancy status, distribution of symptoms, vaccination history, age at receipt of the first two doses of the measles, mumps, rubella (MMR) vaccine, number of years since the receipt of the second MMR dose, and whether cases were outbreak associated. Analyses were performed with SAS statistical software, version 9.4.

RESULTS: Sixty cases met inclusion criteria, among which one (2%) was rubella, 8 (13%) measles, and 51 (85%) mumps. The majority of measles cases were between the ages of 1 – 18 (n=5); whereas, the majority of mumps and rubella cases were between the ages of 19 – 64 (n=37, n=1). The median age of measles cases was 5.5 years (range 1 to 34) compared to mumps cases which were a median age 27 years (range 1 to 81). There were no statistically significant differences between mumps and measles cases by age, gender, race/ethnicity, pregnancy status, or time since vaccination; however, origin of infection was significant. The majority of measles and mumps cases were acquired in Florida, 6 (75%) and 43 (84%), respectively. All measles cases were born after the measles vaccine became commercially available; whereas, 20% of mumps cases and the single rubella case was born before the respective vaccines became commercially available.

CONCLUSIONS: There were significant limitations concerning vaccination history data, as half (53%) of the cases had “unknown” vaccination history. One possible explanation is that 52% of MDC residents are foreign born, and as such, their vaccination history would not be captured in our system. Age differences between measles and mumps cases suggest that the current two dose recommendations may not provide lifelong protection later into adult life, particularly for mumps, which is consistent with the literature. Improved surveillance, with respect to obtaining accurate vaccination history among foreign born cases, is needed to make any further conclusions.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Epidemiology; Surveillance; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Isabel.Griffin@flhealth.gov
Presenting Author(s)	Isabel Griffin
Institution Affiliation	Florida Department of Health in Miami-Dade County Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10807
Abstract Type	Breakout
Abstract Title	HPV Vaccination Among Adolescents and Adults in South Carolina

Abstract

BACKGROUND: The CDC recommends the Human Papillomavirus (HPV) vaccine be routinely administered beginning at age 11 as it protects against both genital warts and cancers caused by HPV. Depending on what age immunization begins, either two or three doses are sufficient. Studies have shown that the prevalence of HPV infection has decreased since the vaccine was introduced in 2006. Although it has been available for 10+ years, immunization rates have not increased like other new vaccines. Using the Children's Health Assessment Survey (CHAS) and the Behavioral Risk Factor Surveillance System (BRFSS), demographic characteristics among adolescents and adults who received 1+ dose of the HPV vaccine were examined in SC.

METHODS: We obtained data about HPV vaccination status among adolescents (11–17 years) from CHAS (2012/2014/2016) and among adults (18–35 years) from BRFSS (2015–2017) in SC. For both surveys, the following characteristics were examined: age, race/ethnicity, sex, health insurance status, SC region; income was also examined among adults. The data were weighted to represent all adolescents and adults eligible for the vaccine. SAS 9.4 software was utilized to obtain weighted prevalence estimates and 95% confidence intervals via survey analysis procedures.

RESULTS: We found that 27% of adolescents ($\pm 4\%$) and 13% of adults ($\pm 1\%$) have received 1+ dose. Among both adolescents and adults, significantly more non-Hispanic blacks and females received the HPV vaccine compared to non-Hispanic whites and males, respectively. Adults with lower ($< \$15K$) annual household income had significantly higher HPV vaccination rates than those of higher ($\$50K+$) income ($15 \pm 3\%$ vs. $10 \pm 1\%$). There were no significant differences by health insurance status, SC region, or age.

CONCLUSIONS: The sex and racial/ethnic disparities found in the current study have been observed nationally for adolescents, but not for adults. For adolescents, the SC estimate from the 2016 National Immunization Survey Teen version (ages 13–17; 1+ dose: $44 \pm 7\%$) is lower than the current study because the age range is narrower. For ages 19–26, CDC national estimates range from 49% (females) to 14% (males) based on the 2016 National Health Interview Survey (no national estimates for 26+). While there is no Healthy People 2020 goal for HPV vaccination among adults, the goal for adolescents (13–15 years) is 80%, which SC falls far below. This has been acknowledged by key partners, and in 2019, targeted marketing around HPV vaccination will begin in places with high cervical cancer rates.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Children and Adolescents; Cancer; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	richardcl@dhec.sc.gov
Presenting Author(s)	Chelsea Richard
Institution Affiliation	University of South Carolina Student

Submission Type	Breakout/Quick/Lightning/Poster
ID	11429
Abstract Type	Breakout
Abstract Title	Interventions to Reduce Measles Exposures in Outpatient Healthcare Facilities — New York City, 2018

Abstract

BACKGROUND: Measles virus is highly contagious and remains airborne for 2 hours after an infected person's cough or sneeze. It causes rare but severe complications including pneumonia, miscarriage, and death. Because patients are infectious before rash onset, preventing measles exposures in healthcare facilities (HCF) is challenging. During September 30–December 10, 2018, New York City (NYC) experienced an ongoing measles outbreak; >2000 persons were exposed to measles in HCF settings. The NYC Department of Health and Mental Hygiene (DOHMH) recommended screening for measles symptoms or exposures, patient education, and alternative isolation procedures when negative pressure rooms were unavailable. We describe interventions taken for reducing measles exposures in outpatient HCFs.

METHODS: A standard questionnaire was used to survey infection control staff from all 17 outpatient HCFs that had measles exposures. HCF exposures occurred when patients with measles entered a facility through 2 hours after departure or appropriate isolation. The questionnaire was administered by telephone on December 10–12, 2018, and included 14 questions about measles screening practices, facility infrastructure, and procedures for seeing patients with suspected measles.

RESULTS: Fifteen (88%) of 17 HCFs responded to the survey. Among responding HCFs, 87% (13/15) instituted telephone-based screening for measles symptoms while scheduling appointments, 73% (11/15) screened at check-in, and 100% (15/15) posted signs about measles symptoms. No HCFs reported having a negative pressure room, and 60% (9/15) had written protocols to minimize measles exposures. Most HCFs, 87% (13/15), established alternative isolation procedures for potentially infectious patients, compatible with their clinic space and acceptable for staff, including separate entrances, examinations outside, after-hours examinations, and at home visits.

CONCLUSIONS: Most HCFs implemented DOHMH-recommended interventions. While negative pressure rooms are uncommon in outpatient settings, HCFs identified creative solutions to prevent healthcare-associated measles exposures. In a postelimination measles era, preventing HCF exposures can contribute to outbreak control.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Infection Control
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kalroy@health.nyc.gov
Presenting Author(s)	Karen Alroy
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Investigating Negative Pertussis PCR Tests: Worth the Effort? An Evaluation of the Impact, Wisconsin, 2016-2018

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) recommends performing Polymerase Chain Reaction (PCR) for pertussis within the first 3 weeks of cough for optimal sensitivity and has specific guidelines on specimen collection. In Wisconsin, both positive and negative results for pertussis PCR tests are reported to the Wisconsin Electronic Disease Surveillance System (WEDSS), an online system for reporting, investigation, and surveillance of communicable disease. While most states do not require follow up on negative PCR test results, Wisconsin encourages Local Health Departments (LHDs) to follow up on negative tests if the case is a known contact of a lab-confirmed pertussis case, is less than one year of age, is at high risk of complications (i.e. immunocompromised), or is symptomatic, as there are reasons this test could provide a false negative result, including timing of the test in relation to symptom onset and technique of specimen collection. However, the investigation of these suspect cases is resource-intensive for LHDs and the reporters. Therefore, we assessed the impact of following up on these negative PCR tests to determine if allocation of resources for these efforts continued to be worthwhile.

METHODS: Data regarding pertussis investigations in Wisconsin from January 1, 2016 through November 30, 2018 were collected using WEDSS and analyzed using SAS 9.4. Investigations with a positive or indeterminate PCR result, only tested by serology or culture, or untested, were excluded from the analysis. Case classification definitions from CDC were used for confirmed and probable. Descriptive statistics were performed for the sample.

RESULTS: From January 1, 2016 through November 30, 2018, 3,261 negative PCR tests were investigated in Wisconsin. Of these, 128 (3.9%) resulted in confirmed cases and 900 (28.3%) were probable. Of the probable cases, 315 (34.2%) were tested 22 days or later after cough onset. Follow up investigation of negative PCR tests have accounted for 98.7% of total probable cases and 7.5% of total confirmed cases of pertussis in Wisconsin from January 1, 2016 through November 30, 2018.

CONCLUSIONS: There were a significant amount of confirmed and probable cases determined from the investigation of negative PCR tests. However, time and resources should be taken into consideration when deciding how to prioritize follow up with negative PCR tests.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	abby.klemp@dhs.wisconsin.gov
Presenting Author(s)	Abby Klemp
Institution Affiliation	Wisconsin Department of Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11768
Abstract Type	Breakout
Abstract Title	Investigation Nuances and Challenges during Outbreak of Measles in Kansas – 2018

Abstract

BACKGROUND: On March 8, 2018, the Kansas Department of Health and Environment (KDHE) was notified of an infant who tested positive for measles. Investigation revealed an infant in the index case-patient's daycare had history of international travel and febrile rash illness. This primary case-patient sought medical advice prior to travel; however, no travel-related recommendations were made and despite presentation and history of travel, measles was never suspected upon return. Retrospectively, cases of measles were identified in infants at the daycare who had been misdiagnosed resulting in further transmission to both unvaccinated and vaccinated persons in other settings. Further complicating matters, a second unrelated measles outbreak was detected in a neighboring state that shares a large metropolitan area with Kansas.

METHODS: Case and contact investigations were conducted by affected jurisdictions and KDHE. Press releases alerting the public of locations where measles exposures may have occurred, and contacts couldn't be identified were published. Bi-daily calls with affected jurisdictions were conducted to streamline the investigation. Specimens were tested by real-time reverse-transcription polymerase chain reaction (RT-PCR) at KDHE or by measles-specific IgM at private laboratories or the Centers for Disease Control and Prevention (CDC). RT-PCR positive specimens were forwarded to CDC for genotyping.

RESULTS: Twenty-two cases of measles residing in three Kansas counties and one in a neighboring state were identified. Several infants diagnosed with other conditions delayed outbreak identification. Places of exposure included the daycare, healthcare settings, private homes, the community, and internationally. Five persons had a prodrome that lasted five days. Twelve case-patients were unvaccinated; nine were ineligible to receive vaccine. Awareness of the outbreak was enhanced through ten press releases detailing dates and times of exposure at 26 public locations. Eleven persons were positive for measles by RT-PCR, six by IgM, and five were epidemiologically linked. RT-PCR specimens were confirmed to be measles genotype B3.

CONCLUSIONS: This is the largest measles outbreak in Kansas in nearly 30 years. Although a major transmission setting was a daycare among an unvaccinated population, almost half with measles were vaccinated and exposed elsewhere. Several persons had a prodrome lasting longer than four days, so extending the infectious period could be considered when reliable prodrome history is available. With high prevalence of international travel, measles should be considered when assessing patients with febrile rash illness consistent with measles. Enhanced communication and coordination among jurisdictions was crucial due to the large numbers of exposure locations and identified contacts.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Infectious Diseases; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	allison.zaldivar@ks.gov
Presenting Author(s)	Allison Zaldivar
Institution Affiliation	Kansas Department of Health and Environment State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Measles Infection Identified in Vaccinated Persons Using Avidity and Plaque Reduction Neutralization Assay—Kansas, 2018

Abstract

BACKGROUND: In March 2018, the Kansas Department of Health and Environment (KDHE) and local partners investigated a measles outbreak in which 22 case-patients were identified; ten had been previously vaccinated. Measles in vaccinated persons may present typically or disease may be less severe with a milder rash and little to no fever. Despite utilizing highly sensitive tests on appropriately collected specimens, measles virus was not always detected in vaccinated symptomatic persons. Utilizing measles-specific immunoglobulin G (IgG) avidity and plaque reduction neutralization (PRN) helped determine whether vaccinated persons were truly infected with measles.

METHODS: Upon suspicion of measles infection, specimens were collected within four days of rash onset and tested at the Kansas Health and Environmental Laboratories (KHEL) using real-time reverse-transcription polymerase chain reaction (RT-PCR). Serum specimens were collected from persons with a known epidemiologic link who tested RT-PCR negative, RT-PCR positive, and persons who were outside of the four-day window from rash onset. These specimens were sent to CDC for measles-specific immunoglobulin M (IgM), IgG avidity, and PRN testing. Patients with a neutralizing antibody concentration $\geq 40,000$ mIU/mL were considered to have high titers to measles.

RESULTS: Ten case-patients reported vaccination. Eight were tested by RT-PCR at KHEL; four tested positive. Two persons were outside the timeframe for RT-PCR testing, but both tested IgM positive. Six serum specimens were sent to CDC; one that tested at the low end of detection by RT-PCR, four that tested RT-PCR negative, and one that was only IgM positive. Four adult specimens had high IgG avidity and high PRN titers indicating secondary vaccine failure but suggesting recent measles infection; one was IgM and RT-PCR positive, one was IgM positive, and two were IgM and RT-PCR negative. Another adult specimen had high IgG avidity, low PRN, and was IgM positive. This adult was considered to have recent measles infection, but PRN titers may have not yet become elevated. One child specimen had low avidity, was IgM positive, and was not tested by PRN indicating primary vaccine failure.

CONCLUSIONS: Vaccinated persons with known exposure to measles may present atypically. Despite collecting appropriate specimens for measles testing, RT-PCR was not adequate for identifying measles virus in some persons with measles. IgG avidity and PRN testing confirmed two cases that were previously IgM and RT-PCR negative. If there is a known measles exposure in a vaccinated person, utilizing IgG avidity and PRN testing could help identify recent measles infection.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Infectious Diseases; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	allison.zaldivar@ks.gov
Presenting Author(s)	Allison Zaldivar
Institution Affiliation	Kansas Department of Health and Environment State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Pneumococcal Disease Outbreak at a State Correctional Facility — Alabama, 2018

Abstract

BACKGROUND: In September 2018, Alabama Department of Public Health was notified of 2 prison inmates with invasive pneumococcal disease. Pneumococcal disease outbreaks are rare, but can occur in institutional settings. We investigated to determine disease severity, risk factors, and intervention strategies.

METHODS: We identified cases using clinic records. A suspected case was defined as respiratory or meningitis symptoms in an inmate or close contact with onset between September 1–November 27, 2018. Probable cases were defined as suspected cases plus radiographically confirmed pneumonia or laboratory evidence of bacterial meningitis with negative testing or unknown etiology. Confirmed cases were defined as suspected cases plus a positive *Streptococcus pneumoniae* test. We performed medical chart review and patient interviews to explore risk factors. We conducted prospective pneumococcal disease surveillance among inmates in the prison clinic between October 5–November 27.

RESULTS: We identified 40 cases (3 confirmed, 2 probable, and 35 suspected) among approximately 1,300 inmates and none among employees. Median patient age was 39 years (range: 22–63 years). All patients with confirmed and probable pneumococcal disease were hospitalized and 1 died; diagnoses included meningitis (2), pneumonia (2), and septicemia with pneumonia (1). All patients with confirmed pneumococcal disease had *S. pneumoniae* serotype 12F, lived in dormitory X, and had symptom onset between September 14–25. Among all 40 patients, 85% reported substance use (cigarettes, alcohol, or illicit drugs) and 33% had medical conditions that increase pneumococcal disease risk. Starting September 29, inmates living in dormitory X (264) were offered pneumococcal disease prophylaxis; 93% received azithromycin and 78% received 23-valent pneumococcal polysaccharide vaccine, which protects against serotype 12F. No *S. pneumoniae* transmission was identified during prospective surveillance.

CONCLUSIONS: Close living quarters, substance use, and underlying medical conditions likely contributed to increased risk for pneumococcal disease. Timely prophylaxis may have interrupted pneumococcal transmission.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Special/Vulnerable Populations; Outbreaks; Respiratory Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	guillermo.sanchez@adph.state.al.us
Presenting Author(s)	Guillermo V Sanchez
Institution Affiliation	Alabama Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10803
Abstract Type	Breakout
Abstract Title	Public Health Impact of Alternative Pertussis Case Classifications for PCR

Abstract

BACKGROUND: Pertussis has persisted at elevated rates in the United States despite high vaccination coverage. Pertussis cases require time-intensive public health follow-up including case finding, patient interviews, patient education, and prophylaxis of exposed contacts. The current national pertussis case definition requires that all PCR-positive cases meet clinical criteria of two weeks of cough along with paroxysms, whoop, or post-tussive vomiting. The goal of this project was to assess the potential impact to pertussis surveillance case counts and follow-up utilizing two alternatives for classifying PCR-positive pertussis cases.

METHODS: Pertussis cases reported January 1, 2014 – October 15, 2018 were identified from Arizona’s infectious disease surveillance system. Pertussis case reports aged >1 year with a PCR-positive result and no other reported laboratory testing were included. Cases were classified using three sets of criteria: national case definition, national case definition with any duration cough (option 1) and acute cough illness of any duration, with or without other symptoms (option 2).

RESULTS: Of 637 cases with only PCR-positive laboratory testing, 496 (78%) were classified as confirmed using the national case definition; 141 were ruled out. Of ruled-out cases: 44 (31%) had no available clinical information, 4 (2%) had no cough, 49 (34%) had cough of less than two weeks or unknown duration, 34 (24%) reported no case-defining symptoms, and 10 (7%) had incomplete information about case-defining symptoms. Thus, applying classification options 1 and 2, 49 and 93 additional cases, respectively, were classified as confirmed. Of the 564 cases with known cough duration, 211 (37%) had coughed for less than two weeks at the time of initial interview. These required additional follow-up by public health officials; most (162, 77%) were later confirmed as having two weeks of cough.

CONCLUSIONS: This analysis of PCR-positive pertussis cases in Arizona shows that these classification options have a relatively small impact on overall surveillance case counts. Even option 2 only increases the number of confirmed PCR-positive cases by 19%, or 11 to 27 additional confirmed cases per year. Importantly, these two classification options for PCR-positive cases could significantly reduce follow-up by public health officials and would mirror the follow-up for culture-positive cases. As diagnostic test utilization for pertussis continues to change, public health officials may receive more and more pertussis reports that include only PCR testing. The burden of disease continues to be high and public health agencies need to be able to adapt to these changing pressures and use limited resources wisely.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Program Evaluation; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Susan.Robinson@azdhs.gov
Presenting Author(s)	Susan Robinson
Institution Affiliation	Arizona Department of Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11192
Abstract Type	Lightning
Abstract Title	Hepatitis A Vaccination Among Health Department STD Clients during a HAV Outbreak: Need and Uptake - Tennessee, 2018

Abstract

BACKGROUND: Tennessee (TN) is experiencing a hepatitis A virus (HAV) outbreak among people who use recreational drugs, people experiencing homelessness, and men who have sex with men. Vaccination is a cornerstone of HAV prevention. As part of its outbreak response, the TN Department of Health (TDH) identified venues serving at-risk populations, including health department (HD) Sexually Transmitted Disease (STD) clinics. HAV vaccination was provided to these STD clinics in an effort to provide routine opt-out vaccine to all incompletely or un-vaccinated clients. We sought to quantify the potential and actual impact of this approach.

METHODS: The TDH Viral Hepatitis program produces a monthly HAV vaccination report among STD clients (most recent study period in November 2018), stratified by public health region as follows: a list of HD clients seeking STD services was extracted from the clinic management information system and de-duplicated by region. Identifying information (first name, last name, DOB, and social security number, as available), was matched to the TN Immunization Information System (TennIIS) to determine the HAV vaccination status of STD clients at the time of the visit: “complete”; “up-to-date” (the first dose was administered within 6 months prior to the month of the STD visit); or “in-need” (previously unvaccinated or received one dose more than six months prior). For clients “in need” of vaccination, TennIIS was checked to determine if HAV vaccination was administered at the current visit.

RESULTS: In the most recent study period, 9,564 HD clinic clients sought STD services in TN. Of these, 20.5% (n=1,956) had previously “completed” their HAV vaccination series, 4.7% (n=447) were “up-to-date”, and 74.9% (n=7,161) were “in-need” of HAV vaccine. Of clients “in-need”, 17.0% (n=1,216) were vaccinated during the current visit (ranging from 0 - 38.5% across all regions).

CONCLUSIONS: STD clinics provide an important opportunity to access a high number of at-risk adults in need of HAV vaccination. Despite implementation of a routine opt-out strategy, uptake was low. In order to maximize the uptake of HAV vaccine to at-risk adults in an outbreak context, it is imperative that each local HD identify and address barriers to vaccination uptake among their STD clients “in-need” of vaccination.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Sexually Transmitted Diseases; Vaccine-Preventable Diseases; Hepatitis
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	lindsey.sizemore@tn.gov
Presenting Author(s)	Lindsey A. Sizemore
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11119
Abstract Type	Lightning
Abstract Title	Taking a Closer Look at Non-Outbreak Associated Mumps Cases, Colorado, 2016-2018

Abstract

BACKGROUND: Colorado experienced an increase in reported mumps cases in 2016 through 2018, many of whom were associated with distinct communities and social networks. In addition, an overall increase of mumps cases in Colorado during that time that were not associated with outbreaks was also observed. While the recent mumps outbreaks both in Colorado and nationwide have been well-described, examining the characteristics of non-outbreak associated mumps cases could improve our ability to detect sporadic cases and prevent continued transmission of mumps in the community.

METHODS: Reported mumps cases were identified through Colorado's Electronic Disease Reporting System from January 1, 2016 to December 21, 2018. Cases from 2016-2018 that met the CSTE mumps confirmed and probable case definitions were analyzed using T-test, Chi-Square tests, and odds ratios (OR). An outbreak was defined as three or more cases linked by time and place. Standard mumps surveillance variables and investigation notes collected during the disease investigations were used to describe demographics and identify potential risk factors.

RESULTS: A total of 134 cases of mumps were reported in Colorado from 2016 to 2018; 76 (57%) were not associated with an outbreak. Non-outbreak associated cases had a higher mean age compared to outbreak associated cases (30.2 vs 23.5 years; $P=0.01$). Most non-outbreak cases were reported by a hospital or emergency department (37%) and primary care providers (37%). Among 95 cases that were tested, IgM detection was more commonly used among non-outbreak cases, and PCR was more often used among outbreak cases ($P<0.001$). Cases vaccinated with at least 1 dose of mumps containing vaccine were significantly less likely to be associated with an outbreak (OR=0.31; 95% CI: 0.13-0.73; $P=0.006$). The most commonly identified risk factors for disease among non-outbreak associated cases were contact with someone with mumps-like illness (24%) and domestic or international travel during exposure period (20%). Most outbreak-associated cases were linked to communities where international travel and group living was common.

CONCLUSIONS: Differences identified between non-outbreak and outbreak associated mumps cases in Colorado include age, vaccination history, risk factors, and laboratory testing. It is challenging to determine if the rise of non-outbreak associated cases is exclusively due to increased awareness about mumps or an actual increase in disease. Strong partnerships with health care providers to identify and test potential cases based on risk factors will help maintain the ability to detect mumps cases in the absence of an outbreak and prevent future outbreaks.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Infectious Diseases; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	amanda.metz@state.co.us
Presenting Author(s)	Amanda R Metz
Institution Affiliation	Colorado Department of Public Health and Environment State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	11265
Abstract Title	Lightning
	Varicella Outbreaks in Long-Term Care Facilities

Abstract

BACKGROUND: In 2018, the Illinois Department of Public Health (IDPH) investigated two outbreaks of primary varicella in long-term care facilities (LTCF) among staff and residents. Many long-term care residents will have birth prior to 1980 and be considered presumptively immune, and few will be able to provide documentation of disease or vaccination. These outbreaks occurred in non-traditional LTCF, and included residents with near life-long history of institutionalization.

METHODS: Clusters and outbreaks of varicella are required to be reported to IDPH. Since implementation of the current outbreak reporting system in 2014, no varicella clusters or outbreaks have been reported in LTCF until 2018. Recommendations for controlling varicella in healthcare settings include: standard, contact, and airborne isolation precautions for cases; only personnel with presumptive evidence of immunity should be exposed to cases; and exposed, susceptible patients should be placed in airborne isolation and contact precautions from days 10 to 21 following exposure.

RESULTS: Outbreak A had six confirmed cases, with an age range of 19-74 years old (median 56.5), consisted of two health care workers (HCW) and four residents. All cases were unvaccinated with no disease history. Three cases were PCR confirmed, but were unable to be genotyped due to specimen availability. Outbreak B had six confirmed cases, with an age range of 21-53 years old (median 29.5), consisted of five residents and one HCW. All cases were either unvaccinated or had unknown status, with either no or unknown disease history. Two PCR confirmed cases were determined to be wild-type virus. The index case in either outbreak was not identified. Cases among residents in both outbreaks ranged in age from 21-74 years, with a median age of 53 years. Comparatively, the median age of varicella cases reported to IDPH in 2018 was 9 years old*.

CONCLUSIONS: Varicella outbreaks in LTCF can be challenging to manage. Recommended isolation precautions are difficult to implement in this setting due to residents with dementia or other mental health conditions, concerns of social isolation, facility capacity and design, and staffing challenges. Employee vaccination status may not be known or readily available, however facilities should consider having immunity status on record. Residents may be considered presumptively immune due to birth year, but are actually non-immune due to individual factors leading to institutionalization. Length of institutionalization should be considered when using birth year as presumptive evidence of immunity. *2018 data are preliminary and subject to change.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	Mallory.Sinner@illinois.gov
Presenting Author(s)	Mallory Sinner
Institution Affiliation	Illinois Department of Public Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	Disparities in Vaccination Coverage By Two Years of Age within States and Selected Local Areas in the United States: An Analysis of 2012-2015 Birth Cohorts

Abstract

BACKGROUND: Data from the National Immunization Survey-Child (NIS-Child) have shown national disparities in vaccination coverage by race/ethnicity, poverty level, health insurance type, and metropolitan statistical area (MSA) status. This study investigates the presence and magnitude of disparities in vaccination coverage for the 50 states and Washington, DC ('states').

METHODS: The NIS-Child is a random-digit-dialed telephone survey of parents/guardians of children aged 19-35 months, followed by a survey of the child's vaccination providers to assess vaccination history. Data from survey years 2013 to 2017 were combined to identify children in birth cohorts 2012-2015. Kaplan-Meier analysis was used to estimate vaccination coverage at age two years for: ≥ 1 dose MMR, ≥ 1 dose varicella, ≥ 3 doses DTaP ('DTaP3'), and ≥ 4 doses DTaP ('DTaP4'). T-tests were used to evaluate significance of differences in coverage within states by race/ethnicity, poverty level, insurance type, and MSA status.

RESULTS: In 47 states, children with household income $<133\%$ federal poverty level (FPL) had lower coverage for at least one vaccine than children with household income $\geq 400\%$ FPL; in 20 states, coverage was lower for all four vaccines. Median percentage point differences in coverage between the income groups ranged from 5.1 for DTaP3 to 13.1 for DTaP4. In 43 states, children with public insurance had lower coverage for at least one vaccine than children with private insurance (range of median percentage point differences: 3.6 for DTaP3 to 8.8 for DTaP4). In 17 of 18 states with adequate sample size, uninsured children had lower coverage for at least one vaccine compared with privately insured children (range of median percentage point differences: 13.9 for DTaP3 to 27.0 for DTaP4). Compared with non-Hispanic white children, non-Hispanic black children had lower coverage for at least one vaccine in 15 states (range of median percentage point differences: 0.9 for DTaP3 to 7.7 for DTaP4). Compared with children in MSA principal cities, children in non-MSAs had lower coverage for at least one vaccine in nine states, but had higher coverage for at least one vaccine in five states; children in MSA non-principal cities had lower coverage for at least one vaccine in six states, but had higher coverage for at least one vaccine in five states.

CONCLUSIONS: Vaccination coverage disparities exist in most states. Identifying these disparities can help immunization programs focus outreach efforts to ensure that vaccines are accessible for all children.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Health Disparities; Immunization; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	woe1@cdc.gov
Presenting Author(s)	Jennifer L. Kriss
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11316
Abstract Type	Poster
Abstract Title	Evaluation of Pertussis Carriage Among a Pediatric and Adolescent Population in Atlanta, Georgia

Abstract

BACKGROUND: Despite high vaccination coverage, pertussis disease rates have been increasing in the United States. While the cause is likely multifactorial, recent data suggest that acellular pertussis vaccines may not prevent bacterial carriage and subsequent transmission. We conducted a cross-sectional study to define the prevalence of *Bordetella pertussis* nasopharyngeal carriage among children seeking care at an emergency department (ED).

METHODS: A convenience sample of patients aged 6-59 months and 11-17 years presenting for any reason to a children's hospital ED in Atlanta, Georgia between December 1, 2017 - May 23, 2018 was enrolled. A nasopharyngeal swab was collected from each participant, and an in-person parent interview was conducted to collect information on demographics and risk factors; pertussis vaccination history was obtained via the state immunization registry. Specimens were tested using a multi-target real-time PCR assay for *B. pertussis* and other *Bordetella* species.

RESULTS: Of 398 enrolled participants, 72% (287/398) were aged 6-59 months (pediatric) and 28% (111/398) were aged 11-17 years (adolescent). Among pediatric participants, 39% (112/287) presented with fever, and 52% (148/287) with cough. Among adolescent participants, 27% (30/111) presented with upper respiratory infection symptoms, and 33% (37/111) with cough. PCR testing was indeterminate for 5 participants (2 pediatric and 3 adolescent) and negative for all others. Of participants with indeterminate results, 2 adolescent participants had cough at enrollment; none reported other symptoms of pertussis; 1 adolescent and 1 pediatric participant were completely vaccinated; 1 pediatric participant was unvaccinated; and 2 adolescent participants were incompletely vaccinated.

CONCLUSIONS: No pertussis carriage was found among nearly 400 pediatric and adolescent ED patients, although indeterminate PCR findings in 1.2% may indicate the presence of bacteria at low levels. Because pertussis incidence in Georgia is lower than the national average, further study in a setting with higher pertussis incidence is needed.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Infectious Diseases; Respiratory Diseases; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	vhy8@cdc.gov
Presenting Author(s)	Anna M. Acosta
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11496
Abstract Type	Poster
Abstract Title	Factors Associated with Meningococcal Disease Mortality— United States, 2010–2017

Abstract

BACKGROUND: Meningococcal disease is a rare but serious infection. In the United States (US), the case fatality ratio (CFR) has ranged from 13.1%-19.4% each year during 2010 through 2017, higher than reported in many other developed countries. We assessed factors associated with meningococcal disease mortality in the US from 2010-2017.

METHODS: Meningococcal disease cases reported through the National Notifiable Diseases Surveillance System from 2010 to 2017 were included in the analysis with additional epidemiologic information provided by state health departments. Isolates were serogrouped using slide agglutination and real-time polymerase chain reaction, while clonal complex (CC) was determined using Sanger sequencing or whole genome sequencing, depending on year. The five most frequently identified serogroups and CCs in the sample were analyzed separately; all others were excluded (serogroup) or classified as “other” (CC). Patient age was analyzed as a continuous variable. CFRs were calculated using the proportion of cases with known outcome as the denominator. Odds ratios were calculated using multivariable logistic regression.

RESULTS: A total of 4229 meningococcal disease cases were reported from 2010 to 2017; outcome was known for 3584 (84.8%). Overall, 16.5% of cases were fatal, and no difference was observed in CFR by sex ($p=.27$), race ($p=.83$), ethnicity ($p=.88$), or outbreak association ($p=.52$). Median patient age was significantly higher for fatal cases (38 years vs 28 years, $p<.0001$). In bivariate analysis, CFR was significantly different by serogroup ($p<.0001$) and CC ($p=.0004$). CFR was significantly higher for serogroups C (22.4%), Y (16.6%), and W (18.7%) compared to serogroup B (12.8%). CFR was significantly higher for CC11 (23.1%) compared to other CCs (14.6%); however CC was only available for 1511 cases (35.7%). In multivariable analysis, CFR increased with patient age (OR 1.01, 95% CI 1.00-1.01), was significantly higher for serogroup C (OR 2.07, 95% CI 1.14-3.77) compared to serogroup B, and significantly lower for CC103 (OR 0.37, 0.17-0.82) compared to other CCs. **CONCLUSIONS:** In a multivariable logistic regression model, patient age, serogroup, and CC were significantly associated with fatal outcome for meningococcal disease cases. It will be important to continue monitoring changes in circulating CCs, along with serogroup and patient age, to better understand the variation in CFR over time in the US.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	wgi9@cdc.gov
Presenting Author(s)	Amy Blain
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	11185
Abstract Title	Poster
	Updating the Advisory Committee on Immunization Practice Recommendations for Prevention of Human Rabies--United States 2018-Present

Abstract

BACKGROUND: Rabies is an acute, progressive encephalomyelitis transmitted to humans by exposure to infected animals; it is nearly always fatal but is preventable. The Advisory Committee on Immunization Practices (ACIP) develops guidance for the safe and effective use of vaccines among civilian populations in the United States (U.S.). ACIP recommendations for rabies were comprehensively updated in 2008, followed by an update to the post-exposure prophylaxis schedule in 2010; since then, data with direct relevance to the vaccination schedules and serologic monitoring recommendations have been published. In response, the World Health Organization (WHO) updated global recommendations in 2018, and we began the multi-year process of updating the ACIP recommendations.

METHODS: The Centers for Disease Control and Prevention's (CDC's) Office of the Associate Director of Science sets rigorous standards and expectations for guideline development. Working group members and ACIP committee members are selected for their experience and expertise. Rabies vaccine working group members have expertise in immunobiologics, vaccine efficacy and safety, and clinical medicine; representatives from relevant professional societies and rabies subject matter experts are also included. We determined the scope of the update after reviewing data published since 2008, recently published WHO recommendations, and rabies questions for which CDC frequently consults. Frequent consultations with subject matter experts are ensuring useful and relevant updates. We identified systematic reviews, economic analyses, and literature searches needed to effectively inform discussions. Unpublished data from pharmaceutical companies are also being gathered.

RESULTS: We formed a working group comprised of 15 experts including stakeholders from the U.S. Food and Drug Administration, National Association for State and Public Health Veterinarians, and clinical professional societies. The scope of the updates was determined to be primary vaccination schedules, serologic monitoring, safety and effectiveness of biologics, cost-effectiveness of some recommendations, and location of immunoglobulin administration. Data to inform intradermal vaccine efficacy and considerations for treatment among special populations (e.g., immunocompromised, pregnant persons, and children) will be considered. Systematic reviews addressing utility of various vaccine schedules and sites for rabies immune globulin administration and economic analyses of various vaccine schedules are ongoing.

CONCLUSIONS: We are leading a comprehensive update of the ACIP recommendations for rabies based on established scientific standards. Steps are being taken to ensure this update is informed by unpublished data from multiple sources, ongoing evaluations that fill literature gaps, new global recommendations, and expert input. Updating these recommendations will take several years and result in new evidence-based recommendations.

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Vaccine-Preventable Diseases
Consider for Different Presentation?	Evidence Based Practice; Vaccine-Preventable Diseases; Zoonotic Diseases
Presenting Author Email Address(es)	Yes
Presenting Author(s)	ige4@cdc.gov
Institution Affiliation	Agam K. Rao
	Centers for Disease Control and Prevention
	CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10917
Abstract Type	Quick
Abstract Title	Analysis of Pertussis PCR-Positive Patients Not Meeting the Case Definition—Florida, 2016–2018

Abstract

BACKGROUND: Since 2016, the Florida Department of Health (FDOH) has noted an increasing number of patients who test positive for pertussis by polymerase chain reaction (PCR) but who do not meet the pertussis case definition. These patients are recorded in Merlin, Florida’s reportable disease surveillance system, marked as “not a case” (NaC), and are not included in case counts. This analysis sought to identify patterns among pertussis PCR-positive patients who were not meeting the case definition to determine if FDOH should recommend updating the pertussis case definition to better reflect the burden of disease. Due to the complexity of the case definition, FDOH included only non-infant patients in this analysis.

METHODS: FDOH individually reviewed NaC patients entered into Merlin January 1, 2016—September 30, 2018 with a positive pertussis PCR result to determine the reason for not meeting the national pertussis surveillance case definition. To meet the case definition, these patients need a cough lasting at least 14 days and an additional symptom of paroxysmal cough, posttussive vomiting, or whoop. FDOH compared pertussis PCR-positive NaC patients to confirmed and probable (reported) pertussis cases during the same timeframe.

RESULTS: FDOH identified 106 pertussis PCR-positive NaC patients: 20 in 2016, 41 in 2017, and 45 in 2018. About one-third (34%) of patients did not have enough information in Merlin to evaluate the reason for not meeting the case definition. Among the 70 (66%) patients evaluated, the most common reason for not meeting the case definition was lack of both cough for at least 14 days and an additional symptom (31%), followed by lack of only cough for at least 14 days (29%), lack of only an additional symptom (27%), and lack of both any cough and additional symptom (13%). Compared to reported cases, pertussis PCR-positive NaC patients started treatment an average of 11 days earlier (20 days after onset compared to 9 days, $p<0.05$).

CONCLUSIONS: Pertussis PCR-positive NaC patients likely presented with milder symptoms due to earlier treatment and should be counted as cases. FDOH recommends changing the national pertussis surveillance case definition to require only a cough of any duration and a positive PCR result. This change would increase pertussis case counts to better reflect the true burden of disease. In Florida, 82% of PCR-positive NaC patients would meet the new case definition, but the overall impact would be minimal since FDOH investigates these patients regardless of meeting the case definition.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Surveillance; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Katherine.Kendrick@flhealth.gov
Presenting Author(s)	Katherine Kendrick
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Characterizing Potential Risk Factors for Serogroup B Meningococcal Disease Among College Students — United States, 2014–2017

Abstract

BACKGROUND: Among persons aged 18–24 years, college students are at increased risk of serogroup B meningococcal disease and since 2013, 11 serogroup B college outbreaks have been reported. The Advisory Committee on Immunization Practices recommends that serogroup B meningococcal (MenB) vaccine may be administered to adolescents aged 16–23 years and should be used for outbreak response. We assessed potential risk factors for serogroup B disease among college students to better define sub-populations of students at increased risk and inform targeted prevention and response measures.

METHODS: For all meningococcal disease cases in persons aged 18–24 years reported through the National Notifiable Diseases Surveillance System during 2014–2017, undergraduate college attendance and outbreak-association were ascertained by state health departments. Jurisdictions submitted additional risk factor information abstracted from existing public health case investigations to CDC. Incidence and risk ratios (RR) were calculated using data from the National Center for Education Statistics and U.S. census data. Proportions were used to describe characteristics of college students developing serogroup B disease.

RESULTS: Of 228 cases reported in persons aged 18–24 years, 122 (54%) were in undergraduate college students. Among these, 91 cases (75%) were due to serogroup B. Incidence of serogroup B meningococcal disease in undergraduates, including sporadic and outbreak-associated cases, increased from 0.116 to 0.276 cases per 100,000 population from 2014 to 2017. Average annual incidence of serogroup B disease was higher among students attending 4- vs. 2-year colleges (0.273 vs. 0.043 per 100,000, respectively; RR: 6.4 [95% CI: 2.9–16.1]). Among serogroup B cases, 80% of outbreak-associated and 58% of sporadic cases were in students aged 18–19 years; among 86% (78/91) of cases with known residence, 70% of outbreak-associated and 60% of sporadic cases were in students who lived on campus. Greek life participation for sporadic cases could not be assessed due to missing data; however, 56% of outbreak-associated cases were in students affiliated with Greek life.

CONCLUSIONS: Among undergraduate college students, serogroup B meningococcal disease incidence was highest in students attending 4-year colleges. The majority of cases occurred in students aged 18–19 years, students living on-campus, and, for outbreak-associated cases, students with Greek life affiliation. These data may be useful to inform priority groups for MenB vaccination during outbreaks and individual clinical decision-making for vaccination of adolescents.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	nsi4@cdc.gov
Presenting Author(s)	Lauren M Weil
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11065
Abstract Type	Quick
Abstract Title	Measles Contact Tracing in the Ridesharing Economy — Oregon, 2018

Abstract

BACKGROUND: On August 10, 2018, the Oregon Health Authority (OHA) was informed that a person with measles visited Oregon during her infectious period. On August 20, a secondary case of measles was reported. While in Oregon, both patients visited public places and used transportation ridesharing companies. To find exposed persons and prevent additional cases, state and local public health officials initiated an investigation, including identification of persons exposed through ridesharing.

METHODS: OHA defines measles-exposed persons as those spending time indoors within 10 meters of a measles patient and for ≤ 20 minutes of a measles patient having been at that location. Patients are infectious for 4 days before and after rash onset. We included ridesharing drivers and passengers who rode in the car ≤ 20 minutes after a patient. We obtained pick-up and drop-off times and locations from patient rideshare accounts, provided this information to rideshare companies, and negotiated release of drivers' and passengers' contact information for follow-up. We ascertained vaccination status of contacts and advised them how to seek care if they experienced measles symptoms.

RESULTS: Patients used two ridesharing companies. Contact by phone was unsuccessful. Information was obtained by visiting Company A's office. In addition to a visit, Company B required a letter citing OHA's legal authority. We obtained contact information for all 14 contacts (9 drivers and 5 passengers) 4 days after confirming patients' trips. Of 14 contacts, 1 driver was incompletely vaccinated; he was instructed to self-monitor and remained symptom-free. Other concerned drivers contacted OHA; their ride details indicated that they had not been exposed to either patient. Company B misinterpreted OHA information request and suspended 1 driver's account, considering him a public health threat.

CONCLUSIONS: No measles transmission through ridesharing was identified. Information available from ridesharing companies complemented traditional methods and proved essential to complete contact tracing.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Data Sharing; Motor Vehicles
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	wny6@cdc.gov
Presenting Author(s)	Steven I Rekant
Institution Affiliation	Oregon Public Health Division EIS/CEFO

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Measles Disease Activity, United States, 2018

Abstract

BACKGROUND: Measles is a highly infectious viral illness that can lead to serious complications. Measles was declared eliminated (i.e., interruption of sustained year-round endemic transmission) from the United States in 2000, yet the U.S. is continually challenged by measles introductions from countries where the disease remains endemic. We aimed to summarize U.S. measles epidemiology in 2018 in the context of prior post-elimination years (2001–2017).

METHODS: We reviewed demographic and epidemiological data from confirmed measles cases reported to the Centers for Disease Control and Prevention by state health departments in 2018. We analyzed the importation status, age, vaccination status, and U.S. residency of cases, and calculated overall and age-specific incidence rates by dividing the number of U.S.-resident cases by U.S. Census population estimates.

RESULTS: From January 1–December 31, 2018, 349 confirmed measles cases and 17 outbreaks (i.e., 3 or more cases linked in time and space; range: 3–109 cases per outbreak) were reported to CDC (incidence of 0.97 per million population), compared to a median of 72 cases (range: 37–667) and 4 outbreaks (range: 2–23) reported annually during 2001–2017 (incidence of 0.21 per million population, range: 0.08–2.06). Reported incidence was highest among infants aged 6–11 months and 12–15 months (18.8 and 16.0 per million population, respectively). Measles cases were reported in 26 states and Washington D.C.; 81 (23%) were internationally imported and 268 (77%) were U.S.-acquired. The median age of cases was 7 years (range: 4 months–62 years). Overall, 301 (86%) measles cases were unvaccinated or had an unknown vaccination status and 317 (91%) were U.S. residents. Outbreak-associated cases accounted for 287 (82%) of reported cases. Imported cases traveled to 26 different countries during their exposure periods. Israel, which has reported over 2,300 measles cases in 2018 (an increase from 16 cases in 2017), was the most common travel destination (18 importations), and these importations resulted in outbreaks in four separate jurisdictions.

CONCLUSIONS: There was an increase in measles cases and outbreaks in 2018, compared to recent years. Travel to countries experiencing measles outbreaks led to importations with subsequent spread within unvaccinated communities, with highest risk among infants too young to be vaccinated and unvaccinated toddlers around the recommended age for the first measles vaccine dose. Our findings emphasize the importance of prompt routine immunization, as well as vaccination prior to international travel, according to Advisory Committee on Immunization Practices recommendations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Infectious Diseases; Vaccine-Preventable Diseases; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	xda5@cdc.gov
Presenting Author(s)	Adria Lee
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11017
Abstract Type	Quick
Abstract Title	Pediatric Mumps during the 2015–2017 Mumps Resurgence in the United States

Abstract

BACKGROUND: Numerous mumps outbreaks occurred in the United States over the last decade, with outbreaks affecting young adults on college campuses being among the largest and most widely publicized. However, at least half of mumps cases and outbreaks occurred in other age-groups and settings. We describe reported mumps cases among children and adolescents during 2015 through 2017.

METHODS: The Centers for Disease Control and Prevention (CDC) analyzed reports of confirmed and probable mumps cases in persons aged ≤18 years (defined here as pediatric mumps) transmitted electronically through the Nationally Notifiable Diseases Surveillance System (NNDSS) by the 52 reporting jurisdictions.

RESULTS: Between January 1, 2015–December 31, 2017, 49 jurisdictions reported 4,886 pediatric mumps cases (35% of all US reported cases, 13,807); 8 jurisdictions reported >100 cases each, representing 82% of all pediatric cases. Overall, 29 (1%) cases were in infants <1 yr, 406 (8%) were in children aged 1–4 yrs, 1,408 (29%) in children aged 5–10yrs, 1,365 (28%) in adolescents aged 11–14yrs, and 1,678 (34%) in adolescents aged 15–18yrs. Most (3,548, 73%) cases did not travel outside the state during their exposure period; only 37 (1%) traveled outside the country. Cases in patients aged 1–4 yr were more frequently non-outbreak associated (38%) than those in patients <1 yr and 5–18 yrs (24% and 9%, respectively). Among 3,309 (68%) patients with known number of MMR doses received, 81% of those 5–18 yrs had ≥2 MMR doses, while 67% of those 1–4 yrs had ≥1 dose. Median time since last MMR dose for patients with 2 doses was 8 years (IQR: 4, 11 years). Four patients had meningitis and 1 had encephalitis; all were ≥10 years old and previously received 2 MMR doses. Of male mumps patients older than 10 years of age (2,113), 46 (2%) reported having orchitis; of these, 33 (72%) had 2 MMR doses. Sixty-four patients were hospitalized and there were no deaths.

CONCLUSIONS: About one-third of cases reported during the recent US mumps resurgence were in children and adolescents. The low rate of mumps complications compared with previous studies suggests mumps complications may not be adequately captured in national surveillance or identified by providers. Providers should remain vigilant that mumps can still occur among fully vaccinated pediatric patients, even those recently vaccinated.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Surveillance; Vaccine-Preventable Diseases; Children and Adolescents
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	klt8@cdc.gov
Presenting Author(s)	Mariel Marlow
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10918
Abstract Type	Quick
Abstract Title	Religious Exemptions to Immunizations in Florida

Abstract

BACKGROUND: Florida Statutes and Florida Administrative Code require all attendees of Florida daycares and grades K–12 of public and private schools to have a certification of immunization or exemption on file. There are four types of immunization exemptions allowed in Florida: religious exemptions (REs), temporary medical exemptions, permanent medical exemptions, and temporary exemptions for homeless, transfer, and juvenile justice students. REs are intended for those whose religious beliefs do not support immunizations; however, there is no way to prevent someone from obtaining an RE for philosophical reasons. While all REs must be recorded in Florida's statewide immunization registry, Florida SHOTS, recording of immunizations is optional. This analysis sought to understand the behaviors of individuals with an RE to better focus efforts to increase vaccination in this population.

METHODS: The Florida Department of Health (FDOH) queried Florida SHOTS for individuals with an RE issued between January 1, 2012 and September 30, 2018. Demographic and immunization data recorded in Florida SHOTS were analyzed.

RESULTS: Florida issued 103,155 REs from January 2012 to September 2018 with the number of new REs steadily increasing each year. One quarter (25%) of all REs were issued in August, coinciding with the start of the school year. Over half (53%) of REs were issued to children ≤4 years old. Overall, 60% of individuals with an RE had at least one immunization recorded in Florida SHOTS, and 29% received at least one immunization after obtaining an RE. The most commonly started vaccine series by age 2 years was the diphtheria, tetanus, and pertussis series (53% of the 97,876 2-year-olds with an RE), followed by the *Haemophilus influenzae* type b (Hib) series (51%) and the polio series (50%). The most commonly completed series by age 2 were the Hib (38%) and polio (37%) series.

CONCLUSIONS: Most individuals with an RE have received at least one vaccination, indicating that they are opting out of specific vaccines rather than all vaccines. Once an individual has an RE, they are less likely to continue to receive vaccinations. Therefore, efforts should focus on reaching parents of children ≤4 years old before they request an RE. Additional information is still needed to understand the reasons for opting out of individual vaccines. Since REs do not appear to be used for their intended purpose, Florida should review and update the process for obtaining an RE.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Surveillance; Immunization; Registry
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Katherine.Kendrick@flhealth.gov
Presenting Author(s)	Katherine Kendrick
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11487
Abstract Type	Quick
Abstract Title	Response to an Outbreak of Measles Associated with an Imported Case, Texas, 2018

Abstract

BACKGROUND: Measles, a highly contagious viral disease, requires immediate public health follow-up to mitigate secondary cases. In January 2018, an imported case was reported to the Texas Department of State Health Services, Public Health Region 2/3 (DSHS PHR 2/3). Investigation of this case and five secondary cases identified multiple high risk contacts and public venues where exposures may have occurred leading to extensive public health prevention and control interventions.

METHODS: Investigation into the index case revealed six close contacts, of which four were high risk due to lack of vaccination and no history of disease, and visits to four public venues while contagious. Amongst the five secondary cases, four additional public venues were identified as requiring public health follow-up. All close contacts of cases and all venues were informed of the exposure and provided information regarding measles infection. DSHS PHR 2/3 issued a media release and health alerts regarding the measles outbreak to increase public awareness and promote case finding amongst other public health entities. Measles cases were classified according to CSTE definition. Diagnostic laboratory testing including serology and polymerase chain reaction were performed.

RESULTS: Six confirmed cases were identified during this outbreak with disease onsets ranging from 1/9/18-1/20/18. Of the six case-patients identified, one (16.7%) was an infant, one (16.7%) was 14-18 years of age, and four (66.8%) were adults. None of the six cases were immunized against measles nor had history of disease. Over half of the secondary cases (80%) were associated with the index case's household and one case (20%) was associated with exposure at a public venue. In total, there were eight venues requiring public health follow-up; two (25%) healthcare facilities, one (12.5%) church, one (12.5%) daycare, one (12.5%) high school, one (12.5%) university, one (12.5%) gym, and one (12.5%) movie theater.

CONCLUSIONS: In January 2018, five persons associated with exposure to an imported case of measles were diagnosed with the disease. The rise of vaccine exemptions and the high secondary attack rate of measles amongst susceptible contacts dictates immediate public health intervention. This outbreak had the potential to develop into a larger event given the public venues involved as well as the fact that measles is transmissible prior to rash onset. The prompt investigation into contacts and activities of cases along with the dissemination of information during this investigation demonstrates a successful public health response.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Epidemiology; Infectious Diseases; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email	heidi.threadgill@dshs.texas.gov
Address(es)	
Presenting Author(s)	Heidi Threadgill Honza
Institution	Texas Department of State Health Services
Affiliation	State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Serogroup B Meningococcal Vaccine Uptake Among People at Increased Risk for Serogroup B Meningococcal Disease Due to Underlying Medical Conditions – United States, 2018

Abstract

BACKGROUND: In February 2015, the Advisory Committee on Immunization Practices (ACIP) recommended serogroup B meningococcal vaccine (MenB) for individuals aged ≥ 10 years with complement deficiency (including eculizumab use), or anatomic or functional asplenia (including sickle cell disease). We used IBM MarketScan Treatment Pathways commercial claims data to estimate MenB vaccination coverage among people with these conditions. **METHODS:** We defined a cohort of people aged ≥ 10 years continuously enrolled from the date of MenB licensure (October 29, 2014) through April 30, 2018. Within this cohort, we identified individuals with at least one procedure code, one inpatient ICD-9/10 diagnosis code, or two outpatient ICD-9/10 codes (≥ 30 days apart) for sickle cell disease, congenital asplenia, partial or total splenectomy, complement deficiency, or eculizumab administration. For all conditions we required at least one code before January 1, 2018 to allow time for MenB receipt after diagnosis. For eculizumab, we also required at least one eculizumab administration code after January 30, 2018 to exclude patients no longer taking eculizumab. Individuals were classified as having received MenB if they had at least one MenB administration code at any time, and as having completed a MenB series if they had been vaccinated with an appropriate number and spacing of MenB doses according to ACIP recommendations. **RESULTS:** Of 3,565 individuals meeting the inclusion criteria, 206 (5.8%, 95% confidence interval [CI] 5.0–6.6%) had received at least one MenB dose. First-dose coverage was lowest in adults aged ≥ 24 years, with 69/2,903 (2.4%, 95% CI 1.9–3.0%) having received at least one dose. In contrast, 55/237 (23%, 95% CI 18.0–29.1%) of those aged 10–15 and 82/425 (19%, 95% CI 15.7–23.4%) of those aged 16–23 years had received at least one MenB dose. Overall 113/3,565 (3.2%, 95% CI 2.6–3.8%) people had completed a MenB series; series completion among those who received at least one MenB dose was similar across age groups. Results by underlying condition were similar to overall results except that higher vaccine uptake was observed among eculizumab recipients aged ≥ 24 years (N = 39; one dose: 15.4%, 95% CI 5.9–30.5%; complete series: 10.3%, 95% CI 3.9–25.1%). **CONCLUSIONS:** MenB coverage is low among individuals at increased risk for serogroup B meningococcal disease due to underlying conditions, especially for adults aged ≥ 24 years. Further evaluation is needed to develop strategies to increase MenB vaccination and series completion in individuals with these underlying conditions.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Special/Vulnerable Populations; Vaccine-Preventable Diseases; Immunization
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	xdf4@cdc.gov
Presenting Author(s)	Lucy McNamara
Institution Affiliation	Centers for Disease Control and Prevention Federal Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11131
Abstract Type	Quick
Abstract Title	Unexpected Change in Pertussis Patterns — Maine, 2018

Abstract

BACKGROUND: Pertussis is a highly contagious vaccine-preventable respiratory disease caused by *Bordetella pertussis*. Since 2014, Maine has had one of the highest pertussis rates in the United States. For 2013–2017, Maine Center for Disease Control and Prevention (MCDCP) identified a median of 51 cases during September–October (range 13–67). During September–October 2018, case counts more than doubled. To better understand pertussis dynamics in Maine, we compared 2018 case reports with those reported during 2011–2017.

METHODS: Pertussis data reported during January 2011–October 2018 were retrieved from Maine’s National Electronic Disease Surveillance System Base System. Incidence rates were calculated by age groups (<1 years, 1 to 6 years, 7 to 10 years, 11 to 18 years, and >18 years) using U.S. Census Bureau data. Proportion of patients with vaccination appropriate for age was calculated based on CDC’s immunization schedule. Comparisons were made between 2018 and 2011–2017 aggregate estimates.

RESULTS: We identified 332 confirmed or probable pertussis cases during 2018. Highest incidence was among children aged <1 year (265.6/100,000 population) followed by children aged 1 to 6 years (131.7/100,000 population); these rates were higher than the 2011–2017 mean incidence for these age groups (156.1/100,000 population and 85.6/100,000 population, respectively). Pertussis incidence decreased in 2018 for all other age groups. Among patients, significantly more were appropriately vaccinated in 2018 versus the 2011–2017 mean (83.3% vs 61.1%, $P<0.05$). In 2018, 87.8% of children with pertussis aged <7 years were appropriately vaccinated, compared to the 2011–2017 mean of 68.8% ($P<0.05$).

CONCLUSIONS: Pertussis incidence among Maine children aged <6 years increased in 2018 despite improved vaccination among patients across age groups. MCDCP is investigating possible reasons for this increase, including non-compliance with vaccine storage recommendations, and potential blunting of the child’s immune response associated with maternal immunization.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jennifer.sinatra@maine.gov
Presenting Author(s)	Jennifer Ann Sinatra
Institution Affiliation	Maine Center for Disease Control and Prevention EIS/CEFO

Submission Type ID	Roundtable
Abstract Type	Roundtable
Abstract Title	Immunization Coverage in Urban and Rural Populations in Nigeria

Abstract

Key Objectives:

*To determine the immunization status and coverage of children in urban and rural populations of Nigeria. * To identify any disparity in immunization coverage in the urban and rural areas of Nigeria, and the factors responsible. *To establish and highlight the role of record keeping in the immunization system.*To recommend, based on findings, the best approaches to improve on the immunization coverage in both urban and rural populations equitably.

Brief Summary:

Immunization against childhood VPDs is an important public health intervention which averts an estimated 2-3million deaths annually.Despite this and disproportionately too, nearly one in five children miss out on basic vaccines.This study aimed to contribute towards achieving the GVAP by determining the immunization coverage of eight childhood VPDs in urban and rural populations in Nigeria. Retrospective, comparative and community-based study was conducted in Owerri Municipal Council and Ideato North LGAs of IMO State, south-east Nigeria as case studies for the urban and rural populations of Nigeria,respectively. This covered the period from 2013-2017. Modified WHO-EPI cluster sampling methods were used for household selection.After adjustment by using finite population correction formula and a design effect of 2.3, the effective sample size was 725children and their mothers/caregivers, 315 per LGA. Data was collected using a pre-tested, interviewer administered questionnaire , focused discussions and review of existing records in the NPI units, PHC departments of the LGAs of study. 590 correctly filled questionnaires, 295 per LGA were collected and analyzed. Factors associated with full immunization were identified and independent predictors investigated for. Significances of all the tests were decided at p-value of 0.05. 81.1% of the children were fully immunized by immunization card-plus history, with coverage of 129.4% from the review of records in the urban LGA while only 18.9% of the children in the rural area were fully immunized by immunization card-plus history, 0% from the review of records. Factors significantly associated with full immunization were maternal education level,technologies for data cataloging and transfer, area of residence, social class and maternal health-care utilization. Salient areas need improvement. It is vital that fully operational immunization information system be established and local programmatic interventions be strengthened to upgrade the awareness of the communities on immunization through information, education and communication, primary and maternal health care utilization, while working on advancing the economic status of the populace.This will ensure the GVAP is met, the gap bridged and is critical in the reduction of childhood morbidity and mortality.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vaccine-Preventable Diseases
Keywords	Immunization; Health Disparities; Vaccine-Preventable Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	omeakuanuli@gmail.com
Presenting Author(s)	Maris Anulika Omeaku
Institution Affiliation	Imo State University Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	11755
Abstract Type	Breakout
Abstract Title	Assessing the Reproducibility and Validity of a Zika Epidemiologic Risk Map

Abstract

BACKGROUND: Following the identification of imported Zika cases in Florida in late 2015, an epidemiologic risk map was created and disseminated to county health departments. This map displayed the proportions of women of childbearing age and sociodemographic factors (race, primary language, and low income) determined in a 2011 Key West study to approximate populations at risk for being missed in dengue (an epidemiologically similar arbovirus) prevention outreach campaigns. The goal of this analysis was to evaluate reproducibility of methodology used to generate risk level for a census tract and to evaluate correlation between case numbers and the designated census tract risk using the defined population risk factors.

METHODS: Epidemiologic risk maps were created county-by-county using census-tract level data from the 2010–2014 American Community Survey (ACS) 5-year estimates (Baseline) or the 2012–2016 ACS 5-year estimates (Updated) and standardized methodology. High-, medium-, or low-risk census tracts were defined based on natural breaks in the distribution of each variable within a county. Baseline map risk levels were compared to the original map (Original) created in 2015; the same data layers and methodology were used for both maps. Validation of risk level definition was conducted by overlaying residential address information from 1,680 confirmed and probable 2016–2017 ZIKV infection cases on both the Baseline and Updated maps and comparing the proportion of cases by risk level aggregate for all census tracts.

RESULTS: Map reproducibility was low. Census tract-defined risk on the Baseline map completely matched those on the Original map in only 20/67 (29.9%) counties; more than 10 census tracts were discordant in each of 12/67 (17.9%) counties. Although most cases (85.5% in Baseline; 84.6% in Updated) lived in high- or medium-risk census tracts, there was no gradient between the two, with an equal distribution of cases in each. Census tract-defined risk was not associated with being travel-related or locally acquired.

CONCLUSIONS: The epidemiologic risk map created and disseminated during the ZIKV outbreak in Florida was not reproducible, and defined risk did not consistently align with case distribution. Updating the map with population data accurate to the time of infections did not improve the map's ability to predict high risk areas. A different methodological approach other than using natural breaks to determine risk classification should be used when creating future maps. Factors influencing communication penetration are not necessarily indicative of risk of infection and should be evaluated further.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Epidemiologic Methods; Geographic Information Systems (GIS); Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Kirtana.Ramadugu@flhealth.gov
Presenting Author(s)	Kirtana Ramadugu
Institution Affiliation	Florida Department of Health CDC/CSTE Fellow

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Comparison on Outcomes of Dogs and Cats Exposed to Rabies before and after Implementation of New Animal Management Recommendations, Kansas 2013-2018

Abstract

BACKGROUND: Rabies is a highly fatal zoonotic disease of mammals. Prior to 2016, Kansas regulation required out-of-date dogs and cats exposed to rabies to be managed like unvaccinated dogs and cats, euthanized or quarantined for six months. Quarantine presents a significant burden on public health resources and owner finances; causing many to opt for euthanasia. In 2016, the National Association of State Public Health Veterinarian's Animal Rabies Compendium recommendations were updated. Management of out-of-date dogs and cats significantly changed from a 6-month quarantine to a 45-day observation. Management of unvaccinated dogs and cats changed from a 6- to a 4-month quarantine.

METHODS: Rabies-positive animals reported to the Kansas Department of Health and Environment were entered into Kansas' electronic disease surveillance system. All dogs and cats exposed to rabies were evaluated for vaccination status, disposition, and outcome. Vaccination status was categorized as current, out-of-date, unvaccinated, or unknown. Disposition was classified as quarantined, observed, or euthanasia. Outcomes of dogs and cats exposed to a rabies-positive animal from January 1, 2013 – December 31, 2015 (period 1) were compared to those from January 1, 2016 – December 10, 2018 (period 2).

RESULTS: In period 1, 184 dogs and cats were exposed to rabies; 81 (44%) were currently vaccinated, 26 (14%) out-of-date, 67 (36%) unvaccinated, and 10 (6%) unknown. Of 26 out-of-date contacts, 13 (50%) were euthanized and 13 (50%) were quarantined for six months (11 survived, one exhibited signs and tested rabies negative, one was euthanized). Of 67 unvaccinated contacts, 51 (76%) were euthanized, 12 (18%) were quarantined for six months (8 survived, one exhibited signs and tested rabies positive, one lost to follow-up, two died from unrelated causes), and four (6%) were killed by the rabies-positive animal. In period 2, 126 dogs and cats were exposed to rabies; 43 (34%) were currently vaccinated, 20 (16%) out-of-date, 62 (49%) unvaccinated, and one unknown. Of 20 out-of-date contacts, three (15%) were euthanized and 17 (85%) were observed for 45 days (all survived). Of 62 unvaccinated contacts, 42 (68%) were euthanized and 20 (32%) were quarantined for four months (all survived).

CONCLUSIONS: No exposed out-of-date dogs or cats developed rabies during quarantine or observation. Fewer out-of-date and unvaccinated dogs and cats were euthanized following rabies exposure after new recommendations were implemented. The updated guidelines have reduced the number of animals euthanized, decreased the burden of public health follow-up, and continue to prevent the spread of rabies in Kansas.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Veterinary Public Health; One Health; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Chelsea.Raybern@ks.gov
Presenting Author(s)	Chelsea Raybern
Institution Affiliation	Kansas Department of Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10677
Abstract Type	Breakout
Abstract Title	Factors Associated with Inappropriate Administration of Rabies Post-Exposure Prophylaxis in Suburban Cook County, Illinois, 2015-2018

Abstract

BACKGROUND: Rabies is nearly 100% fatal in humans but is preventable when post-exposure prophylaxis (PEP) is given promptly and correctly. The Advisory Committee on Immunization Practices (ACIP) publishes guidelines that detail when animal exposure circumstances warrant PEP administration. Failure to adhere to these guidelines results in unnecessary cost, inconvenience, and minor medical risks to the patient when PEP is given but not indicated. Potential human rabies exposures, including the initiation of PEP, are reportable in Illinois. Since 2015, the Cook County Department of Public Health (CCDPH) has engaged in continuous quality improvement initiatives to increase reporting and improve clinical quality measures related to rabies exposures. In this study, we assessed factors associated with inappropriate administration of PEP.

METHODS: Individuals who received PEP in Suburban Cook County between January 2015 and October 2018 were retrospectively evaluated for appropriateness of treatment according to ACIP guidelines. A multivariable logistic regression model was used to evaluate predictors of inappropriate PEP administration.

RESULTS: During our study period, 279 (54%) of 519 reported individuals received inappropriate administrations of PEP. Individuals who received PEP were 84% less likely to have been treated inappropriately if a local or state health department was consulted (OR 0.16, 95% CI 0.11-0.26). A health department was consulted for 163 (31%) reported PEP recipients. Exposing animal species was also associated with appropriateness of PEP administration. Compared to bats, exposure to a dog or cat was associated with greater odds of inappropriate PEP administration (OR 2.69, 95% CI 1.52-4.76; OR 5.61, 95% CI 1.73-18.14, respectively), while exposure to a raccoon was associated with reduced odds of inappropriate PEP administration (OR 0.25, 95% CI 0.09-0.72). Patient age and sex were not significantly associated with inappropriate PEP administration.

CONCLUSIONS: Consultation with a health department was the single most protective factor against inappropriate administration of PEP in Suburban Cook County. As the majority of patients were given PEP without consulting a health department, this is an area where substantial improvement can be made to reduce the burden of unnecessary PEP. Healthcare providers should be especially mindful when considering PEP for domestic animal exposures, as the likelihood of inappropriate PEP administration was significantly higher for dog and cat exposures than for bats or raccoons. The results from this analysis will allow CCDPH to implement more informed education efforts with local hospitals.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vaccine-Preventable Diseases; Local Epidemiology; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	hannah.steinberg@cookcountyhhs.org
Presenting Author(s)	Hannah Steinberg
Institution Affiliation	CSTE Applied Epidemiology Fellowship Program CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11770
Abstract Type	Breakout
Abstract Title	Fight the Bite: Using Local Data to Inform West Nile Virus Mitigation in Mesa County, Colorado

Abstract

BACKGROUND: Between 2013 and 2017, 18 cases of West Nile Virus were reported to Mesa County Public Health (MCPH) in Colorado. During that time, MCPH focused on reactionary methods of dealing with cases of West Nile Virus by following up with cases after they were reported. We wanted to use our experience with data visualizations to shift that focus toward prevention. The Grand River Mosquito Control District (GRMCD) is the lead agency for local mosquito control efforts. GRMCD focuses on controlling the *Culex* species of mosquitoes in the area, which is the species that can carry West Nile Virus. A partnership was formed to utilize data to inform mosquito control efforts in 2018.

METHODS: GRMCD allowed MCPH to access their mosquito trap data which includes mosquito count by trap, species, and year dating back to 2013. GRMCD collects mosquitos from each of the 83 traps and updates their data weekly. With a direct connection to these real-time data, MCPH was able to use Tableau to visualize which traps were seeing the most *Culex* activity and whether or not that was above or below the historical average for that particular trap and week over the past five years. We were also able to look at data from Colorado's disease reporting system to see the number of West Nile Virus cases in Mesa County and surrounding counties. We had a weekly conference call with staff at GRMCD and MCPH to discuss what the data were telling us.

RESULTS: Overall, the ability to visualize data helped to influence disease prevention decisions at the local level. The data obtained from this partnership between GRMCD and MCPH were used to influence prevention decisions and when press releases were issued. At the end of 2018, Mesa County had an incidence rate of 1.3 cases of West Nile Virus per 100,000 population. For comparison, two counties bordering Mesa had incidence rates of 26.1 cases per 100,000 and 18.9 cases per 100,000, respectively, in 2018.

CONCLUSIONS: The new partnership and data-sharing between GRMCD and MCPH allowed for more timely information on when and where to focus mosquito control efforts. The success of this partnership has encouraged us to form similar partnerships with other local organizations in the community.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	andrew.tyler@mesacounty.us
Presenting Author(s)	Andrew Tyler
Institution Affiliation	Mesa County Public Health Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10750
Abstract Type	Breakout
Abstract Title	Knowledge and Practices Regarding Zoonotic Disease Exposure Risks and Personal Protective Equipment Use Among Arizona Wildlife Professionals, 2008 and 2018

Abstract

BACKGROUND: Over half of all emerging infectious diseases are zoonotic; >70% of those are wildlife-associated. Wildlife professionals are at increased risk of occupational disease exposure. In 2008, after an Arizona wildlife biologist died from plague after necropsying an infected mountain lion without adequate personal protective equipment (PPE), the Arizona Department of Health Services (ADHS) surveyed wildlife professionals from multiple Arizona agencies. ADHS revised the survey in 2018 to assess changes in practice and culture, and to address additional factors identified since 2008. The purpose of both studies was to assess the risk of disease exposure to wildlife professionals, their PPE use, and zoonoses knowledge; these results would identify targets for education to improve practices.

METHODS: In 2008, a 12-question survey was distributed in-person at a state wildlife professional meeting using an anonymous email link to wildlife agency employees. In 2018, a revised 20-question survey was created in Qualtrics® and distributed using an anonymous email link to state and federal wildlife agencies, licensed wildlife rehabilitators, and other wildlife control groups through their own list serves.

RESULTS: We received 162 and 81 complete responses in the 2008 and 2018 surveys, respectively. Over half of respondents (54% in 2008; 59% in 2018) had >10 years of experience. In 2018, fifty-one percent were male, and respondents represented all 15 Arizona counties. Respondents reported similar bite frequencies in 2008 (27%) and 2018 (23%), but bites from rabies reservoir (bats, foxes, or skunks) or spillover species (bobcats and coyotes) was higher in 2008 (42%) than in 2018 (16%). Among the 58% of respondents in 2018 that performed necropsies or collected animal samples within the previous five years, only 60% always wore latex or nitrile gloves, and 79% never wore a facemask. In 2018, reasons for PPE non-use included: not necessary in given scenarios (79%), not readily available (27%), and practicality (19%). Respondents indicated awareness of certain zoonoses, including the risk of plague (96%), rabies (91%) and hantavirus (91%); however awareness was lower for brucellosis (72%), leptospirosis (60%), and tuberculosis (59%).

CONCLUSIONS: Approximately one quarter of Arizona wildlife professionals reported experiencing wildlife bites in 2008 and 2018, although the frequency of high-risk rabies exposures in 2018 was lower. In 2018, questions pertaining to zoonoses awareness and reasons for non-use of PPE highlighted targets for education to improve practices, which should be pursued. Development of educational materials and facilitation of personal protection training for wildlife professionals could prevent future disease transmission.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Occupational Health; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	heather.venkat@azdhs.gov
Presenting Author(s)	Heather Venkat
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Monitoring Rabies Epizootics in the United States: Balancing the Need for a Sensitive Rabies Surveillance System with Reasonable Expectations for Laboratory Monitoring

Abstract

BACKGROUND: A standardized rabies virus (RABV) surveillance system that includes virus characterization information could enhance early detection of: host-shift events, translocation of RABV variants, and discovery of novel variants. Given the severe implications that RABV have for both human and animal health, understanding the transmission dynamics of RABV variants within and between animal species is crucial. To date, there has been no systematic evaluation of either the representativeness or completeness of the virus characterization data in animals submitted to the U.S. national animal rabies surveillance system.

METHODS: The authors discussed epidemiologically important events likely to yield actionable information relevant to rabies control. Specimens likely to identify significant epidemiologic events (e.g. host-shift, translocation, novel variant, or epidemiologically unusual events) were considered of epizootiological importance (SEI). The 2010–2015 U.S. public health rabies surveillance data were used to project the additional burden for laboratory testing if all SEI underwent virus characterization. Data were analyzed and the total number of positive samples obtained for each SEI category across the six year time span was used to calculate the estimated number of samples and confidence intervals that public health laboratories could expect if all SEI underwent RABV characterization. Terrestrial animal data was included in this analysis; however, bats were not included.

RESULTS: Four epidemiologically relevant events critical to rabies surveillance were determined based on discussion and previous literature findings: introduction of novel RABV variants; translocation of variants; host-shift events; and rabies events that may affect future testing guidelines. Twelve SEI categories, based on one of the four events, were evaluated. During 2010–2015, there was an annual average of 855 (95% CI, 739–971) rabies positive SEI; an average of 270 (95% CI, 187–353) (31.6%) SEI underwent virus characterization. Virus characterization of all SEI would be expected to increase laboratory testing by approximately 584 (95% CI, 543–625) samples per year.

CONCLUSIONS: Prioritizing RABV characterization of SEI may improve early detection of rabies events associated with host-shifts, translocations, and importation. Characterization of SEI may help refine wildlife rabies management practices. Laboratory testing of SEI should be evaluated by each public health laboratory to ensure testing does not strain routine diagnostic laboratory capacity.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Epidemiology; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ydi7@cdc.gov
Presenting Author(s)	Emily G Pieracci
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Polar Bears in the Desert: Rickettsia Parkeri Rickettsiosis in Southern Arizona, 2016-2017

Abstract

BACKGROUND: *Rickettsia parkeri* is an emerging tick-borne disease in the United States (US), transmitted by the bite of *Amblyomma maculatum* (the Gulf Coast tick). Clinical manifestations can include fever, headache, fatigue, myalgia, and maculopapular rash. A characteristic eschar forms at the site of the tick bite. Arizona's index case of *R. parkeri* rickettsiosis was reported in 2014. In 2018, the Arizona Department of Health Services sought to describe and characterize additional cases of this emerging disease identified during 2016-2017.

METHODS: We identified cases through routine investigation in conjunction with electronic laboratory reports, and three cases self-reported to public health authorities. Serum samples were evaluated for IgG antibodies reactive with antigens of *Rickettsia rickettsii* and *R. parkeri* using indirect immunofluorescence antibody testing. Samples were initially screened at a 1/32 and diluted serially to endpoint; those with IgG antibody titers ≥ 64 were considered positive. DNA was extracted from eschar swab specimens and screened using a real-time PCR assay targeting a segment of the 23S rRNA gene of all known *Rickettsia* species.

RESULTS: We identified seven cases (3 confirmed, 4 probable) of *R. parkeri* rickettsiosis; patients (6 male, 1 female) ranged in age from 29-69 years (median, 41 years), and became ill between July and September. Fever (6/7), myalgia (5/7), and arthralgia (5/7) were most commonly reported and 5/7 patients had a documented eschar. All patients reported a tick bite acquired in southern Arizona within 2-8 days prior to illness onset. Four patients worked as US border patrol agents. Antibodies reactive to *R. rickettsii*, *R. parkeri*, or to both antigens, were detected in all patients; titers reactive with *R. parkeri* were two- to four-fold greater for six patients. Seroconversions between acute and convalescent-phase samples were identified for two patients. The panRickettsia real-time assay was positive for two patients.

CONCLUSIONS: *R. parkeri* rickettsiosis is endemic to a region of the southwestern US and could present an occupational risk; prevention messaging could be provided to border patrol agents. Four cases initially misdiagnosed despite the presence of an eschar suggests a lack of regional clinician awareness. *R. parkeri* rickettsiosis is the second tick-borne rickettsiosis identified repeatedly in Arizona since 2003. Rocky Mountain spotted fever, a closely related and significantly more clinically severe spotted fever rickettsiosis, is also endemic in portions of Arizona. Public health agencies need to provide further information to clinicians to help distinguish these two infections clinically and apply species-specific diagnostic assays to improve surveillance.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Occupational Exposure; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	hayley.yaglom@azdhs.gov
Presenting Author(s)	Hayley Yaglom
Institution Affiliation	Arizona Department of Health Services State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Probable Transfusion-Associated Transmission of Powassan Virus, 2018

Abstract

BACKGROUND: Powassan virus (POWV) is a tick-borne flavivirus and rare cause of encephalitis. In the United States, POWV disease is most commonly reported from the Northeast and Upper Midwest; no cases have been reported in Indiana. Transmission of POWV via blood transfusion or organ transplantation has not been documented. We investigated a case of encephalitis in an Indiana resident with recent history of kidney transplantation and red blood cell transfusions.

METHODS: Medical records of the encephalitis patient, the organ donor, and the recipient of a lung from the same donor were reviewed. The encephalitis patient and blood donors were interviewed. Specimens from the encephalitis patient, lung recipient, organ donor, and blood donors were tested for evidence of POWV infection by reverse transcription-polymerase chain reaction (RT-PCR), IgM capture enzyme-linked immunosorbent assay, and/or plaque reduction neutralization test. An environmental investigation was conducted to assess the encephalitis patient's risk of tick exposure.

RESULTS: The patient had onset of encephalitis in July 2018, approximately three weeks after a kidney transplant and three red blood cell transfusions. The patient was hospitalized, but survived. Serum and CSF collected 13 days after encephalitis onset had detectable POWV IgM antibodies but no detectable RNA. The POWV neutralizing antibody titer was 10 in this serum specimen and 320 in a serum specimen collected five days later. POWV neutralizing antibodies were not detected in the CSF. Serologic testing for other flaviruses was negative. The patient's pre-transplant serum had no detectable POWV RNA, IgM, or neutralizing antibodies. Post-transplant serum from the lung recipient had no detectable POWV IgM or neutralizing antibodies. Banked organ donor serum had no detectable POWV RNA, IgM, or neutralizing antibodies. A plasma co-component from one of the three blood donors had no detectable POWV IgM or neutralizing antibodies, but RT-PCR test results were equivocal. A serum specimen collected from this donor 174 days after donation had detectable POWV IgM antibodies and a neutralizing antibody titer of 40. The blood donor lived in the Upper Midwest and reported a tick bite one month prior to donation. Follow-up sera from the other two blood donors had no detectable POWV neutralizing antibodies. The encephalitis patient's only reported outdoor exposure was in Indiana, at home and a park; no ticks were found at either location.

CONCLUSIONS: Blood transfusion was the likely mechanism of POWV transmission in this case. While POWV disease is rare, healthcare providers should consider POWV to be a possible transfusion-associated pathogen.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Infectious Diseases; Emerging Infections
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	tastevens@isdh.in.gov
Presenting Author(s)	Taryn Stevens
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Rabbits: Canary in the Coalmine or Public Enemy #1? a One Health Approach to a Kentucky Tularemia Investigation

Abstract

BACKGROUND: Tularemia, a bacterial Category A bioterrorism agent, can infect both people and animals, and can be fatal if not treated appropriately. In April, 2018 a rabbit die-off and subsequent positive culture for tularemia in one rabbit initiated an investigation into a 240-acre beagle hunt club enclosure in western Kentucky. The Kentucky Department for Public Health (KDPH) and Kentucky Department of Fish and Wildlife Resources (KDFWR) closed the field, halting scheduled field trials due to the potential exposure risk and began immediate coordination to investigate. Recent hunt club trials potentially exposed dozens of people and beagles in 22 states and Canada through tick and rabbit exposure. Literature review showed no precedent for investigation and mitigation of high tularemia levels in an enclosed environment. We initiated a multiagency, federal, state and local response.

METHODS: Invoking a one-health approach, experts in entomology, human healthcare, veterinarian medicine, wildlife biology and incident management convened. We developed a five-step approach to assess and mitigate the threat: 1): notification and risk assessment of those exposed; 2) site evaluation; 3) tick drags for identification and pathogen testing; 4) rabbit density reduction; 5) exposure mitigation and release of fields back to the hunt club. Materials were created for phone and voicemail notification, including testing and clinical guidance for physicians and veterinarians. The KY State Health Operations Center (SHOC) was activated. Health departments in all 22 states and Canada were notified; participants were contacted and a risk assessment conducted. An Epi-X alert was sent for additional case finding. Site assessment and rabbit harvesting (live and deceased) occurred in May, 2018. Two tick drags were conducted for speciation and testing in May and October.

RESULTS: Of 99 people contacted, six people and four dogs had symptoms mirroring tularemia. Seven dogs had ticks. One dog tested positive; two were treated empirically and improved. Four rabbits (two live, two carcasses), with embedded ticks, were tested; two rabbits (one live, one carcass) and ticks were positive. The initial tick drag collected 116 ticks; one group of 12 tested positive. The second tick drag yielded zero ticks.

CONCLUSIONS: Artificial lack of natural predation likely amplified the presence of tularemia in an enclosed canine hunt club field. A One-Health approach was implemented to successfully respond in a situation that lacked scientific precedence for evaluation and mitigation. Subject matter experts collaborated to produce a synergistic response. A public health threat was recognized and contained.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	One Health; Vectorborne Disease; Environmental Health
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kelly.giesbrecht@ky.gov
Presenting Author(s)	Kelly Giesbrecht
Institution Affiliation	Kentucky Department for Public Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Syndromic Surveillance of Emergency Department Visits for Tick Bites and Lyme Disease — Three Regions, 2017

Abstract

BACKGROUND: Surveillance for Lyme disease can be resource intense in endemic areas due to high case volume. Syndromic surveillance of emergency departments (ED) visits may offer an efficient approach to monitor tick bite and Lyme disease cases. We described the frequency and seasonality for these outcomes in regions with high, medium, and low Lyme disease incidence. In addition, we evaluated the utility of tick bite visits to predict the seasonal peak in Lyme disease visits.

METHODS: We developed algorithms for tick bite and Lyme disease using combinations of *International Classification of Diseases* Tenth Revision (ICD-10) diagnostic codes and key word search terms in the chief complaint field of ED visit data. Algorithms were applied to data submitted through the National Syndromic Surveillance Program (NSSP) during 2017 in three regions with known high, medium, or low Lyme disease incidence. We compared number and seasonality of ED visits by region for tick bite and Lyme disease. We calculated Lyme disease incidence using total ED visits and compared to National Notifiable Diseases Surveillance System (NNDSS) data. We also calculated the time lag between peak number of ED visits for tick bite and for Lyme disease.

RESULTS: In 2017, the number of ED visits in the high, medium, and low incidence regions was 13,804 (346/100,000 ED visits), 6,536 (29/100,000 ED visits), and 764 (20/100,000 ED visits) for tick bite and 4,749 (119/100,000 ED visits), 3,946 (17/100,000 ED visits), and 170 (5/100,000 ED visits) for Lyme disease, respectively. For comparison, Lyme disease incidence was 53, 12, and 1 case per 100,000 persons in the high, medium, and low incidence regions, as reported through NNDSS. In the high incidence region, 44% of the ED visits for Lyme disease occurred during June and July, as compared with 53% of cases reported through NNDSS. Peak daily ED visits for tick bites preceded the peak for Lyme disease by 50 and 42 days in the high and medium incidence regions, respectively; no temporal pattern for Lyme disease ED visits was observed in the low incidence region.

CONCLUSIONS: Syndromic surveillance demonstrates substantial ED burden by patients with tick bite and Lyme disease. In high incidence areas, ED visits for Lyme disease have similar relative incidence and seasonality as data reported to NNDSS. In high and medium incidence areas, peak ED visits for tick bites may provide a guide for optimal timing of Lyme disease prevention messages.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Syndromic Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	GMarx@cdc.gov
Presenting Author(s)	Grace E Marx
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11217
Abstract Type	Lightning
Abstract Title	Beyond Case Counts—Capturing Record Number of Deaths Due to West Nile Virus in Los Angeles County By Enhancing Monitoring of Patients

Abstract

BACKGROUND: Los Angeles County Department of Public Health (LACDPH) documents cases of West Nile virus (WNV) every year. As WNV can cause prolonged illness, case investigations frequently occur while the patient remains hospitalized. Patients alive at the time of case investigation have been recorded as surviving the disease. In 2017, the outcome monitoring protocol was enhanced for patients who remained hospitalized at the time of case investigation and LACDPH documented a record-breaking 27 deaths.

METHODS: Medical records were requested for each hospitalized WNV patient reported to LACDPH. Patients with discharge summaries unavailable at the time of investigation due to prolonged hospitalization were flagged for additional follow-up every two weeks and up to three months, until a discharge summary was available for review. For patients discharged to rehabilitation centers, death certificates were reviewed five months after the initial investigation.

RESULTS: In 2017, 18 deaths were identified through routine surveillance. Approximately 80 patients remained hospitalized at the time of case investigation and were flagged for additional follow-up. Nine more deaths were identified for a total of 27 deaths. Among all 27 deaths, the average length of time between disease onset and death was 29 days (range of 8 to 144 days). This average was longer among the nine additional deaths (45 days, range of 15 to 144 days) compared to deaths identified through routine surveillance (21 days, range of 8 to 46 days). The average length of hospitalization for those nine patients was also longer than those deaths identified by routine surveillance (41 vs. 14 days). All nine additional deaths died during hospitalization compared to 3 of the 18 deaths found through routine surveillance.

CONCLUSIONS: The additional deaths identified from the new protocol revealed that many WNV deaths can go unreported without active monitoring. Though the deaths all occurred in the hospital, reliance on passive reporting from the hospital is insufficient for deaths that can occur up to five months after onset. A substantial number of deaths also occurred after hospitalization. Under-estimation of fatalities contributes to a false perception that WNV is not a severe and significant threat to the public. The record number of deaths documented in 2017 prompted an unprecedented educational campaign in which approximately 100 public health teams distributed mosquito-borne disease materials to thousands of public venues across LAC. Having an accurate count of deaths played a key role in garnering public interest and promoting behavior change, which is imperative to preventing WNV.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Epidemiologic Methods; Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ebarnes@ph.lacounty.gov
Presenting Author(s)	Emily Barnes
Institution Affiliation	Los Angeles County Department of Public Health Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11826
Abstract Type	Lightning
Abstract Title	Hantavirus Infection on the Navajo Nation 1992-2016

Abstract

BACKGROUND: Hantavirus is a genus of viruses in the Bunyaviridae family. The primary species of hantavirus in the American Southwest is Sin Nombre Virus. Its main host, the deer mouse (*Peromyscus maniculatus*), can carry the virus in feces, urine, and saliva. The most common mode of transmission to humans is inhalation of aerosolized particles containing the virus. The purpose of the project was to assess the burden of hantavirus among Navajo residing in the Four Corners (AZ, NM, UT, CO) area. The goal of the project was to quantify available data in order to serve as a platform for future surveillance efforts and to reveal patterns that may assist in targeting prevention.

METHODS: The Navajo Epidemiology Center received data from the CDC Viral Special Pathogens Branch for 139 hantavirus cases between November 1992 and May 2016 that were linked to a city of residence or city of exposure in one of 10 counties in and around Navajo Nation. Two methods were used to restrict analysis to Navajo cases. First, data were included for all individuals listed as American Indian with a community of residence on the Navajo Nation. Second, cases with a community of residence outside Navajo Nation were evaluated individually. Data was managed in Microsoft Excel 2013 and analyzed using SAS 9.3.

RESULTS: One hundred and eight cases that were potentially Navajo occurred between November 1992 and May 2016. The highest numbers of cases occurred during the late spring and early summer months – April, May, June, and July – with a slight peak again in November. Women appear to have a higher risk of mortality compared to men. This difference is largest among women in the 40-49, 50-59, and 60-69 age groups. Approximately half of cases occurred in Eastern Agency (Navajo Nation contains five geopolitical regions called agencies). Most cases had exposure to mice in or around the home. Many cases lived in mobile homes, at altitudes between 6000 and 7000 feet, and in piñon/juniper woodland and/or high desert areas.

CONCLUSIONS: Hantavirus surveillance data suggest that persons in certain occupations and certain populations may be at increased risk because of potential for rodent exposure. Educational efforts and awareness focused on high-risk populations should continue so that persons can decrease their risk of acquiring hantavirus disease.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Tribal Epidemiology; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Del.Yazzie@nndoh.org
Presenting Author(s)	Del Yazzie
Institution Affiliation	Navajo Department of Health Tribe

Submission Type	Breakout/Quick/Lightning/Poster
ID	11651
Abstract Type	Lightning
Abstract Title	Review of Pennsylvania's 2018 Arbovirus Season: A Blip on the Radar or Is This the New Norm?

Abstract

BACKGROUND: In response to the emerging threat of West Nile virus (WNV) and other arboviruses, a multi-agency task force was established in 2000 to reduce expected morbidity and mortality through comprehensive human and animal surveillance and a mosquito control program. Since its emergence in 1999, WNV has been the most frequently reported arbovirus in Pennsylvania; typically averaging 11 human, 4 equine, 25 avian cases and 1504 positive mosquito pools annually. The 2018 mosquito season created unique challenges in the wake of the National Weather Service reporting record rainfalls across the state. The purpose of this review is to describe the burden of WNV and other mosquito-borne arboviruses during 2018 and to illustrate the importance of an interagency response during a high burden season.

METHODS: The multi-agency task force includes three state agencies: Department of Environmental Protection (DEP), leading mosquito surveillance; Department of Health (DOH), leading human case surveillance; and Department of Agriculture, leading veterinary surveillance. As outlined in the Commonwealth of Pennsylvania's WNV and Other Arboviruses Prevention and Control Plan (WNV plan), interagency coordination and weekly data sharing updates promotes a targeted approach for mosquito control efforts in areas with elevated human and animal infection rates. The WNV plan was routinely monitored and response efforts by the appropriate agency were initiated when tiered thresholds were achieved (phases 0-4).

RESULTS: During 2018, routine surveillance identified 120 human, 111 equine, and 107 avian cases of WNV. A record 4,729 WNV-positive mosquito pools were identified in 63 of 67 Pennsylvania counties, requiring large mosquito-control efforts statewide. In addition, other rarely reported mosquito-borne arboviruses were identified including a human and emu case of Eastern Equine encephalitis, and a human case of Saint Louis encephalitis virus. For only the second time in Pennsylvania, DEP identified an *Aedes aegypti* mosquito. The highest phase of response (phase 4) in the WNV control plan was reached and prevention activities including health alerts and enhanced communication efforts were carried out accordingly.

CONCLUSIONS: Environmental factors, including record rainfall across Pennsylvania, promoted ideal mosquito breeding conditions which contributed to record numbers of WNV-infected mosquitoes and greater than expected human, equine, and avian cases. The established task force and WNV plan promoted a coordinated, rapid response and allowed for interagency sharing of key information necessary to reduce risk of human illness. As the threat from arbovirus diseases continues, it is crucial to remain vigilant with surveillance activities and coordinated mosquito control prevention efforts.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Collaboration; Data Sharing
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	krymason@pa.gov
Presenting Author(s)	Krystal Mason
Institution Affiliation	Pennsylvania Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Lightning
Abstract Title	Tail of a Rabid Puppy: Lessons Learned

Abstract

BACKGROUND: In Minnesota, skunks and bats are the main rabies reservoirs. Livestock and pets generally develop rabies following a bite from a rabid skunk. People are generally exposed to rabies by bats, livestock, and unvaccinated pets. The Minnesota Department of Health (MDH) utilizes interagency cooperation with the Minnesota Board of Animal Health (BAH) when investigating exposures to potentially rabid animals. On September 17, 2018, BAH notified MDH that a 4 month-old puppy with progressive paralysis and other neurological symptoms had been euthanized and submitted for rabies testing at a regional veterinary diagnostic laboratory (VDL). An interagency investigation was initiated to determine possible animal and human exposures.

METHODS: MDH contacted the puppy's owners and the submitting veterinarian and obtained names of persons who had contact with the puppy during September 2-17. All contacts were interviewed by MDH to discern potential exposures and, if needed, recommend post-exposure prophylaxis (PEP). BAH conducted field investigations to evaluate animal exposures to the puppy.

RESULTS: From interviews with the owners and two veterinarians on September 17, MDH learned that the puppy was attacked by a skunk July 1, and developed symptoms consistent with rabies September 12. Due to overwhelming clinical and epidemiological evidence for rabies, MDH initially interviewed 11 potential contacts obtained from initial owner interview, and advised 8 to initiate PEP on September 17. On September 18, the VDL notified the submitting veterinarian, MDH and BAH that the rabies direct fluorescent antibody (DFA) test was negative, resulting in some contacts discontinuing PEP. The VDL performed a second rabies DFA and rabies PCR test due to concerns of a false negative test. On September 21, the second rabies DFA and rabies PCR were positive. In total, 49 contacts were interviewed, many of whom expressed doubt about the positive results following the previous negative results. Twenty-five (51%) contacts were advised to start rabies PEP treatment, including 5 international visitors and 6 children. Coordination between four healthcare facilities in Minnesota and North Dakota was needed to ensure adequate PEP for contacts with high-risk exposures. BAH placed one animal into 180-day quarantine.

CONCLUSIONS: While typically very reliable, false-negative DFA results do occur, and repeat testing should be performed when the animal's clinical presentation and exposure history is consistent with rabies. Strong relationships and good communication between public health and animal health agencies and VDLs are essential for a successful rabies surveillance program and to empower all program participants to investigate unexpected results.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Stephanie.s.Johnson@state.mn.us
Presenting Author(s)	Stephanie Sikavitsas Johnson
Institution Affiliation	Minnesota Department of Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11585
Abstract Type	Poster
Abstract Title	A Review of Powassan Virus Cases in Pennsylvania Residents (2011–2017) and Novel Evidence Found in Locally Collected Adult Black-Legged Ticks (2013–2015)

Abstract

BACKGROUND: Powassan virus (POWV) is a zoonotic, tick-borne RNA virus that can infect the central nervous system and cause severe illness such as meningitis in humans. POWV is transmitted by the black-legged tick, *Ixodes scapularis*. Since surveillance began in 2003, more than 100 cases of POWV have been reported in the United States. Over half of these were reported in 2016–2017, suggesting an increase in incidence in recent years. The purpose of this review is to describe the epidemiology of recent human disease cases and better define the geographic areas of POWV risk in Pennsylvania.

METHODS: Pennsylvania residents were identified through passive surveillance when POWV lab results were reported to the Pennsylvania Department of Health (PADOH). Suspected POWV cases were investigated and reported to the national surveillance system, ArboNET, if they met case definition. Adult ticks were recovered from deer heads during late Fall hunting seasons. Ticks identified as adult *Ixodes scapularis* were grouped into pooled tick samples by year and region of collection. PCR testing was performed and ticks making up a positive pool were then tested individually for POWV.

RESULTS: There were a total of five human cases of POWV reported to PADOH, one case in 2011 and four cases in 2017. POWV patient characteristics include: all were male and resided in northeast Pennsylvania, four (80%) were >65 years old, none had traveled the month before symptom onset, all five were hospitalized with neuroinvasive symptoms, and two reported tick bites prior to symptom onset. During 2013–2015, 1,990 adult *Ixodes scapularis* ticks were recovered from 9,930 harvested deer heads. One of the 409 (0.2%) pooled tick samples tested positive for POWV. The positive tick sample was collected in 2014 from a collection site in southeast Pennsylvania, and the state-wide individual tick pathogen prevalence rate for the three-year collection period was 0.05%.

CONCLUSIONS: This study provides evidence that POWV is present in *Ixodes scapularis* ticks in Pennsylvania and suggests that the patients who tested positive for POWV could have acquired their infection locally. Considering the potential for severe disease, primary care physicians should become familiar with signs and symptoms of this emerging pathogen to properly diagnose and treat patients who become infected with POWV. Also, Pennsylvanians should be educated on prevention of tick-borne diseases such as practicing strict tick avoidance measures and locating and removing ticks as soon as possible after exposure.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Infectious Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email	krymason@pa.gov
Address(es)	
Presenting Author(s)	Krystal Mason
Institution	Pennsylvania Department of Health
Affiliation	State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Poster
Abstract Title	Anticipating Years with Weather-Related Increased Risk of West Nile Virus to Humans in Nebraska

Abstract

BACKGROUND: To complement Nebraska's vector-borne disease surveillance, we looked for a statistical connection between weather and human cases of West Nile Virus (WNV) that would let us issue warnings of higher annual risk at the start of the infection season. We investigated which time lags of key variables explained most.

METHODS: We created 12, 18, 24, 30 and 36-month lags of temperature and drought data. Human cases per county-year was the response variable. From the number of cases, we computed cumulative incidence (previous exposure). We used the R package mgcv (Wood) to fit general additive models with functional smoothing curves, essentially letting the data speak for itself. We fit models based on 2002-2015, and used 2016 for out-of-sample predictions. We used Akaike information criterion to select models that best fit the data, and contrasted the performance of our best-fit models with the performance of the naïve model (the assumption that each year would be the same as the preceding one). Because more than half of the county-years in our data had zero cases, we converted predictions to presence-absence, and mapped predictions for which of Nebraska's 93 counties would have cases in 2016. We used McNemar's test of statistical significance.

RESULTS: The best-performing model used 24-month temperature lags, 12-month lags of the Standardized Precipitation and Evapotranspiration Index, cumulative incidence, county and year, and had an R-square of 0.917. It out-performed the naïve model in 10 out of 13 years, 2003-2015, and in 2016. In presence-absence predictions for 2016, our model outperformed the naïve in 30% of counties, with exponentially small probability of this difference happening by chance.

CONCLUSIONS: Our model has predictive value. We anticipate that different combinations of precipitation and temperature will work better for different places, and that the best-fit model may evolve over time, but that the method of identifying a best model and then using it to make predictions will be widely applicable, for West Nile Virus and for other annual effects of temperature and drought. To deploy this method operationally, we recommend model refitting and evaluation after each year's infection season, incorporating the most recent numbers of human cases, and then making predictions in May or June, as soon as drought indices can be computed. Timely availability of infection data and drought indices may be a constraint.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Risk Assessment; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	jeff.hamik@nebraska.gov
Presenting Author(s)	Jeffrey J. Hamik
Institution Affiliation	Nebraska Department of Health and Human Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10735
Abstract Type	Poster
Abstract Title	Correlation between West Nile Virus Surveillance Data in Louisiana and National Data, 2002-2018

Abstract

BACKGROUND: West Nile virus (WNV) is a mosquito-borne disease that was introduced to the United States in 1999, with the first human case identified in Louisiana in 2001. Less than one percent of all WNV infections develop neuroinvasive disease (NID) that can be associated with encephalitis or meningitis. With the assumption that transmission is affected by local ecologic conditions, we intended to determine if Louisiana WNV-NID case counts would correlate with national data from 2002–2018 despite regional variances in ecologic factors.

METHODS: Suspected arboviral infections were reported to the Infectious Disease Epidemiology Section of the Louisiana Department of Health, Office of Public Health, through laboratory reports and physician inquiries. Clinical symptoms, exposure information and laboratory results were evaluated against the Council of State and Territorial Epidemiologists (CSTE) case definitions and entered into the Louisiana web-based surveillance system, Infectious Disease Reporting Information System (IDRIS). While diagnosis and reporting is incomplete, most cases of WNV-NID are severe enough to cause hospitalization and receive laboratory testing. Hence the reporting of WNV-NID cases is considered the best indicator for comparisons of WNV activity. Louisiana WNV-NID cases were extracted from IDRIS from 2002–2018 (only 1 case was reported in 2001); national WNV-NID data were obtained from CDC from 2002–2018. A linear regression analysis was performed and a coefficient of determination was calculated.

RESULTS: As of January 7, 2019 Louisiana has identified 1,095 WNV-NID cases and there have been 24,463 WNV-NID cases reported nationally. The number of WNV-NID cases in Louisiana has shown wide variations, ranging from a high of 204 cases in 2002 and 160 cases in 2012, to a low of 6 cases in 2011. The number of national WNV-NID cases also had wide variation, ranging from a high of 2,946 cases in 2002 and 2,873 cases in 2012, to a low of 386 cases in 2009. Over the past 17 years, Louisiana represented 4.48% of all WNV-NID national cases. The highest and lowest proportions for Louisiana data were respectively: in 2005 twice the national proportion (9.01%) and in 2011 less than half of that proportion (1.23%). The coefficient of determination equals 72.67%.

CONCLUSIONS: Overall, there is a strong positive linear relationship between the WNV-NID cases reported from Louisiana to the national data. This is supported by the coefficient of determination and similar variation in the high and low WNV-NID years. Future analysis may investigate how national factors determine local case counts despite regional variations in ecological factors.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Zoonotic Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	cwaldron@la.gov
Presenting Author(s)	Christine Scott-Waldron
Institution Affiliation	Louisiana Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11705
Abstract Type	Poster
Abstract Title	Evaluation of a Community-Based Mosquito Trapping Program in Sedgwick County, Kansas, 2018

Abstract

BACKGROUND: In 2013, the Sedgwick County Division of Health (SCDOH) began collaborating on mosquito surveillance with the Kansas Department of Health and Environment (KDHE), the City of Wichita Stormwater Program (CoW), and the Kansas Biological Survey (KBS). In Sedgwick County, mosquito surveillance guides larvicidal mosquito abatement efforts to protect the health of Sedgwick County residents. From 2013 to 2017, mosquito trapping was performed by KBS. In 2018, changes to the program resulted in trapping performed by SCDOH-coordinated community volunteers and, also, a new ArcGIS application.

METHODS: Mosquito surveillance was conducted weekly from May 17 through October 25, 2018 (24 weeks). Encephalitis Vector Surveillance (EVS) traps were set in five pre-determined locations every Tuesday night and collected Wednesday morning (240 trap-days) by four trained Sedgwick County Master Gardeners volunteers, one student and, later in the summer, four SCDOH staff. Mosquitoes were packaged on dry ice and sent to the KBS for enumeration and species identification. Standing water around traps with >20 *Culex* species mosquitoes were treated with larvicidal dunks. One CoW field staff entered larvicidal dunk application into an ArcGIS online survey which SCDOH used to track mosquito numbers and abatement. A mosquito program survey was sent to all volunteers and analyzed by SCDOH at the end of the surveillance season.

RESULTS: In 2018, mosquito traps were set up and removed 100% of total season trap-days. Community volunteers spent 144 trap-days and accrued 3,864 mileage. After two volunteers dropped out of the program, SCDOH staff spent 96 trap-days and accrued 1,064 mileage to complete trapping. Of the participants, 78% responded to the end of season survey. Volunteers identified strong partnerships, an easy to understand program structure, and a well-organized SCDOH staff as the program's strengths. Volunteers identified insufficient volunteers, difficulty submitting mileage, commuting time, and insufficient dry ice as barriers. The ArcGIS application allowed field staff to easily identify trap and abatement location. The application was utilized consistently by CoW staff, who reported the system was easy to use and more efficient for reporting abatement. For SCDOH reports, the ArcGIS application saved approximately two hours in staff time compared to 2017.

CONCLUSIONS: Although more labor intensive when compared to previous years' trappings, Sedgwick County successfully coordinated a mosquito surveillance program in 2018. Community volunteers were dedicated to the program, but the logistics and sustained need from May through October were obstacles. Sustainability remains a top concern.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Sonali.kurlekar@sedgwick.gov
Presenting Author(s)	Sonalli Kurlekar
Institution Affiliation	Sedgwick County Division of Health, Wichita, Kansas Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11459
Abstract Type	Poster
Abstract Title	Evaluation of Immunoglobulin G Titers for Determining Spotted Fever Group Rickettsioses —Tennessee, 2013-2017

Abstract

BACKGROUND: Tick-borne disease cases more than doubled during 2004 – 2016 making up 77% of all vector-borne disease reports. Spotted fever group rickettsioses (SFGR) have been reported throughout most of the continental United States although >60% of cases are reported by North Carolina, Oklahoma, Arkansas, Tennessee, and Missouri. Surveillance approaches in these states vary. From 2013 – 2016, there was a 27% increase in reported SFGR cases. We reviewed clinical symptoms and testing of Tennessee SFGR cases to assess our surveillance approach.

METHODS: We analyzed cases with SFGR immunoglobulin G (IgG) titers $\geq 1:64$ during 01/01/2013 – 12/31/2017 collected through passive surveillance. Strengths and limitations of various SFGR IgG titers for determining case classifications were compared. Data in this retrospective cohort analysis were analyzed using two-way frequencies, Pearson's Chi-square test and Fisher's exact test to evaluate the distribution of the input variables, and logistic regression to measure associations between patient's IgG titers, onset and sample collection dates, and case classification status.

RESULTS: 7,459 cases were reported with 30% being probable cases. Investigations with a single IgG titer of 1:64 resulted in the highest number of non-case classifications (72%) and had the lowest positive predictive value (PPV), 27%. In comparison, investigations with a single IgG titer of 1:128 had a higher PPV (38%). Receiver operating characteristic (ROC) analyses indicated that eliminating 1:64 IgG titers and increasing the titer cut-off to 1:128 or above, increased the accuracy of single IgG tests in identifying clinically compatible cases.

CONCLUSIONS: In Tennessee, the number of people tested for SFGR continues to increase, causing a high burden of investigations. A single IgG titer of 1:64 was a poor indicator of a clinically compatible case. Convalescent titers are a more reliable approach for determining case status however, in practice, this is rarely performed. To prioritize the large volume of laboratory reports, health departments may consider giving highest priority to investigations of patients with IgG titers $\geq 1:128$. Investigations for patients with an IgG titer of 1:64 could be limited to those with a convalescent titer. Standardized approaches to surveillance will facilitate consistent case reporting and monitoring of SFGR trends.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kelly.orejuela@tn.gov
Presenting Author(s)	Kelly Orejuela
Institution Affiliation	Tennessee Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10733
Abstract Type	Poster
Abstract Title	Kentucky's Mosquito Surveillance and Arbovirus Testing, 2018

Abstract

BACKGROUND: Diseases transmitted by mosquitoes and other arthropods are an important public health concern. To better understand the threat of potential mosquito-borne disease events, the Kentucky Department for Public Health (KDPH) along with partners, initiated a mosquito surveillance program in 2017 set out to identify and describe mosquito species present across our state. These surveillance efforts continued in 2018, applying lessons learned from 2017. Kentucky completed its second Mosquito Surveillance season utilizing ELC funds provided by the CDC.

METHODS: Fourteen local health departments (LHD's) participated in mosquito surveillance during the 2018 mosquito season. Environmental staff collected mosquito pools at designated collection sites in 24 counties for 16 weeks between June and October. Mosquito pools were sent to one of three designated laboratories. The laboratories are testing for St. Louis Encephalitis virus (SLE), West Nile Virus (WNV), or Zika virus based on the anticipated presence of the viruses in the mosquito species and historical disease transmission patterns. Protocols are set in place for public health response to any positive pools.

RESULTS: During the 2018 mosquito season, 980 mosquito pools were collected. From those pools, 15,720 individual mosquitoes representing 29 species were identified. The most commonly identified species was *Culex pipiens* (n=4,392) at 28%. The next most commonly identified species was *Aedes albopictus* (n=2,618) at 17%. Of the 980 mosquito pools, 480 pools have been tested for WNV with 77 testing positive in five distinct geographic regions. In 2017, 119 mosquito pools were tested and 17 were positive for WNV in three distinct regions. In addition, in 2018, 374 of the mosquito pools were tested for SLE virus with no positives, as well as 370 of the mosquito pools tested for Zika virus with no positives.

CONCLUSIONS: Kentucky needs to increase surveillance more evenly across the state. Due to the 15.9% positivity rate for WNV, an increase in public awareness and intervention efforts are priority. For example, 75% of mosquito pools submitted from Daviess County was positive for WNV, and this was unexpected. This indicates Kentucky may have a higher rate for WNV than what is currently known. KDPH is increasing public awareness by utilizing surveillance efforts, so these will aid in developing additional prevention initiatives.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; One Health; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Tori.Amburgey@ky.gov
Presenting Author(s)	Victoria Amburgey
Institution Affiliation	Kentucky Department for Public Health State Public Health Agency

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	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	erica.mendoza2@dshs.texas.gov
Presenting Author(s)	Erica Mendoza
Institution Affiliation	Texas Department of State Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10935
Abstract Type	Poster
Abstract Title	Skunk Rabies Epizootic Impact on the Recommendation for Rabies Post-Exposure Prophylaxis El Paso County, CO 2017-2018

Abstract

BACKGROUND: Bats are the traditional rabies reservoir in Colorado, however, since 2009 the state has experienced a skunk rabies epizootic. Before 2009, the last rabid terrestrial animal in El Paso County (EPC) was a skunk in 1974. While relatively few skunks tested positive for the rabies virus between 2009 and 2016, the number increased dramatically to 21 skunks in 2017, followed by 61 in 2018. The increase in skunk rabies was most noticeable during March and April of 2018, which corresponds to the skunk mating season in Colorado. Prior to 2017, the only rabies season that had a higher number of positive skunks than bats was 2009. We hypothesized that due to the increase in rabid skunks, the number of people requiring post-exposure prophylaxis (PEP) would increase in EPC.

METHODS: All animal bites by a rabies reservoir species are reportable to the health department within 24 hours. El Paso County Public Health (EPCPH) receives calls from citizens to evaluate exposures from potentially rabid animals and utilizes REDCap, an open-source database, to triage them. If an animal tests positive for rabies it is recorded in the Colorado Zoonotic Disease Animal Surveillance Reporting Database; if a person is recommended PEP, the exposure is documented in the Colorado Electronic Disease Reporting System (CEDRS). A report was created in CEDRS to pull data on PEP recommendations for people and cross-referenced with the rabies-positive animals in EPC recorded in the zoonotic database. REDCap brings the two information streams together to associate a specific animal with the PEP recommendations.

RESULTS: Analysis included 179 people recommended for rabies PEP between January 2012 and December 2018. Of those people, 96 were exposed to bats, 25 to cats, 22 to skunks and 36 to other animals. By year: 38 people were recommended for PEP in 2018, 34 in 2017, 34 in 2016, 64 in 2015, 8 in 2014, 0 in 2013 and 1 in 2012.

CONCLUSIONS: Recommendations for Rabies PEP did not increase with the number of rabid skunks; the majority of PEP recommendations are due to bat exposures. Skunk exposures are more evident whereas bat exposures are often nuanced, requiring a more conservative approach to recommendations. This dynamic is reversed in pets, with more animals being recommended for rabies vaccines due to skunks than bats.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	haleyzachary@elpasoco.com
Presenting Author(s)	Haley Zachary
Institution Affiliation	El Paso County Public Health Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11213
Abstract Type	Quick
Abstract Title	<i>Salmonella</i> Serovar Fluntern Illnesses Linked to Leopard Geckos— United States, 2018

Abstract

BACKGROUND: Reptile contact is an important cause of zoonotic non-typhoidal salmonellosis (NTS) in the United States. In April 2018, Oregon Public Health Division contacted CDC about a temporal cluster of four *Salmonella* serovar Fluntern (SF) illnesses in four states; ill people reported contact with geckos, a popular reptile pet. PulseNet, the national molecular subtyping network of foodborne disease surveillance, subsequently identified additional SF clinical isolates. We sought to characterize the magnitude of illness and prevent further transmission.

METHODS: A case was defined as isolation of SF from an ill patient during July 1, 2017, through March 1, 2018. Public health personnel interviewed patients to assess reptile exposure, and conducted traceback for reported purchase locations. Environmental samples were taken from patients' pet gecko habitats. Animal isolate data regarding SF from the U.S. Department of Agriculture National Veterinary Services Laboratories (NVSL) were obtained to determine if SF had been isolated from animal sources. Whole genome sequencing (WGS) core genome multi-locus sequence typing (cgMLST) was performed to determine relatedness between clinical and animal isolates.

RESULTS: We identified 12 cases in 11 states; 8 (67%) were female, and median age was 5 years (range: <1–58 years). Three patients were hospitalized; no deaths were reported. Of those with exposure information (n=10), all reported reptile exposure; 9 (90%) specified contact with leopard geckos. No common source of geckos was identified from reported purchase locations. Health officials in Los Angeles County (LAC) isolated SF from one patient's leopard gecko. Five reptile/gecko isolates were identified from NVSL from 2015–2018. WGS cgMLST analysis revealed substantial genetic diversity between clinical and animal isolates; however, gecko and clinical isolates from LAC were highly related (1 allele difference).

CONCLUSIONS: This investigation linking SF illness to leopard gecko exposure highlights an important public health risk of NTS transmission. A better understanding of how geckos are distributed in the United States could improve gecko traceability to points of origin and mitigate *Salmonella* transmission at breeders. Identification of historic gecko isolates suggests the potential for transmission of SF from geckos to humans in the United States has existed for several years. This investigation demonstrates a need to educate gecko breeders, retailers, and the public about the risk of *Salmonella* infection from pets, and the value of continual prevention efforts among those who own and care for leopard geckos.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Epidemiology; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	njq5@cdc.gov
Presenting Author(s)	Lia Koski
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Animal Bites and Rabies Post-Exposure Prophylaxis: An Evaluation of Public Health Surveillance Data in the United States—November 2018

Abstract

BACKGROUND: Rabies is a fatal viral illness that is preventable with post-exposure prophylaxis (PEP). Robust animal bite and PEP data would be useful in evaluating appropriate use of PEP, measuring public health costs, assessing adherence to PEP schedules, and monitoring supplies nationwide. However, neither are nationally notifiable and the quality of state-level data is unknown.

METHODS: The National Association of State Public Health Veterinarians with assistance from the Centers for Disease Control and Prevention designed a cross-sectional web-based survey to evaluate the availability and quality of surveillance data for animal bites and PEP. Surveys were sent to state public health veterinarians in the 50 U.S. states, Puerto Rico, New York City, and Washington DC in November 2018. Questions were designed to determine which jurisdictions have surveillance data at the state level, how those systems are managed, what data are collected and used, and which entities outside of public health participate in information flow. The survey included multiple choice questions, likert scales, and free texted response fields organized with skip patterns.

RESULTS: Of 53 jurisdictions, 39 (73.5%) responded including 37 states, New York City and Philadelphia. No state-level data on animal bites or PEP was available in 7 (17.9%) jurisdictions; 3 (7.7%) jurisdictions had only ad hoc data available such as rabies hotline calls. Of the 29 jurisdictions with some state-level animal bite or PEP data available, 15 jurisdictions (38.4%) had data from animal bite surveillance; of those, 7 (46.7%) reported electronic reporting platforms and 5 (71.4%) reported platforms integrated with other reportable conditions. Models for capturing PEP data ranged from standard local health department follow-up of suspected rabies exposures to integrated electronic surveillance systems that collected more data. Jurisdictions reported inconsistent availability of personally identifying data (e.g., age) and type of animal exposure; they estimated 50% of data were shared between state and local jurisdictions. Few responders supported making PEP nationally notifiable but 30 (79.0%) of 38 supported improving standards for data collection.

CONCLUSIONS: PEP and animal bite surveillance is variable among jurisdictions. Lack of standardized definitions and protocols contributes to the inability to interpret data at the national level. Setting data standards for animal bite and PEP surveillance may facilitate improved data collection so that practices and burden of rabies, animal bites, and PEP across jurisdictions can be compared. Alternatively, data sources such as syndromic surveillance or distribution data from PEP manufacturers could circumvent the limitations of existing surveillance.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Zoonotic Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	okp7@cdc.gov
Presenting Author(s)	Erin R Whitehouse
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Clusters of Cat and Raccoon Rabies in Florida, 2018

Abstract

BACKGROUND: Rabies is a preventable viral infection transmitted through the saliva of an infected animal, typically through bites. Rabies is nearly 100% fatal in humans who do not receive timely post-exposure prophylaxis (PEP), which costs approximately \$5000 in a 165-pound adult. In Florida, although raccoons are the terrestrial wildlife rabies reservoir, most instances of PEP use are related to domestic animal (dog and cat) exposure even though state law requires vaccination for all dogs, cats, and ferrets over 4 months of age. Rabies infections in people or animals or any recommendation to administer PEP are reportable conditions in Florida. In 2018, the Florida Department of Health investigated clusters of terrestrial animal rabies in three counties; the main types of animals in these clusters were cats and raccoons. All three counties have community cat trap-neuter-release ordinances. The goal of this analysis was to characterize and compare these clusters to statewide cat and raccoon rabies cases from previous years.

METHODS: Cat and raccoon rabies reports (both positive laboratory tests and PEP-related exposures) from January 1, 2009 to December 31, 2018 were characterized. Temporal and geographic data from 2018 were compared to aggregated data from 2009–2017 (baseline years).

RESULTS: There were 15 rabies-positive cats and 59 rabies-positive raccoons in 2018, a 46.7% increase in cats and no change in raccoons compared to baseline years. The three counties with rabies clusters reported 10 positive cats (67% state total) and 17 positive raccoons (29% state total). All cats and 35.3% of raccoons in the three counties exposed humans. Most cats were stray (90%) and all were either unvaccinated or had unknown vaccination status. The three counties reported a 94.3% increase in cat-related PEP and an 87.2% increase in raccoon-related PEP recommendations while statewide cat-related and raccoon-related PEP recommendations only increased 38.7% and 29.2%, respectively, between baseline years and 2018. PEP recommendations related to stray cats increased 3.5% in the three counties and 7.8% statewide, while the proportion related to unvaccinated cats or cats with unknown vaccination status remained unchanged for both.

CONCLUSIONS: The number of rabid cats and the PEP due to contact with stray cats and raccoons increased in Florida in 2018. Cat rabies vaccination policies should be reinforced with community members, veterinarians, and other stakeholders. Targeted education should emphasize avoiding direct contact with wildlife and unowned animals. Further studies should be conducted to evaluate the impact of community cat policies on rabies and PEP incidence.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Environmental Exposures; Infectious Diseases; Injury
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Kirtana.Ramadugu@flhealth.gov
Presenting Author(s)	Kirtana Ramadugu
Institution Affiliation	Florida Department of Health CDC/CSTE Fellow

Submission Type	Breakout/Quick/Lightning/Poster
ID	11728
Abstract Type	Quick
Abstract Title	Eastern Equine Encephalitis Activity in Emus, Florida, 2018

Abstract

BACKGROUND: Eastern equine encephalitis virus (EEEV), an endemic arbovirus in Florida, can be transmitted year-round. Emus are particularly vulnerable to infection, typically resulting in rapid death following onset of severe gastrointestinal illness. Emus develop high levels of viremia and can infect competent vectors. Exposure to bodily fluids or feces from infected birds can lead to possible exposure for people and other animals. A EEEV horse vaccine is available for off-label use in emus. During 2018, the Florida Department of Health (Florida Health) and Florida Department of Agriculture and Consumer Services (FDACS) received reports of seven emu flocks with symptoms consistent with EEEV infection. Joint investigations were initiated with FDACS and local mosquito control.

METHODS: Emu owners were interviewed and provided recommendations related to proper personal protective equipment (PPE), mosquito bite prevention, carcass and egg disposal, and emu vaccination. Molecular testing was conducted by Florida Health on bloody fecal samples and when available, tracheal, cloacal, or choanal swabs or serum from recently deceased or sick birds. Representative tissues were collected from two emus that were autopsied. Symptom monitoring was conducted for 10 days post-exposure on individuals caring for the emus. Serum samples were also obtained for molecular and serologic testing to evaluate for possible EEEV exposure. Public health advisories were also issued to the public.

RESULTS: EEEV infections were confirmed in emus at seven of the farms, with five farms reporting illness in more than one emu. Symptom onset dates ranged from 2/13/18–11/1/18. Farm A had the highest rate of transmission, where more than half of the 28 emus were symptomatic. The remaining emus were euthanized due to the high rate of transmission at the location and lack of veterinary care. Overall, 44/60 (73%) of the emus among the seven locations became ill or were euthanized. Twenty-two samples were positive for EEEV by molecular testing, including six fecal samples, six tracheal swabs, two cloacal swabs, two serums, one heart, one brain, one spleen, two livers, and one intestine. A single ostrich was also symptomatic at one of the farms. EEEV testing was negative for 18 human contacts.

CONCLUSIONS: Most of the emu flocks had no history of previous vaccination. Investigations were complicated due to owners' limited resources, including no regular veterinary care. There were also differences in risk perception among individuals caring for infected emus; only two owners routinely used the provided PPE. The joint investigations were critical to preventing further spread of EEEV.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Environmental Health; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Andrea.Morrison@flhealth.gov
Presenting Author(s)	Andrea Morrison
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11310
Abstract Type	Quick
Abstract Title	Epidemiologic Features of an Outbreak of Human Jamestown Canyon Virus Disease, Wisconsin, 2017-2018

Abstract

BACKGROUND: Jamestown Canyon virus (JCV) is a mosquito-borne *Orthobunyavirus* that can cause neuroinvasive disease. Nationally, JCV disease is most commonly reported in Wisconsin. During 2012 to 2016, a median of five cases of JCV disease (range 1 – 11) were reported annually among Wisconsin residents. Then in 2017 and 2018, 43 cases and 20 cases of JCV were reported respectively, representing a >500% increase in the average annual number of cases compared to the previous five years. We report on the epidemiologic features of this JCV disease outbreak during 2017 and 2018.

METHODS: JCV cases were classified using both laboratory and clinical criteria from the arboviral diseases national surveillance case definition. Wisconsin State Laboratory of Hygiene (WSLH) performed JCV-specific IgM enzyme-linked immunoassay on specimens submitted to WSLH for arbovirus testing and on specimens from commercial laboratories with evidence of arboviral antibodies from patients with clinical evidence of an arboviral illness. Specimens with presumptive evidence of JCV IgM antibodies were confirmed at CDC using plaque reduction neutralization test. Clinical information, demographics, travel history, and potential modes of transmission were collected through patient interviews, and clinical information was confirmed by medical record abstraction.

RESULTS: A total of 63 cases of JCV disease were reported from 35 (49%) Wisconsin counties. Illness onsets occurred during each month of the year except February, March, and December, with 53 (84%) cases occurring between June and September. The median patient age was 57 years (range 19 – 83), and 41 (65%) were male. Fifty (79%) cases were classified as neuroinvasive disease, and 38 (60%) were hospitalized. The most common symptoms reported were fatigue (87%), fever (84%), headache (71%), chills (65%), myalgia (60%), and disorientation (57%). Encephalitis was diagnosed in 22 (35%) of the cases, meningitis in 11 (17%), and acute flaccid paralysis in 3 (5%). Infections were presumably transmitted by mosquitoes, since all patients denied blood transfusion, organ transplantation, or laboratory exposure in the 30 days prior to illness onset. Of the 63 cases, 13 cases also had laboratory evidence of another arboviral infection (West Nile, Powassan, or eastern equine encephalitis virus).

CONCLUSIONS: JCV infections in 2017 and 2018 contributed to significant morbidity among Wisconsin residents. The abrupt increase in cases, in the absence of substantial modifications in surveillance practices, suggests potential change(s) in disease transmission dynamics resulting in more human infections. Accurate diagnosis of JCV disease and further characterization of transmission dynamics in Wisconsin can inform public health prevention strategies.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Vectorborne Disease; Outbreaks
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	rebecca.osborn@dhs.wisconsin.gov
Presenting Author(s)	Rebecca A Osborn
Institution Affiliation	Wisconsin Department of Health Services State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11410
Abstract Type	Quick
Abstract Title	Epidemiology of Ehrlichiosis Caused By Ehrlichia Chaffeensis and Ehrlichia Ewingii— United States, 2013–2016

Abstract

BACKGROUND: Human ehrlichiosis is a tickborne disease caused by bacteria from the *Ehrlichia* genus. The majority of reported cases in the United States are due to infection by *E. chaffeensis*. Ehrlichiosis can cause moderate to severe illness and is potentially fatal. Symptoms can include fever, headache, malaise, and myalgia. Rash is reported in approximately one-third of patients with *E. chaffeensis* infection. Infection caused by *E. ewingii* usually results in milder illness compared with *E. chaffeensis*. Presumptive treatment with doxycycline is recommended for patients of all ages with suspected ehrlichiosis. Presented here is a summary of *E. chaffeensis* and *E. ewingii* cases reported to the Centers for Disease Control and Prevention (CDC) with illness onset during 2013–2016.

METHODS: Cases of ehrlichiosis are reported to CDC through two national surveillance systems: the National Notifiable Diseases Surveillance System (NNDSS) and tickborne rickettsial disease case report forms (CRFs). Demographic data reported through NNDSS were used to calculate incidence rates. Data from CRFs describe clinical course and patient outcome.

RESULTS: From 2013–2016, a total of 5,733 cases of ehrlichiosis were reported through NNDSS (60.4% male, 68.0% white, median age 58 years). The majority of cases were reported as *E. chaffeensis* infection (n=5,648, 98.5%). The incidence rate (IR) of *E. chaffeensis* infection was 4.6 cases per million persons. Most cases reported illness onset from May–August (n=3,477, 79.1%). The hospitalization rate (HR) was 53.7%, and the case fatality rate (CFR) was <1.0%. No fatalities in persons under 30 years old were reported. Eighty-five (1.5%) cases were reported through NNDSS as *E. ewingii* infection. The IR of *E. ewingii* infection was 0.07 cases per million persons. Most cases reported illness onset between June and August (n=61, 78.2%). The HR was 57.9% and no deaths were reported.

CONCLUSIONS: The incidence of human ehrlichiosis cases in the United States has continued to rise since becoming nationally notifiable in 1999. A national surveillance summary of cases with illness onset during 2008–2012 showed children aged <5 years with ehrlichiosis were more than twice as likely to experience fatal outcome compared to the rest of the population. This report found no fatalities in persons aged <30 years, which may be due to educational efforts urging physicians to treat young patients with suspected rickettsial infection with doxycycline. Ongoing surveillance and reporting of tickborne diseases are critical in understanding the epidemiology of ehrlichiosis in the United States.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Epidemiology; Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kzy2@cdc.gov
Presenting Author(s)	Dena Cherry-Brown
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10632
Abstract Type	Quick
Abstract Title	Eschar-Associated Rickettsiales: Clinical Clue or Misunderstood Element?

Abstract

BACKGROUND: Eschars are necrotic lesions found at the site of tick or mite attachment and can be a common clinical feature of certain rickettsial diseases. Eschars result from a number of domestic pathogens, including *Rickettsia parkeri*, *R. species 364D* and *R. akari*, and several imported *Rickettsiae* including *R. africae* and *R. conorii*, but have not been linked to *Ehrlichia* and *Anaplasma* species. In 2010, the Centers for Disease Control and Prevention began collecting information on eschars on their tickborne rickettsial disease (TBRD) case report form (CRF). The purpose of this analysis is to summarize U.S. eschar-associated rickettsioses.

METHODS: We summarized supplemental data collected by state and local health departments and submitted to the Rickettsial Zoonoses Branch via CRFs or similar sources. Data with illness onset from 2010–2016 were included in this summary. Case classifications were made according to CSTE case definitions.

RESULTS: From 2010–2016, 484 TBRD cases were reported with the presence of an eschar. Of those, 387 (80.0%) were classified as a spotted fever rickettsiosis, 64 (13.2%) were *E. chaffeensis* ehrlichiosis, 30 (6.2%) were *A. phagocytophilum*, 1 (0.2%) was *E. ewingii* ehrlichiosis, and 2 (0.4%) were undetermined ehrlichiosis/anaplasmosis. Of eschar-associated spotted fever rickettsiosis cases, 11 identified *R. africae* as the suspected agent, 2 listed *R. parkeri*, and one case each specified *R. conorii*, *R. species 364D*, and *R. akari*. Only 8.7% of eschar-associated infections met the criteria for a confirmed case. Eschar-associated illnesses were more common in men than women (59.9% vs 39.0%), most were white (68.4%) and non-Hispanic (83.1%). Nineteen percent (n=90) of eschar-associated cases were hospitalized, and only one person reportedly died because of their illness. Thirty-four cases were positive by PCR, yet only six were reported as a spotted fever rickettsiosis.

CONCLUSIONS: The presence or absence of eschars can provide valuable data and help clinically differentiate spotted fever group rickettsioses; however, the value and validity of eschars in cases of ehrlichiosis and anaplasmosis have not yet been defined. Cases of eschar-associated ehrlichiosis and anaplasmosis are not reported in the literature, yet 20% of eschar-associated illnesses were reported as one of these agents. It is possible that some of these instances arise from misunderstanding of the term. Further clinical research is needed to clarify if these reports reflect a mistake, a new discovery, or if they are a result of co-infection with another eschar-causing rickettsial pathogen.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	isj3@cdc.gov
Presenting Author(s)	Naomi Drexler
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	11172
Abstract Type	Quick
Abstract Title	Evaluating the Efficacy of Community-Level Interventions during Outbreaks of Flea-Borne Typhus Fever

Abstract

BACKGROUND: The city of Pasadena is a known endemic area for flea-borne typhus fever, with several documented outbreaks within the last 30 years. In 2016 and 2018, Pasadena experienced epidemic levels of typhus fever across the city. Our objective was to evaluate the effectiveness of community interventions, including educational mailers and media messaging, for the management of typhus fever outbreaks and assess the efficacy of these interventions.

METHODS: Face-to-face interviews were conducted among a simple random sample within a cluster area of flea-borne typhus fever using a semi-structured questionnaire. Among the 2,309 residential addresses that received the initial mailer, 200 were randomly selected to be interviewed, and a total of 37 (18.5%) interviews were completed. Participants were asked whether they had heard of typhus and from what source, what their level of concern was about the disease, and whether they took any preventive actions. Residents who voluntarily reported seeing the educational mailer and/or the press coverage following our health alert, were compared to those residents who heard about the typhus outbreak from other outlets or did not hear about it at all to assess the value of the educational materials for vectorborne disease prevention.

RESULTS: Among the respondents who completed the interview (n=37), almost 46% (17/37) of the sample reported seeing the educational mailer from the health department and nearly 22% (8/37) reported hearing about the outbreak from traditional news outlets (e.g. newspapers, television). Of those who reported seeing the mailer, 76% (13/17) did at least one preventive control activity to mitigate typhus fever risk. Specifically, all four of the pet owners who reported seeing the mailer discontinued backyard feeding. Finally, people who reported seeing the mailer reported higher, but not significant, levels of concern about flea-borne typhus fever ($p=0.14$) but more knowledge about how typhus is transmitted ($p=0.01$).

CONCLUSIONS: Broad, community-level mailers appear to be an effective strategy for motivating individuals in high-risk areas to change behaviors to prevent environmental infectious diseases like flea-borne typhus fever.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Evaluation; Local Epidemiology
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	mfeaster@cityofpasadena.net
Presenting Author(s)	Matthew M Feaster
Institution Affiliation	City of Pasadena Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10992
Abstract Type	Quick
Abstract Title	Evaluation of Commercial Insurance Claims As a Component of Lyme Disease Surveillance

Abstract

BACKGROUND: In high incidence areas, traditional case-based surveillance for Lyme disease (LD) can require substantial resources while yielding little new information for public health action. Commercial claims data, a growing source of epidemiologic information, could supplement case-based surveillance to provide a more complete picture of disease burden, geographic spread, and factors linked to severe illness while requiring fewer resources. We evaluated population characteristics and LD patterns in a large national insurance claims database to evaluate its utility as a component of LD surveillance.

METHODS: We examined the annual variability of enrollee data in MarketScan® Commercial Claims and Encounters databases during 2010-2016 and its representativeness compared to the US population. Analyzed records were restricted to those with full-year enrollment and associated prescription data. We identified records of enrollees as clinician-diagnosed cases of LD using International Classification of Disease codes for LD and related clinical conditions with antimicrobial prescriptions for LD treatment. Case characteristics were compared to those in the National Notifiable Diseases Surveillance System (NNDSS). US Census regions were used to describe geographic distribution.

RESULTS: During 2010-2016, annual enrollment in the MarketScan database varied between 19,004,365 (in 2016) and 28,757,701 (in 2012). Proportions of the MarketScan population in each region remained consistent and closely aligned with the US population (regional proportions differed by 0-8% between the two populations). Females were slightly overrepresented in MarketScan, as were adults aged 45-55, compared to the US population. We identified 111,006 individuals diagnosed with LD; annual incidence per 100,000 enrollees ranged from 49 (2010) to 79 (2014) and was equal between sexes. Median annual incidence per 100,000 enrollees in the Northeast, North Central, South and West census regions was 277, 25, 29, and 14, respectively. Age-specific incidence in MarketScan was bimodal with a consistent peak in males 5-9 years and a second peak in adults that was variable across years. In NNDSS, annual incidence ranged from 10 to 12; a bimodal age distribution consistently occurred, with the majority of cases among males, irrespective of age group. Comparatively, relative incidence of LD in adult women was much higher in the MarketScan database.

CONCLUSIONS: Despite yearly variation in MarketScan enrollment, several epidemiologic characteristics of clinician-diagnosed LD were similar to those of national surveillance data. Differences between MarketScan and NNDSS data require further consideration; however, MarketScan could serve as a complementary surveillance tool and provide new insights into burden, demographics, and clinical picture of LD that inform education and prevention activities.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	ICD; Vectorborne Disease; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ltp9@cdc.gov
Presenting Author(s)	Amy Schwartz
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Evaluation of the West Nile Virus Risk Level Model in Kansas, 2018

Abstract

BACKGROUND: West Nile virus (WNV) is the leading cause of domestically acquired arboviral disease in the United States and Kansas. *Culex* species mosquitoes are the primary vector for transmission. Mosquito-based surveillance (MS) is the primary tool for quantifying WNV transmission risk. WNV risk levels (RL) were developed in 2017 and modified in 2018. RLs were evaluated to determine if current factors used to calculate RLs accurately reflected the risk of transmission.

METHODS: MS was conducted weekly with fifteen traps among three counties, in 2 of 6 regions in Kansas, from 5/13/2018 to 10/23/2018. RL threshold measures were based on California's Mosquito-Borne Virus Risk Assessment. Percent change of *Culex spp.* mosquitoes from the same week the previous year, average daily temperature over the previous two weeks, and five-year historical case data were used (Model 1). Weekly average numerical values were calculated and assigned to one of four RLs (minimal, low, moderate, high). In post-season analysis, a second model was explored where, if ≥ 40 *Culex spp.* mosquitoes were trapped in a county during a week, that factor increased to the maximum value (Model 2). One week was subtracted from onset dates of cases to determine the region's RL during the likely exposure period. RLs in all six regions, positive predictive value (PPV), and sensitivity of both models were compared.

RESULTS: As of 12/11/18, 40 confirmed or probable WNV cases had completed investigations and were reported to ArboNet; two cases occurred prior to MS and were excluded from analysis. In Model 1, 23 weeks were high risk, 89 moderate, and 26 low. In Model 2, 28 weeks were high risk, 92 were moderate, and 18 were low. In Model 1, 10 (26%) persons had likely exposure during high risk weeks compared to 25 (66%) in Model 2. In Model 1, 28 (74%) persons had likely exposure during moderate risk weeks compared to 13 (34%) in Model 2. Zero cases in either model were likely infected during a low risk week. PPV increased from 0.22 in Model 1 to 0.38 in Model 2 and sensitivity increased from 0.19 in Model 1 to 0.56 in Model 2.

CONCLUSIONS: Addition of the two-tier factor for *Culex spp.* in Model 2 increased predictability and sensitivity of Kansas' WNV risk model. Routine evaluation of the WNV surveillance system is crucial to ensure stakeholders receive accurate RL classification to provide appropriate mosquito control and prevention messages to the public.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Disease Prevention; Risk Assessment; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	amie.cook@ks.gov
Presenting Author(s)	Amie Cook
Institution Affiliation	Kansas Department of Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10595
Abstract Type	Quick
Abstract Title	Increasing Incidence of Anaplasmosis in the United States, 2013–2017

Abstract

BACKGROUND: Anaplasmosis, caused by the bacterium *Anaplasma phagocytophilum*, is a tickborne disease of national concern due to its increasing incidence in the United States. The blacklegged tick, *Ixodes scapularis*, is the primary vector in the Northeastern and Midwestern United States where anaplasmosis is most commonly reported. Illness can range from mild to moderate, the most common symptoms are fever, chills, headache, myalgia, and malaise. While the reported case-fatality rate is <1%, predictors of a more severe course of illness include advanced age, immunosuppression, comorbid medical conditions, and delay in diagnosis and treatment.

Doxycycline is the treatment of choice for rickettsial diseases in patients of all ages.

METHODS: Cases of anaplasmosis reported to the Centers for Disease Control and Prevention National Notifiable Diseases Surveillance System (NNDSS) during 2013–2017 were included in this analysis. Incidence rates (IRs) were calculated using U.S. Census Bureau population estimates.

RESULTS: During 2013–2017, 19,151 cases of anaplasmosis were reported to NNDSS, for an average annual IR of 1.3 cases per 100,000 persons. The number of cases doubled from 2,782 in 2013, to 5,762 in 2017, with IRs also increasing from 0.9 to 1.8, respectively. During this time period, the East North Central region reported the most cases with 9,553 (IR=4.1). When adjusting for population, New England had the highest IR of 10.7; this increased from 5.1 in 2013 to 19.0 in 2017. States with the highest IRs included Vermont (27.1), Maine (22.64), New Hampshire (13.1), Minnesota (11.2), Massachusetts (11.1), Rhode Island (10.9), and Wisconsin (10.5); these seven states accounted for 70.3% of all reported cases. Most cases (n=15,740; 82.2%) were reported in persons aged ≥40 years. While the number of cases was highest among persons aged 40–64 years (n=8,323), the IR was highest among persons aged ≥64 years in 2017 at 5.1. Only 78 cases were reported in children aged <5 years.

CONCLUSIONS: During 2013–2017, there was an increase in total number of cases and in the incidence rates of anaplasmosis reported through national surveillance. While anaplasmosis is endemic in the Northeastern and Midwestern states, the Northeastern states have experienced a dramatic increase in cases in recent years. Explanations for this trend may include expansion of the geographic range of *I. scapularis* and increased awareness and testing among providers. The older age predominance is also concerning given the risk of more severe outcomes in these vulnerable populations.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	wwd7@cdc.gov
Presenting Author(s)	Kristen Nichols Heitman
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Investigation of a Bite Inflicted By a Privately Owned Macaque on a Child – Indiana, 2018

Abstract

BACKGROUND: Primates belonging to the genus *Macaca*, also known as macaques, are reservoirs for *Macacine herpesvirus* (B virus), which is a rare cause of neurologic illness and death in humans. B virus can be transmitted via bites, scratches, or contact with body fluids of infected animals. Bites inflicted by nonhuman primates (NHPs) can also transmit rabies virus (RABV), which is endemic in bats in Indiana. Indiana does not regulate the private ownership of NHPs. In July 2018, the Indiana State Department of Health (ISDH) was notified that a privately owned macaque had escaped from its outdoor enclosure and bitten a child.

METHODS: The macaque owner declined humane euthanasia at an exotic animal veterinary clinic and elected instead to dispatch the macaque himself via gunshot to the left lateral chest wall. No veterinary diagnostic laboratories in Indiana accept NHPs, so the cadaver was shipped to a neighboring state for necropsy and pathogen testing. Brain tissue specimens were tested for evidence of RABV and B virus infection by direct fluorescent antibody (DFA) test and polymerase chain reaction (PCR), respectively. Risk assessments were conducted for all potentially exposed persons. Medical records for the bite victim were reviewed. Serum specimens from the bite victim were tested for evidence of B virus infection by Western blot at the National B Virus Resource Center.

RESULTS: The macaque necropsy revealed no gross or microscopic evidence of infectious disease; no evidence of RABV or B virus infection was found. Both the bite victim and the macaque owner received recommendations to complete antiviral prophylaxis and undergo testing for evidence of B virus infection. The owner declined both. The bite victim completed antiviral prophylaxis and also received a course of antibiotics. Serum specimens collected from the bite victim 3 days and 25 days after the bite had no detectable B virus antibodies.

CONCLUSIONS: Privately owned macaques and other NHPs can pose serious health risks to their communities. Injuries inflicted by NHPs therefore require a prompt public health response. Public health and veterinary diagnostic laboratories that routinely test for RABV may not accept or be equipped to test specimens from NHPs due to human health risks. Private owners of NHPs may be reluctant to comply with public health recommendations. Health departments should be prepared for these challenges when responding to bites inflicted by NHPs.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	One Health; Veterinary Public Health; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	tastevens@isdh.in.gov
Presenting Author(s)	Taryn Stevens
Institution Affiliation	Indiana State Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11742
Abstract Type	Quick
Abstract Title	Lyme Disease Cases Acquired in Europe Reported to the Florida Department of Health, 2009–2018

Abstract

BACKGROUND: The majority of Lyme disease cases reported to the Florida Department of Health (Florida Health) are acquired outside the state. This includes cases acquired abroad. Lyme disease outside North America is caused by different serotypes or genospecies. Differences in testing and lack of awareness of Lyme disease among travelers abroad may lead to under-reporting of internationally acquired cases. Multiple health agencies in Europe have reported increased geographical distribution of tick vectors and a rise in incidence of cases being reported. This study analyzes Lyme disease cases with exposure in Europe.

METHODS: Probable and confirmed cases of Lyme disease were classified per the Council of State and Territorial Epidemiologists' national case definition. Cases investigated and reported to Florida Health between January 1, 2009, through December 31, 2018, (as of January 2, 2019) were reviewed and sorted according to import status of acquired outside of the U.S. and origin of exposure in Europe or a European country. Lyme disease incidences in European countries were obtained from data reported by European Centre for Disease Prevention and Control (ECDC) and the World Health Organization.

RESULTS: Twenty-eight cases of Lyme disease with exposure in Europe were reported, with an average of three cases and range of one to five cases per year. Countries of exposure included Austria, Belgium, Czech Republic (3), Denmark, Finland (2), France (3), Germany (5), Hungary, Netherlands, Poland, Scotland, Sweden (2), Switzerland (2), Ukraine, and unspecified European countries (3). Sixteen cases (57%) reported known tick bites abroad, with an additional six (21%) reporting exposure to tick habitats. The majority of cases reported exposure in central Europe, which the ECDC recognizes as the highest area for Lyme disease infection rates on the continent.

CONCLUSIONS: The ECDC currently provides specific Lyme disease educational materials for travelers to Europe. Centers for Disease Control and Prevention has online resources where travelers can search disease information by country of destination, but these resources do not include information on Lyme or other tick-borne diseases by location of travel. Including tick-borne disease risk information in the destination query would be helpful for both travelers and their health care providers. Florida Health is adding information on international tick-borne disease risks to existing resources. A protocol was also created for county epidemiology staff to use when investigating Lyme disease cases with exposure in other countries, as the current Lyme disease case definition only references exposure in high and low incidence U.S. states.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	International Health; Infectious Diseases; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	dana.giandomenico@flhealth.gov
Presenting Author(s)	Dana A. Giandomenico
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Monitoring Bat Rabies in the United States: Considerations for Improved Species Identification and Virus Characterization.

Abstract

BACKGROUND: Species identification and virus characterization data for rabid bats in the United States is limited. Given the implications that bat rabies virus (RABV) variants have for human health, understanding the transmission dynamics of RABV variants within and between bat species is crucial. To date, there has been limited systematic evaluation of virus characterization data of bats submitted to the U.S. national animal rabies surveillance system.

METHODS: The authors evaluated submitted specimens and selected those that merit prioritization for virus characterization. These samples of epizootiological importance (SEI), were selected based on characteristics that would improve detection of sentinel events in disease dissemination. National animal rabies surveillance data, years 2010–2015, were analyzed and the total number of positive samples obtained for each SEI category across the six-year time span was used to calculate the estimated number of samples and confidence intervals that public health laboratories could expect if all SEI underwent RABV characterization. Additionally, we evaluated the number of bats submitted for rabies testing in which species was identified.

RESULTS: The SEI were defined as: rabid non-indigenous bats; rabid bats in southern U.S. border states, Florida, Puerto Rico and the U.S. Virgin Islands; and rabid bats not commonly found to be infected with RABV. During 2010–2015, there were 160,017 bats submitted for testing, including 74,928 (47%) where bats were identified by species. Among the bats with species information included, 33,882 (45%) were defined as SEI. Annually, 692 (95% CI, 600–784) SEI were rabid and 295 (95% CI, 148–442) underwent virus characterization. Performing virus characterization of SEI would result in 387 (95% CI, 287–506) samples each year. In total, 9,552 rabid bats were identified over the six year period, and 2,029 (21.2%) underwent virus characterization.

CONCLUSIONS: Increased RABV characterization of SEI and identification of bat species would help inform our understanding of RABV epizootiology in bat species, some of which have frequent human contact. Laboratory testing of SEI should be evaluated by each public health laboratory to ensure testing does not strain routine diagnostic laboratory capacity.

Submission Complete?	Yes
Committee Topic	Infectious Disease Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Epidemiology; Sustainability
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ydi7@cdc.gov
Presenting Author(s)	Emily G Pieracci
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10857
Abstract Type	Quick
Abstract Title	Potential for Zoonotic Parasitic Transmission in Dog Parks in the Birmingham- Alabama Metropolitan Area

Abstract

BACKGROUND: Visiting dog parks and dog-friendly parks is a popular activity among dog owners. With the rise in the popularity of dog park visits in the Birmingham metropolitan area, the risk of transmission of parasitic infections might be a concern. The objective of this pilot study was to assess the prevalence of parasites in dog stools from dog parks in the Birmingham metro area.

METHODS: In this study, dog fecal samples were collected from dog parks and dog-friendly parks around the Birmingham metro area in two different years (2016 and 2018) and tested for intestinal parasites. Stool sedimentation technique was used and samples were examined microscopically for parasites.

RESULTS: Ten percent of dog fecal samples collected in 2016 were found to be positive (3/30) for larvae and hookworm eggs that may be transmitted to humans. Only one (out of 40) of the samples that were tested in 2018 (2.5%), tested positive for hookworm eggs. The overall percent of specimens positive for parasites in dog feces from the dog parks surveyed was 5.71% (4/70) when using the traditional parasitological method (low sensitivity).

CONCLUSIONS: Even though the overall prevalence of positive dog stool samples and the worm burden were low, this findings indicates that there is a potential risk of zoonotic infection transmission while visiting dog parks and dog friendly parks. Users of parks should be informed and educated on the risk of infection and how to prevent and lower the risk of infection. Specimens from 2018 will be tested using molecular techniques (PCR) next in order to get a better picture of the prevalence of parasites of zoonotic importance in dog feces from dog parks in Birmingham.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Disease Prevention; Zoonotic Diseases; Veterinary Public Health
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	analuna@uab.edu
Presenting Author(s)	Ana L Oliveira
Institution Affiliation	University of Alabama at Birmingham Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	10890
Abstract Type	Quick
Abstract Title	Public Health Response to a Human Rabies Case – Utah, 2018

Abstract

BACKGROUND: On November 3, 2018, the Utah Department of Health (UDOH) was notified of a suspect human rabies case. The patient had onset of symptoms 18 days earlier and was hospitalized for 15 days before rabies was suspected. Laboratory specimens were collected and sent to Centers for Disease Control and Prevention (CDC), which confirmed the patient was infected with a strain of rabies virus associated with the Mexican free-tailed bat. Public health, in partnership with impacted healthcare facilities, conducted an investigation to identify and assess the risk of potentially exposed persons and distribute post-exposure prophylaxis (PEP).

METHODS: Due to the complex nature of the response, UDOH initiated an Incident Command System (ICS) structure to develop and coordinate response activities. The ICS team hosted regular calls for stakeholders and Incident Action Plans were distributed following each meeting outlining actions for the following operational period. To efficiently assess potentially exposed health care workers, an online exposure assessment tool was developed using REDCap and distributed to affected health care facilities. Responses were collected at UDOH and distributed to the health care facilities for distribution of PEP. As UDOH and local health departments were notified of community members who were potentially exposed, public health assessed the exposure risk and individuals recommended to receive PEP were referred to local hospitals.

RESULTS: Investigators learned that the patient handled several bats in the weeks before symptom onset. The patient was hospitalized and received supportive care, but subsequently died as a result of the rabies infection. UDOH held regular ICS calls for three weeks. Overall, public health assessed 30 family and community members who were potentially exposed to the patient and recommended to receive PEP. During the course of illness, the patient was seen at four local hospitals, including two emergency departments, as well as a chiropractic office. The affected health care facilities identified and assessed health care workers who were potentially exposed and 242 completed the online exposure assessment. PEP was provided to 74 (31%) health care workers. The supply of PEP used during the response was coordinated and administered by health care facilities throughout Utah.

CONCLUSIONS: The delayed diagnosis resulted in over 300 individuals potentially exposed to rabies. Structured collaboration between public health partners and health care facilities, as well as the use of online exposure assessment tool allowed for rapid assessment of exposures and timely recommendation of PEP.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Epidemiology; Zoonotic Diseases; Collaboration
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	bbarbeau@utah.gov
Presenting Author(s)	Bree Barbeau
Institution Affiliation	Utah Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	10950
Abstract Type	Quick
Abstract Title	Quantifying Vector Control Response to Human Arboviral Disease

Abstract

BACKGROUND: In New Jersey, vector-borne disease surveillance/control is coordinated between state and local public health and vector control agencies. The New Jersey Department of Health (NJDOH) shares information on human cases of mosquito-borne disease with vector control partners for timely surveillance and control. Although there has been anecdotal evidence on actions taken in response to human case notifications, these actions have not been documented. In 2018, NJDOH implemented a survey to document these efforts.

METHODS: NJDOH designed an online survey (NoviSurvey) that collected information about vector control response, including site visits, public education, surveillance and pathogen testing, and control. After receiving acute arboviral disease laboratory reports, NJDOH notified the New Jersey Department of Environmental Protection (NJDEP), providing the disease, patient address, and date of specimen collection. NJDEP provided this information to the appropriate county mosquito control agency (CMCA) and sent a survey link to the CMCA to complete for each notification. At the end of the season, the data was exported into Excel for analysis.

RESULTS: There were 121 human arboviral notifications between 6/5/18 and 11/18/18. 92 surveys were completed, for a 76% response rate. After human case notification, 39% CMCA's made a home visit and 83% visited the patient's neighborhood. Visits were conducted more often for West Nile virus (WNV) and CA serogroup virus (1 case) and less often for travel associated diseases. Visits were conducted a median of 1 day after notification. Findings included stagnant water, containers or plants holding water, and tires/tire swings. When speaking with homeowners (42%) and neighborhood residents (31%), educational topics included habitat reduction/eliminating standing water, mosquito repellents, and residential spraying. None educated homeowners to treat clothing/gear, or to avoid mosquito bites 3 weeks after travel. CMCA's set mosquito traps during 39% of home visits and 49% of neighborhood visits. When visits were made in response to a WNV human case, 36-38% of sample submissions were positive for WNV. Mosquito control measures included larviciding, adulticiding, and environmental remediation. Control measures were implemented a median of the same day as the visit and 1 day after notification.

CONCLUSIONS: CMCA's provided timely response and control measures after 85% of human arboviral disease notifications. Several CMCA's reported strong collaboration with local health departments to coordinate response and implementation of additional area-wide surveillance and control measures. CMCA response included mosquito control, environmental remediation, and community education. Opportunities exist to improve educational messaging, particularly for travel-associated diseases.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	kim.cervantes@doh.nj.gov
Presenting Author(s)	Kimberly B. Cervantes
Institution Affiliation	New Jersey Department of Health State Public Health Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Rabies Post-Exposure Prophylaxis of Veterinarians and Veterinary Staff Following Contact with Rabid Animals, Kansas 2013 – 2017

Abstract

BACKGROUND: The Advisory Committee on Immunization Practices (ACIP) classifies veterinarians and veterinary staff (VS) at frequent risk for rabies exposure. The most common route of rabies exposure is from a bite; however, non-bite exposures, which rarely cause rabies in the United States (US), should be evaluated on a case-by-case basis. In Kansas, local health departments (LHDs) perform rabies exposure risk assessments and provide rabies post-exposure prophylaxis (PEP) recommendations per ACIP guidelines. Rabies surveillance data was evaluated to characterize veterinarians and VS rabies exposures and to determine if ACIP PEP recommendations were followed.

METHODS: All rabies diagnostic test results were submitted to the Kansas Department of Health and Environment daily from the Kansas State University Rabies Laboratory. Rabies-positive animals were entered into Kansas' electronic disease surveillance system and assigned to the LHD in the county where the animal resided or was found. A standardized rabies risk assessment form, based on ACIP guidelines, was utilized for investigation. LHD investigation included evaluation of all veterinarians and VS in contact with the rabid animal. PEP was recommended based on ACIP exposure risk. From 2013 – 2017 veterinarians and VS contacts of rabies-positive animals were evaluated for: 1) exposure status, 2) PEP recommendation, and 3) compliance with PEP recommendation.

RESULTS: There were 324/5515 rabies-positive animals; 76% wildlife and 24% domestic. Cattle (n=32) and cats (n=28) were the most frequent rabid domestic animals. Sixty-one veterinarians and VS were evaluated; 52 for exposure to livestock and 9 for exposure to small animals. PEP was recommended for 16/52 veterinarians and VS exposed to livestock of which 63% (10/16) were non-bite exposures. Eleven veterinarians and VS considered not exposed and 23 with unknown exposure to rabid livestock received PEP outside of ACIP recommendations. Nine of sixty-one veterinarians and VS were potentially exposed to a rabid small animal. PEP was recommended for 56% (5/9); all for non-bite exposures. No additional veterinarians or VS received PEP due to a small animal exposure.

CONCLUSIONS: To our knowledge, this is the first evaluation of PEP recommendations and compliance of veterinarians and VS in the US. Despite ACIP recommendations for PEP based on exposure risk, veterinarians and VS received PEP outside of ACIP guidelines. Veterinarians and VS should adhere to veterinary standard precautions to reduce potential non-bite exposures. It is crucial that veterinarians and VS understand ACIP recommendations to make informed decisions regarding PEP and to provide accurate information to clients with rabid animals.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Occupational Health; One Health
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Chelsea.Raybern@ks.gov
Presenting Author(s)	Chelsea Raybern
Institution Affiliation	Kansas Department of Health and Environment State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11125
Abstract Type	Quick
Abstract Title	Raccoons, Cats, and the Odd Otter, Oh My! - Rabies Virus Surveillance, Identification, and Prevention in Miami-Dade County, 2018

Abstract

BACKGROUND: In Florida, it is estimated that at least 60,000 residents and visitors are bitten each year by a domestic or wild animal. A *rabies virus exposure* is any bite, scratch, or other contact in which saliva or nervous tissue of a suspect or known rabid animal enters an open or fresh wound or encounters mucous membranes by entering the eye, mouth, or nose of another animal or person.

METHODS: The Florida Department of Health in Miami-Dade County (DOH Miami-Dade) monitors possible animal-to-human rabies transmission through the investigation of all individuals exposed to a suspected rabid animal and/or those that receive or are recommended to receive post-exposure prophylaxis (PEP). Data for animal bites/exposures and animals sent for rabies virus testing between January 1 and December 31, 2018 were abstracted from Merlin, the Florida Department of Health Surveillance System and analyzed using SAS v9.4.

RESULTS: Between January 1 and December 31, 2018, DOH Miami-Dade received 2,094 reports of animal bites/exposures among Miami-Dade County residents, of which 449 (21.4%) met case definition as a possible exposure. Among these, 249 (55.5%) occurred among women, and 266 (59.2%) occurred among individuals of Hispanic ethnicity. Median age was 33 (range 0 to 99). The vast majority (426, 94.9%) of exposures were bites with most individuals sustaining a single bite/wound in a specific area (351, 78.2%). Among individuals with a single exposure site, exposures to the arm or hand were most frequently reported (197, 56.1%). High priority exposures, defined as those occurring to the head or neck, occurred in 7.3% of all reports, regardless of if the individual sustained bites/wounds in a single area or multiple areas. Among the 449 individuals who met case definition as a possible exposure, 336 (74.8%) were recommended PEP of whom 166 (49.4%) initiated treatment; 160 (47.6%) were lost to follow-up. Among all reported animals involved in potential exposures, dogs accounted for the majority of events (301, 67.0%) followed by cats (108, 24.1%) and other wild animals, including raccoons, monkeys, rats, and bats (21, 4.7%). Of 195 animals sent for rabies virus testing, 11 (5.6%) were positive, a nine-fold increase from the previous three-year average.

CONCLUSIONS: In 2018, Miami-Dade County saw a significant increase in rabies positive animal identification. Although human rabies is rare, the potential risk of transmission from animals and humans remains. Enhanced surveillance is necessary to ensure that individuals potentially exposed to rabies virus undertake the proper preventative measures to mitigate infection.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Surveillance; Infectious Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Danielle.Fernandez@flhealth.gov
Presenting Author(s)	Danielle Fernandez
Institution Affiliation	Florida Department of Health in Miami-Dade County Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11653
Abstract Type	Quick
Abstract Title	Raising the Standard: Reviewing Positive Predictive Values of Spotted Fever Rickettsiosis Titers and Assessing Surveillance in the Context of the Current National Case Definition -- Georgia, 2018

Abstract

BACKGROUND: Spotted fever rickettsioses (SFR) are tickborne bacterial diseases caused by pathogens in the genus *Rickettsia*. The indirect immunofluorescence assay (IFA) is the most common reference test for laboratory identification of SFR. The current national case definition for a confirmed case of SFR (2010) requires clinically compatible symptoms and an IFA immunoglobulin G (IgG)-specific antibody titer of at least 1:64 drawn in the first week of illness, with a fourfold change in convalescent titer drawn 2-4 weeks later. This study reviews positive predictive values of SFR titers and assesses SFR surveillance in Georgia in the context of the current national case definition.

METHODS: The Georgia Department of Public Health receives electronic and paper reports of SFR via notifiable disease reporting. Suspect case-patient data are uploaded to the State Electronic National Disease Surveillance System (SendSS). Epidemiologic, clinical, and IFA IgG laboratory testing data from 2018 were analyzed and characterized according to the SFR national case definitions and positive predictive values (PPV) for different titer levels were calculated. This analysis was restricted to suspect-cases with laboratory draw dates in 2018 and investigations completed by December 18th, 2018.

RESULTS: IFA IgG results were analyzed from 478 suspect SFR case-patients. Sixty eight percent (326) of these reports were fully investigated, of which 18% (58) were found to meet clinical criteria for a case, with one confirmed SFR case in 2018. The PPV was 0.15 for an initial titer of 1:64, 0.20 for an initial titer of 1:128, and 0.20 for an initial titer of 1:256 or greater. Only 7% (33) of cases reported a convalescent draw, with 1% (5) during the appropriate time frame to meet the case definition. Eleven percent (55) of investigations had a date of onset that differed from the date their lab was drawn.

CONCLUSIONS: Cases with an initial titer of 1:64 had the lowest PPV but none were greater than 0.20, demonstrating a high background of SFR seroprevalence in Georgia. Many cases who met clinical criteria remained classified as probable because they lacked a convalescent titer in the appropriate time period. Additionally, as the lab date is often used as the default date of onset, it is difficult to determine how long after onset of symptoms a patient is tested. These limitations question the accuracy of diagnosis of SFR in Georgia and highlight sensitivity flaws with the most commonly reported form of SFR laboratory testing.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Local Epidemiology; Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	skyler.brennan@dph.ga.gov
Presenting Author(s)	Skyler Brennan
Institution Affiliation	Georgia Department of Public Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11208
Abstract Type	Quick
Abstract Title	Record Number of Malaria Cases Imported into the United States, 2016

Abstract

BACKGROUND: Malaria is a potentially life-threatening disease caused by *Plasmodium* parasites, transmitted through infective mosquitos. Typically, malaria infections in the United States (U.S.) are imported among persons who traveled to regions with ongoing malaria transmission. Rarely, malaria is acquired within the U.S. through exposure to contaminated blood products, congenital transmission, nosocomial exposure, or local mosquito-borne transmission.

METHODS: Confirmed malaria cases diagnosed by microscopy and polymerase chain reaction (PCR) were reported to health departments, who conducted case investigations. Case reports were transmitted to CDC through the National Malaria Surveillance System, the National Notifiable Diseases Surveillance System, or direct CDC consultations.

RESULTS: In 2016, CDC received 2,078 confirmed malaria case reports, including two congenital cases, three cryptic cases, and one case acquired through blood transfusion. This is the highest number of imported malaria cases in the U.S. since 1972. Compared to recent years, the number of cases reported in 2016 is an 18% increase from the 2010 – 2014 average (1,754 cases annually), and a 36% increase from 2015 (1,524 cases). Note that in 2015, coinciding with the Ebola virus disease (Ebola) outbreak in West Africa, the associated health notices and post-travel monitoring, there was an 11.6% decrease in malaria cases (1,524 cases), compared to 2014 (1,725 cases). In 2016, approximately 80% of cases originated from Africa, and more than 60% of these were from West Africa. In 2016, *P. falciparum* accounted for more than two-thirds of the infections, followed by *P. vivax* (12%), fewer than 5% of cases were infected with *P. ovale*, *P. malariae*, or mixed species infections; the species was not known for approximately 10% of cases. PCR testing confirmed approximately one-third of cases. Approximately 15% of patients had severe malaria, and seven people died. Of the U.S. resident patients who reported purpose of travel, approximately 70% were visiting friends or relatives. Among U.S residents, 94% of patients with malaria did not adhere to, or take a CDC-recommended chemoprophylaxis regimen.

CONCLUSIONS: After the U.S. observed a decrease in imported malaria cases in 2015, likely associated with the Ebola outbreak, cases rebounded from West Africa and across Africa, and a record number of malaria cases were imported in 2016. Since the early 2000s, there has been worldwide success to reduce the malaria disease burden, although progress has plateaued in recent years and malaria remains endemic in many regions, and the use of appropriate chemoprophylaxis medications by travelers is inadequate.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	igd3@cdc.gov
Presenting Author(s)	Kimberly E Mace
Institution Affiliation	Centers for Disease Control and Prevention Federal Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11798
Abstract Type	Quick
Abstract Title	Selected Cardiac Abnormalities in Trypanosoma Cruzi Serologically Positive, Discordant, and Negative Government Working Dogs

Abstract

BACKGROUND: Chagas disease is increasingly recognized in the southern U.S., where triatomine vectors transmit *Trypanosoma cruzi* among wildlife and domestic dogs with occasional vector spillover to humans. Clinical outcome in canines is variable ranging from asymptomatic infections to chronic heart disease to acute death. In order to characterize cardiac manifestations of *T. cruzi* infections, we tracked a cohort of naturally-infected government working dogs and a matched cohort of uninfected dogs. We hypothesized that selected measures of cardiac disease (abnormal rate, abnormal rhythm, and elevated cardiac troponin I (cTnI; a biomarker of cardiac injury)) would occur more commonly in infected than uninfected dogs matched by age, breed sex and location.

METHODS: We placed an ambulatory ECG monitor (Holter) on 41 dogs including 17 *T. cruzi* -infected, 18 uninfected dogs and 6 dogs with discordant results as measured by three independent serological tests.

RESULTS: The presence of ECG abnormalities varied by *T. cruzi* infection status ($p=0.006$), where 76.5% of positive, 100 % of discordant, and 33.3% of negative dogs showed ≥ 1 abnormality. The most common cardiac abnormalities included supraventricular and ventricular arrhythmias and atrioventricular block. Infected dogs had more distinct types of ECG abnormalities than uninfected dogs, with discordant dogs not different from either group ($(2) = 7.95, p=0.019$). Infected dogs had higher serum concentrations of cTnI than both uninfected dogs ($p=0.044$) and discordant dogs ($p=0.06$). Based on dog handler reports, nearly all (4/5; 80%) dogs with reported performance decline or fatigue were infected dogs.

CONCLUSIONS: Understanding the cardiac manifestations of natural *T. cruzi* infections in dogs is critical for prognostication and to establish a baseline for interpreting data from intervention studies. The cardiac manifestations of Chagas disease in these highly valued working dogs is likely associated with a yet- unquantified impact on their ability to work, economic and security consequences.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	ameyers@cvm.tamu.edu
Presenting Author(s)	Alyssa Meyers
Institution Affiliation	Texas A&M University Academic Institution

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Tick-Borne Relapsing Fever in an Area with a Previous Known Cluster

Abstract

BACKGROUND: In September 2018, the National Park Service (NPS) Office of Public Health (OPH) learned of a confirmed Tick Borne Relapsing Fever (TBRF) case in an NPS employee who lived in a group of cabins where there had been a cluster of at least four TBRF cases two years prior. Because the development of a new case suggested ongoing exposure risk, we investigated in order to identify areas for potential improvement in communication and education, integrated pest management (IPM), and illness recognition and reporting.

METHODS: The NPS OPH led a collaborative effort with the park, the NPS IPM, and the California Department of Public Health that included a site visit. Prior to the visit, we distributed a survey to employees aimed at better understanding current thoughts and practices related to TBRF and other rodent-associated diseases. During and prior to the visit, the team met with various work groups in the park, as well as a physician who lived at the site and was instrumental in diagnosing the most recent case. The team also toured park cabins and facilities to help identify areas of rodent ingress and offer recommendations for rodent exclusion.

RESULTS: The majority of the 62 park employees who completed the pre-visit survey identified rodent-related concerns in their home or workplace. Barriers to removing/excluding rodents included the high numbers of rodents in the areas, difficulty excluding them, limited resources for maintenance work, and lack of information on best practices. During the building inspections, we noted areas of potential rodent inclusion. In response to these findings, the team developed an integrative, multi-faceted approach aimed at empowering employees. This approach included education about rodent-exclusion techniques, suggestions for and some provision of materials, including copper mesh, snap traps, spray foam, and hardware cloth, suggestions for enhancing integrated pest management within the park, and information for employees to help them seek medical care when appropriate. Tools developed included an internal employee web page on preventing rodent-associated diseases, a rodent-exclusion supply list, a reporting scheme for employee illness, an employee handout on diseases encountered in a wilderness setting designed them to recognize possible exposures and symptoms, and an employee wallet card to present to healthcare providers when seeking medical care.

CONCLUSIONS: A case of TBRF in a National Park site where there had been a previous cluster demonstrated the need for ongoing efforts to prevent rodent-associated disease. XX

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Disease Prevention; Infectious Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	maria_said@nps.gov
Presenting Author(s)	MA Said
Institution Affiliation	National Park Service Federal Agency

Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Understanding the Burden of Typhus Group Rickettsioses in the United States Using a Large, Insurance Claims Database

Abstract

BACKGROUND: Typhus group rickettsioses (TGR) are vector-borne diseases that include *Rickettsia typhi* (murine typhus) and *R. prowazekii* (epidemic typhus). Improvements in pest management, hygiene, and sanitation led to dramatic decreases in disease incidence during the 20th century. While both diseases are still present in the United States, little is known about their national prevalence, as neither is nationally notifiable. In order to understand the TGR burden in the United States, we summarized nationally representative administrative claims data from a large, commercially insured population.

METHODS: We conducted a descriptive retrospective analysis using the 2003–2016 Truven Health MarketScan® Commercial Claims and Encounters databases. We included any individual <65 years of age with an inpatient admission or outpatient visit with a TGR code from the International Classification of Diseases, Ninth or Tenth Revisions, Clinical Modification (ICD-9/10-CM). The first record with TGR was considered the incident diagnosis. Epidemiologic characteristics associated with the incident diagnosis were summarized for all individuals, and changes in disease patterns during the study period were evaluated.

RESULTS: From 2003–2016, we identified 1,799 unique patients with an ICD-9/10-CM code for a TGR. Average annual incidence was 4.5 patients per 1,000,000 person-years (range: 2.3–5.8/1,000,000 person-years). Epidemic typhus was the most common typhus group rickettsiosis diagnosed among 931 patients (51.8%), followed by murine typhus (n = 722; 40.1%). Recrudescence infection with *R. prowazekii*, known as Brill-Zinsser disease, occurred in 146 patients (8.1%). The majority of patients diagnosed with a TGR were female (n = 1019; 56.6%) and the median age was 42 years (range: 0–64 years). Most patients resided in the Northeast (n=695; 38.6%) and South (n=661; 36.7%) regions, though the incidence rate was almost three times higher in the Northeast (11.6/1,000,000 person-years) compared to the South (4.1/1,000,000 person-years). Hospitalizations were rare (n=74; 4.1%).

CONCLUSIONS: TGR are rarely diagnosed diseases among the U.S. commercially-insured population. More patients were diagnosed with epidemic typhus than murine typhus, even though *R. prowazekii* transmission requires body louse or flying squirrel exposure. Patients from all geographic regions were diagnosed with murine typhus and epidemic typhus, despite both diseases having limited geographical ranges. Insurance claims data do not incorporate symptoms or diagnostic information making validation of cases impossible. The misalignment of the epidemiology of insurance claims data versus historic, published TGR data suggests more studies are needed to determine the true burden of TGR in United States.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	ICD; Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	imv5@cdc.gov
Presenting Author(s)	Cara C. Cherry
Institution Affiliation	Centers for Disease Control and Prevention CDC

Submission Type	Breakout/Quick/Lightning/Poster
ID	10605
Abstract Type	Quick
Abstract Title	Using Citizen Science to Enhance Surveillance of the Mosquito Vector <i>Aedes Aegypti</i> in Arizona, 2015–2017

Abstract

BACKGROUND: Vector surveillance is an essential component of vector-borne disease prevention, however, some communities lack resources to support extensive mosquito surveillance. *Aedes aegypti* mosquitoes have an established presence in Arizona and are one of the primary vectors of the arboviruses Zika, dengue, and chikungunya, remaining a threat for local disease transmission. To better describe *Ae. aegypti* distribution statewide, the Great Arizona Mosquito Hunt (GAMH) was launched during 2015–2017 in a collaboration between the Arizona Department of Health Services and other public health and academic partners. We aimed to assess the utility and feasibility of enlisting citizen scientists (general citizens who contribute their knowledge, tools, or resources) to add to *Ae. aegypti* surveillance efforts with a focus to enhance surveillance capacity in more rural Arizona regions.

METHODS: In August 2015, all 415 Arizona high schools were automatically enrolled using an introductory email unless they specifically opted out. We sent participating schools and youth organizations instructions and oviposition trap (ovitrap) kits which collect only mosquito eggs. They then conducted ovitrapping for 1–4 weeks during peak *Ae. aegypti* season in Arizona and returned the egg sheets to collaborating entomologists for identification. In 2016 and 2017, all schools that returned egg sheets the previous year were automatically enrolled. Schools who did not participate in the previous year(s) were invited to register to participate using an online enrollment form.

RESULTS: During the three years of the GAMH, 120 different schools or youth organizations participated. A total of 879 egg sheets were received and checked for *Aedes* eggs; during 2015–2017, respectively, 51%, 67%, and 48% of respondents indicated they believed they caught eggs. In contrast, relatively few participants had confirmed positive egg sheets (4%, 38%, 13% respectively). Three new areas in Arizona were identified that were not previously reported to have presence of *Ae. aegypti*. In 2017, 95% of respondents indicated that GAMH increased student engagement in classroom science.

CONCLUSIONS: Overall, the GAMH successfully engaged Arizona schools in mosquito surveillance, created hands-on educational opportunities in classrooms, and documented *Ae. aegypti* populations within Arizona from several areas that were not identified by routine mosquito surveillance during previous years. Our results suggest this youth-based citizen science approach could be a useful tool; collaborations between public health officials and the general public can improve the public's knowledge of mosquito-borne disease while providing valuable information for public health response planning and increasing overall preparedness to meet emerging arboviral threats.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Collaboration; Surveillance; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	heather.venkat@azdhs.gov
Presenting Author(s)	Heather Venkat
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type	Breakout/Quick/Lightning/Poster
ID	11351
Abstract Type	Quick
Abstract Title	West Nile Virus Disease Burden in the City of Houston, 2014-2018

Abstract

BACKGROUND: West Nile Viral disease (WNV) is a vector-borne condition that is transmitted through an infected mosquito. It is considered the leading cause of domestically acquired arboviral disease in the United States. In general, majority of the cases are asymptomatic. One in five people who are infected will display mild symptoms like fever, headache, body ache, nausea and vomiting. Only about 1 in 150 infected people will develop serious neurologic complications such as encephalitis and meningitis. According to CDC, in 2017, in the State of Texas, there were total of 133 confirmed cases including 5 deaths and 14 presumptive blood donors. Out of the confirmed cases, there were 85 neuroinvasive and 48 non-neuroinvasive cases. The purpose of this study is to present and summarize the epidemiologic and clinical distribution of confirmed West Nile cases in Houston, Texas, from 2014-2018.

METHODS: Data were extracted from Houston's Electronic Disease Surveillance System (HEDSS) from January 1, 2014 to December 31, 2018. A total of 130 confirmed cases were analyzed to examine the epidemiologic and clinical characteristics of confirmed WNV cases. SAS statistical software was used to conduct statistical analyses. Case severity was determined (West Nile neuroinvasive disease [WNNV] and West Nile fever [WNF]) according to CDC's criteria, 2014.

RESULTS: During 2014-2018, a total of 531 human WNV cases were reported to Houston Health Department (HHD). 130 cases were confirmed, including 98 (75%) WNNV, (25%) WNF and 4 deaths. Males accounted for 68% of cases. About 60% of all cases occurred in persons aged 50-79. Whites (42%) had the highest number of confirmed cases followed by Hispanics (26%). Approximately 87% of the cases resulted in hospitalization. WNF cases mostly presented with fever (92%), headache (67%) followed by chills (62%). WNNV cases showed up with altered mental status (47%), stiff neck (37%), Ataxia (8%), and seizure (8%).

CONCLUSIONS: WNV is mostly prevalent in males, White adults over 60 years of age, with majority of cases has common neuroinvasive symptoms like altered mental status, stiff necks, Ataxia. For non-neuroinvasive cases has clinical symptoms like fever, headache, and chills and rigors. WNV infection is a markedly underreported disease as most of the infected people do not seek medical care due to mild or no symptoms. Currently there are no specific treatment available. Thus, continued monitoring and surveillance activities are warranted for prevention and control of WNV complications as well as decreasing the risk of infection.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Waterborne Disease; Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	razina.khayat@houstontx.gov
Presenting Author(s)	Razina Khayat
Institution Affiliation	City of Houston Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11721
Abstract Type	Quick
Abstract Title	Why Should We Do PCR? Assessment of Clinician Acute Arboviruses Test Ordering Practices

Abstract

BACKGROUND: Zika (ZIK) and dengue (DEN) viruses are flaviviruses with similar geographic distributions and clinical presentations and can be cross-reactive on antibody testing. Polymerase chain reaction (PCR) testing can detect viral ribonucleic acid (RNA) in acute infections and is available commercially. Additionally, secondary DEN infections may result in a low immunoglobulin (Ig)M antibody titer and early IgG elevation, making PCR the best way to confirm an acute DEN infection. Understanding provider test ordering practices can help inform clinician outreach and improve public health surveillance.

METHODS: Florida Department of Health epidemiologists work with commercial laboratories to forward select flavivirus positive samples to the state public health laboratories (SPHL) for confirmatory testing. Obtaining acute symptom onset date, required symptoms, recent travel history, and sample collection dates are pivotal to the laboratory testing algorithm. SPHL relies on state and county epidemiologists to acquire this information before assigning testing, if samples arrive without appropriate paperwork. Epidemiologists confirm and evaluate other epidemiologic information from providers to request additional arboviral testing from SPHL and to obtain convalescent samples as needed. SPHL and commercial laboratory results from confirmed and probable DEN and ZIK cases with symptom onset between January 1, 2016, and December 18, 2018, were reviewed to assess gaps in testing requested by providers.

RESULTS: Of the 70 PCR-positive DEN cases at SPHL, only one had provider-ordered PCR testing. Sixty-seven of these had DEN serology ordered commercially; thirteen had only significantly elevated IgG, which does not meet national DEN case definition criteria. Two additional cases had only ZIK or chikungunya commercial testing ordered. Among the 76 PCR-positive ZIK cases at SPHL, 51 had provider-ordered PCR and nine had only ZIK serology ordered. Commercial DEN serology was ordered for 62 of the ZIK cases.

CONCLUSIONS: Thirteen DEN and sixteen ZIK cases were identified that likely would not have been reported due to initial testing selection. Arboviral disease reporting helps drive mosquito control activity in Florida. In addition, molecular testing provides more disease-specific testing, which is particularly relevant for ZIK-linked birth defects. PCR serotyping of acute DEN cases also provides important epidemiologic information. The Centers for Disease Control and Prevention recommends both DEN and ZIK PCR when either is suspected as an acute illness; relying exclusively on IgM testing is not recommended. Health care providers should be encouraged to order PCR testing for suspected acute flavivirus patients and consider all clinically similar arboviruses endemic to the exposure location.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Epidemiology; Infectious Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	Blake.Scott@flhealth.gov
Presenting Author(s)	Blake L. Scott
Institution Affiliation	Florida Department of Health State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11530
Abstract Type	Quick
Abstract Title	Zika Virus — U.S. Virgin Islands, January 2016–January 2018

Abstract

BACKGROUND: Zika virus (ZIKV) is a mosquito-borne flavivirus that can cause asymptomatic infection, or fever, rash, and congenital malformation, including microcephaly. In the U.S. Virgin Islands (USVI), *Aedes aegypti*, the primary ZIKV vector, caused prior arbovirus epidemics, including the 2014 chikungunya virus epidemic that ceased after ~1 year. ZIKV emerged from Brazil and rapidly spread during 2015–2016 throughout the Americas. USVI consists of 3 main islands, including St. John (population ~4,000), St. Thomas (population ~52,000), and St. Croix (population ~51,000). We describe the epidemiology of the USVI ZIKV outbreak.

METHODS: ZIKV confirmed disease was defined according to the CSTE case definition. During January 2016–December 2018, serum samples and case-report forms were obtained from all pregnant women seeking prenatal care and persons who sought health care in USVI with ≥2 of the following clinical signs: fever, rash, arthralgia, conjunctivitis, or myalgia. ZIKV immunoglobulin M antibody, polymerase chain reaction, and plaque reduction neutralization testing were used to confirm ZIKV infection.

RESULTS: In total, 1,031 clinical cases were detected during January 3, 2016–January 24, 2018 (no additional cases have been detected as of January 3rd, 2019), with 919 (89%) detected during July–December 2016. Of those with data, patients' median age was 37 years (range: 0–84 years); 680/1028 (66%) were female, including 136 pregnant women. Rash (763/1030; 74%) and arthralgia (647/1030; 63%) were the most commonly reported clinical signs. ZIKV rates were higher on St. John (89 cases; 2225 cases/100,000 persons) and St. Thomas (685 cases; 1317 cases/100,000 persons), compared with St. Croix (257 cases; 504 cases/100,000 persons).

CONCLUSIONS: ZIKV affected populations throughout USVI. The majority of transmission occurred during July–December 2016 and ceased in January 2018, possibly because of herd immunity, environmental factors, or declining circulation of ZIKV in the Americas.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Epidemiology; Outbreaks; Vectorborne Disease
Consider for Different Presentation?	Yes
Presenting Author Email Address(es)	springer.browne@doh.vi.gov
Presenting Author(s)	A. Springer Browne
Institution Affiliation	Centers for Disease Control and Prevention EIS/CEFO

Submission Type ID	Roundtable
Abstract Type	11331
Abstract Title	Roundtable
	Haemaphysalis Longicornis: Collaborating to Explore the Implications of a Newly Emerging Tick Species

Abstract

Key Objectives:

- Discuss the surveillance methods used to collect *Haemaphysalis longicornis* where this tick has been detected
- Discuss the latest findings and diagnostic options for both genotyping and human pathogen detection in *Haemaphysalis longicornis*
- Describe state responses and interstate collaboration efforts in conducting surveillance and outreach for the emergence of *Haemaphysalis longicornis*

Brief Summary:

In November 2017, the New Jersey Department of Agriculture confirmed the presence of *Haemaphysalis longicornis*, also known as the Asian longhorned tick, in Hunterdon County on a sheep that had not traveled off the property in years. As of December 2018, *H. longicornis* has been confirmed in eight additional states, mostly in the eastern United States. *H. longicornis* is an ixodid tick with a wide host range and complex life cycle that is native to East Asia and commonly found in New Zealand and Australia. In these areas, *H. longicornis* has been associated with animal and human health conditions such as *Theileria* infections in cattle and severe fever with thrombocytopenia syndrome virus and *Rickettsia japonica* in people. In addition, studies in Asia have identified *H. longicornis* infected with various species of pathogens capable of causing tickborne disease such as *Borrelia* and *Anaplasma*. No established population of this tick species, native to Asia, has ever been previously documented in the United States. Historical records, however, indicate individual ticks of this kind have been collected in the United States before 2017. Multiple partners from agriculture and public health agencies as well as academic institutions have engaged in efforts to assess the epidemiology and potential public health impact of this tick in the United States. A roundtable discussion is needed to discuss the ongoing efforts and challenges including (1) surveillance methods used to detect *H. longicornis*, (2) potential range and distribution of this tick (3) genetic testing of *H. longicornis* as it relates to geographic origin, (4) human pathogen testing to inform public health impact, (5) assessing human encounter rates with *H. longicornis*, and (6) intervention strategies. Further, opportunities for continued collaboration among stakeholders in the areas of tick surveillance, testing and control, and public health messaging will be discussed.

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Collaboration; Zoonotic Diseases
Consider for Different Presentation?	No
Presenting Author Email Address(es)	carl.williams@dhhs.nc.gov; julia.murphy@vdh.virginia.gov
Presenting Author(s)	Carl Williams; Julia Murphy
Institution Affiliation	North Carolina Department of Health and Human Services State Public Health Agency