

Submission Type

ID

Abstract Type

Abstract Title

Abstract

Committee

Topic

Keywords

Consider for
Different
Presentation?

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Submission Type Breakout/Quick/Lightning/Poster

ID 10252

Abstract Type Breakout

Abstract Title Automated Electronic Lab Reporting for Antibiotic Resistance Surveillance through Statewide Susceptibility Reporting on an Expanded List of Isolates

Abstract

BACKGROUND: Antibiotic resistance is a growing public health problem and requires public health best practices for detection/tracking emerging resistance for emergency response/containment, and for assessing judicious antibiotic prescribing initiatives. Described here is a unique statewide antibiotic resistance surveillance initiative incorporating: 1) reportable disease regulations mandating the reporting of susceptibilities and expanding the list of reportable organisms; 2) automated electronic laboratory reporting(ELR) into a NEDSS application; 3) SQL/SAS processing of data to generate an antibiotic datamart for analysis, assessment, and response.

METHODS: Iterations of the Nebraska Reportable Disease regulations from 2001, 2010, and 2017 progressively expanded the laboratory requirement to report bacterial isolates with associated antimicrobial susceptibilities, formatted per national ELR guidelines. By 2017, there were 36 mandated reportable bacterial isolates, including all Staph aureus, enterococcus, Klebsiella, Enterobacter, Pseudomonas, pneumococcus, and Serratia isolates. All designated reportable organisms are routinely included as part of the overall interface development work for automated ELR. Successful interfaces have been implemented with Cerner, Sunquest, Epic Beaker, McKesson, Meditech, and Orchard lab information systems. SQL/SAS programs extract and process the data into a simple spreadsheet where each isolate represents a record in the database, and include patient name/demographics, date of specimen collection, specimen source, reporting facility, MIC/interpretation, date of admission/discharge and patient location within the hospital (PV1 data). Isolates are deduplicated based on patient name, organism, and date of specimen collection (only one species isolate per patient per 30 day period). Classes of antibiotics (n=18) were defined in collaboration with antibiotic resistance experts to assess for multiclass resistance (Ansamycin, Aminoglycosides, Cephalosporins, Folate, Glycopeptides, Lincosamides, Lipopeptides, Macrolides, Metronidazole, Monobactams, Nitrofurantoin, Oxazolidine, Penicillins, Phenicol, Phosphonics, Polymyxin, Quinolones, Tetracyclines).

RESULTS: Analysis of 2017 data showed the following: total isolates (n= 66,654), deduplicated isolates (n= 51,550), top five genera (Staphylococcus aureus [22%], E coli [38%], Klebsiella [12%] enterococcus [9%] and Pseudomonas [6%]). The distribution of multiclass resistance was: 11%, 6%, 2%, 0.9%, 0.2%, 0.02% for 4, 5, 6, 7 and 8 class-resistance, respectively. E coli (46%), Klebsiella (15%), and Staph aureus (14%), accounted for 75% of the 534 isolates with >=6-class resistance. Carbapenimase resistance was detected in 465 (0.9 %) of de-duplicated isolates (Pseudomonas [n=363, 78%], Enterobacter [n=41, 9%], and Strep pneumo [n=17, 4%]).

CONCLUSIONS: Meaningful-use approved LISs can meet antibiotic susceptibility reporting requirements of current implementation guides. This system tracks carbapenimase resistance, anticipates broader antibiotic resistance challenges, and can track the need for and impact of judicious antibiotic prescribing intervention programs.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Antimicrobial Resistance; Electronic Laboratory Reporting (ELR); Meaningful Use

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10141

Abstract Type Breakout

Abstract Title Development of a State-Wide Antibigram Using Electronic Lab Reporting

Abstract

BACKGROUND: Antibigrams are an important tool for informing appropriate antibiotic selection. Typically, antibigrams are developed by a hospital or laboratory in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines for selecting one isolate per patient per 30 days and only reporting susceptibilities on organisms for which at least 30 isolates were tested. Several state health departments have been able to obtain and combine data from multiple facilities in order to develop state or regional antibigrams. This approach is limited since it relies on facilities to comply with CLSI guidelines and report accurately. Further, an institution would likely not report on organisms for which fewer than 30 isolates were tested. The Nebraska Department of Health and Human Services (NDHHS) sought to use electronic lab reports of organisms along with susceptibility results to develop a novel approach to creating a state-wide antibigram.

METHODS: In accordance with state regulations, electronic reports of culture results with susceptibility patterns were received in real-time into the Nebraska Electronic Disease Surveillance System (NEDSS). For results reported in 2017, custom Statistical Analysis Software (SAS) code was developed to create a line list of all organisms with culture results as well as demographic variables and information on ordering and reporting facilities. Additional SAS code was developed to reflect CLSI guidelines and restricted to Nebraska residents only. This information was used to populate a state-wide antibigram.

RESULTS: During January 1, 2017 to December 31, 2017 there were 51,550 unique isolates reported from 27 facilities. The antibigram includes 4 gram positive and 14 gram negative organisms. In particular, among *Streptococcus pneumoniae*, 4% (N = 21) of 593 isolates tested were intermediate to penicillin and 12% (N = 72) were resistant. Additionally, among *Klebsiella pneumoniae*, 0.2% (N = 12) of 5,111 isolates tested were intermediate to a third generation cephalosporin and 4% (N = 190) were resistant.

CONCLUSIONS: We used a novel approach to develop a state-wide antibigram based on electronic laboratory reports. This data is received in real-time and allows for a more direct, comprehensive, and timely assessment of antimicrobial susceptibility patterns across the state. This data can be customized to evaluate a particular geographic region, facility, or type of specimen and will provide critical guidance for providers, especially in remote or resource-limited areas as well as valuable insight into resistance trends across the state, such as for community acquired pneumonia due to *Streptococcus pneumoniae* and *Klebsiella pneumoniae*.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Electronic Laboratory Reporting (ELR); Informatics; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9448
Abstract Type	Breakout
Abstract Title	Identification of Facilities at-Risk of Receiving Patients Colonized with Carbapenem-Resistant Enterobacteriaceae

Abstract

BACKGROUND: When patients are admitted over time to multiple healthcare facilities (“patient sharing”), the risk for transmission of multi-drug resistant organisms (MDRO), specifically carbapenemase producing Carbapenem-Resistant Enterobacteriaceae (CP-CRE), is increased. We developed an interactive web interface for visualization of the patient sharing network among healthcare facilities in Tennessee (TN). The goal of this tool is to assist team members to identify facilities at-risk of receiving patients with a MDRO for public health interventions.

METHODS: Using the statewide hospital discharge data (HDDS) from 2014 -2016 and aggregated facility-level patient sharing data from the Centers for Medicaid and Medicare Services' (CMS) Minimum Dataset (MDS) 2014, we constructed patient sharing networks through direct patient transfers and total patient transfers including indirect transfers with up to 30, 56, and 365 days of intervening stays in community. HDDS data contains all admissions to 154 TN hospitals and MDS data contains admissions of all CMS fee-for-service beneficiaries to 138 TN hospitals and 327 TN nursing homes. Year-to-date CP-CRE TN surveillance case counts for 2017 from the National Electronic Disease Surveillance System (NEDSS)-base system was aggregated by facility. Social network analysis and visualization and were conducted using STATNET and visNetwork packages in R. The interactive web platform was developed using the Shiny package in R and hosted locally within Tennessee Department of Health

RESULTS: Authorized users can access the Shiny web application to visualize the patient sharing network of a facility of interest (ego) without having to develop code. Users can tailor visualization based on the year, data source (HDDS or MDS), length of intervening stays in the community, ego facility, and the lower threshold of the number of transfers. The interface visualizes the ego facility and other facilities that receive or send patients to that facility and the number of transfers between pairs of facilities. A tooltip and additional tabs display the facility's CP-CRE year-to-date case counts, and facility characteristics. The analysis tab displays facility names that are most at-risk to receive transfers from the ego facility in the event of any CP-CRE transmission within the ego facility.

CONCLUSIONS: The interactive web platform of patient sharing network allows public health professionals to easily identify facilities at-risk of receiving patients colonized by CP-CRE from an index facility.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Informatics; Infection Control; Antimicrobial Resistance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9916
Abstract Type	Breakout
Abstract Title	Investigation of an Outbreak of VIM-Producing <i>P. Aeruginosa</i> in a Long-Term Acute-Care Hospital, Orange County, Florida 2017

Abstract

BACKGROUND: Verona integron-encoded metallo-beta lactamase (VIM)-producing *Pseudomonas aeruginosa* (Pa) and *Klebsiella pneumoniae* carbapenemase (KPC)-producing carbapenem resistant Enterobacteriaceae (CRE) are multidrug-resistant organisms that can cause health care-associated infections. VIM-Pa is rare in the United States and previously has not been identified in Florida. On July 5, 2017, the Florida Department of Health in Orange County was notified of a VIM-Pa and KPC-CRE isolated from a long-term acute care hospital (LTACH) patient. Local, state, and CDC public health officials investigated to determine the source of exposure and scope of colonization with a goal to prevent further transmission.

METHODS: Investigators conducted non-regulatory site visits to evaluate infection prevention practices and identify opportunities for improvement and a baseline point-prevalence survey to identify additional patients colonized with VIM-Pa or KPC-CRE. Subsequent point-prevalence surveys every two weeks assessed the effectiveness of control measures; all new admissions were screened for carbapenemase-producing organisms beginning August 17, 2017. A cohort study (n=129) of patients present in the facility was conducted to identify risk factors for VIM and KPC acquisition. Additionally, the patient environment and shared medical devices were cultured for VIM- and KPC-producing organisms.

RESULTS: The infection control assessment identified gaps in hand-hygiene (adherence rate=61%), use of personal protective equipment, including adherence to contact precautions, (gown adherence rate= 61%; glove adherence rate= 67%), and environmental cleaning. From July 13 to November 13, 2017, 7 LTACH patients with VIM-Pa, 20 with KPC-CRE and 5 with both organisms were identified. Exposure to hemodialysis (RR 2.25, 95% CI 1.16-4.35), mechanical ventilation (RR 1.60, 95% CI 1.09-2.33), and presence of a tracheostomy (RR 1.36, 95% CI 1.10-1.68) were associated with VIM-Pa acquisition. The risk of KPC-CRE colonization was associated with exposure to mechanical ventilation (RR 1.50, 95% CI 1.07-2.12) and hemodialysis (RR 2.18, 95% CI 1.21-3.91). KPC-CRE were detected in handwashing in 2 of 3 rooms sampled; VIM-*Pseudomonas putida* was identified from a swivette toilet.

CONCLUSIONS: Colonization screening performed in response to a single case of VIM-Pa identified large undetected outbreaks of KPC-CRE and VIM-Pa in an LTACH. Poor adherence to hand hygiene and contact precautions and gaps in cleaning patient rooms and mobile medical equipment likely contributed to transmission. Improvements in infection control have decreased but not entirely halted transmission; the role of contaminated sink drains in ongoing transmission and the means to address this requires further investigation. Ongoing on-site infection control assessments, biweekly point-prevalence surveys, and enhanced laboratory surveillance have been essential to slow this outbreak.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Infection Control
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9652

Abstract Type Breakout

Abstract Title Multidrug Resistant *Shigella Flexneri* Infections in Tennessee, 2015-2016

Abstract

BACKGROUND: Shigellosis is the 3rd most common bacterial enteric infection in the US. Transmission is primarily person to person and *Shigella sonnei* outbreaks are common in daycare settings. *Shigella flexneri* is less commonly reported but multi-state outbreaks are increasingly recognized. We reviewed *S. flexneri* cases from 2015-2016 to assess involvement in multi-state clusters, and describe resistance profiles and risk factors

METHODS: Data was collected on cases including completion of standard case report forms, supplemental interviewing, and medical record review. Collaboration with the state HIV/STD program facilitated risk factor assessment including HIV status and sexual orientation. Isolates were subjected to antimicrobial susceptibility testing and PFGE. Analyses were performed using Epi Info 7

RESULTS: Twelve Tennessee cases were included in 5 multi-state clusters of antimicrobial resistant *S. flexneri*. Six PFGE patterns were identified. All cases were males; 11 (92%) resided in large metropolitan areas. Eight (67%) were African-American, 2 (17%) White, and 2 (17%) were unknown race. Median age was 33 years with a range of 17-51 years. Epidemiological data was available for 8 cases. Three cases were hospitalized. Duration of illness ranged from 5 to 7 days. Three were treated with antibiotics. Four (50%) self-identified as MSM, 6 (75%) were HIV/immune-compromised, and 2 (25%) reported a STD. One case (13%) reported drug use, and 2 (25%) reported recent domestic travel. All denied international travel. Antibiotic susceptibility results were available for 7 cases. All (100%) were resistant to ≥ 4 antimicrobial classes. One was a highly drug resistant, resistant to at least ampicillin, azithromycin, and TMP/SMX.

CONCLUSIONS: Emergence of domestically acquired antimicrobial resistant *S. flexneri* is a growing public health concern. We identified common features among Tennessee cases including male sex, MSM, HIV and other immunosuppressive conditions, and residing in metropolitan areas. Partnership with the HIV/STD staff facilitated data collection and education of cases and high-risk groups. Joint investigation and outreach between health department programs may assist in surveillance and prevention efforts for multidrug *S. flexneri*.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Outbreaks; Risk Factors; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9711
Abstract Type	Breakout
Abstract Title	Novel Carbapenemase-Producing Carbapenem-Resistant Enterobacteriaceae Transmission in a Long-Term Care Facility - North Carolina, 2017
Abstract	BACKGROUND: In April 2017, the North Carolina Division of Public Health (NC DPH) was notified by a local health department (LHD) of a cluster of infections of extended-spectrum β-lactamase (ESBL)-producing organisms and carbapenem-resistant Enterobacteriaceae (CRE) among long-term care facility (LTCF) and community residents in County A. In consultation with the Centers for Disease Control and Prevention (CDC), NC DPH coordinated an investigation to: enhance surveillance; assess infection prevention practices at three impacted LTCFs; and prevent further transmission. METHODS: We used local hospital surveillance data to establish baseline prevalence. We conducted site visits to all LTCFs in County A to assess infection control practices and opportunities for disease transmission. NC DPH and CDC performed additional testing on one available CRE isolate to characterize the resistance mechanism. We conducted point prevalence surveys at one LTCF in June and August to identify individuals colonized with Carbapenemase producing CRE (CP CRE). RESULTS: Between October 22, 2016 and September 30, 2017, we identified 77 cases of ESBL and/or CRE in County A, twice the average monthly number of cases observed in the county in the preceding 21 months. Thirty-six (47%) infections were identified in residents of three LTCFs (N=198). An additional 9 cases (12%) had a history of exposure to other LTCFs within the county. Among the 77 cases, we identified four cases of CRE infections (5%); three were LTCF residents. One CRE isolate was identified through PCR as producing Imipenemase (IMP) Metallo-β-lactamase Carbapenemase. The LTCF case had numerous recent healthcare exposures, but no recent travel outside of NC. Site visits to the LTCF with the IMP case (LTCF 1) revealed numerous lapses in infection prevention and opportunities for transmission. Caregiver staff lacked understanding of multi-drug resistant organisms and measures to prevent transmission. Initiation of contact precautions was delayed and not adequately maintained. Hand hygiene and personal protective equipment was applied inconsistently. Annual staff competency checks were not conducted. Two sequential point prevalence surveys of LTCF 1 residents identified three additional residents colonized with IMP producing CRE. These three residents had no recent travel outside of NC or healthcare exposures outside of LTCF 1. All four cases of IMP producing CRE were geographically clustered within LTCF 1. CONCLUSIONS: We detected the first introduction and subsequent transmission of a resistance mechanism in a LTCF in NC. As a result, there is an unmet need for infection prevention education in LTCFs to ensure appropriate identification, containment and prevention of emerging CRE.
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Healthcare Associated Infections (HAI); Outbreaks
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9161

Abstract Type Breakout

Abstract Title Prevalence of Antibiotic Use and Knowledge and Attitudes Toward Antibiotic-Free Meat, Pennsylvania — 2016

Abstract

BACKGROUND: Antimicrobial resistance is recognized as one of the greatest threats to human health worldwide. Inappropriate use of antibiotics in human medicine and in food-animal production exacerbates emergence of resistance. Understanding the public's knowledge and attitudes can inform multifaceted interventions to achieve judicious use of antibiotics.

METHODS: In 2016, a weighted probability sample (n=6,810) of Pennsylvania adults was surveyed regarding antibiotic prescriptions and attitudes toward antibiotic-free meat using a state-specific module in the national Behavioral Risk Factor Surveillance System (BRFSS).

RESULTS: Among Pennsylvania adults, 40.9% (95% confidence interval [CI], 39.2%–42.6%) responded that they had been prescribed antibiotics in the previous 12 months and 6.2% (95% CI, 5.0%–7.7%) of these adults reported that they had persuaded their providers to prescribe these drugs. Asthmatic adults were significantly more likely to report receiving antibiotics (59.0% (95% CI, 53.6% - 64.3%)) than non-asthmatic adults (38.6% (95% CI, 36.8%-40.4%)) as were diabetic (55.1% (95% CI, 50.2%–60.0%)) versus non-diabetic (39.1% (95% CI, 37.3%–40.9%)) adults. Females were more likely than males to have been prescribed antibiotics (45.1% of females (95% CI, 42.7% – 47.4%) vs. 36.3% of males (95% CI, 33.8% –38.8%)). Of respondents, 25.2% (95% CI, 23.6%-26.9%) thought that antibiotics are always appropriate to treat non-bacterial illnesses (e.g., common cold). Although knowledge varied by demographic characteristics, it increased with education and income and was lowest among adults with chronic illnesses (e.g., asthma, diabetes). Additionally, among males, younger adults (18-29), 32% (95% CI, 27.8%–37.1%) also thought that antibiotics should be used to treat viral illnesses as did 27.7% (95% CI, 21.1%-35.5%) of uninsured Pennsylvanians. Overall 42% (95% CI, 40–44%) of the survey participants reported that that they try to purchase antibiotic-free meat. This preference was higher among females (48.8% (95% CI, 46.0%–51.5%)) than males (34.8% (95% CI, 32.1%–37.7%)).

CONCLUSIONS: Inappropriate prescriptions in ambulatory care settings and deficiencies in the public's knowledge about ineffectiveness of antibiotics to treat viral infections call for simultaneous interventions among clinicians and patients. To promote judicious use of antibiotics in food animals, additional One Health measures are needed to engage consumers and to address their expectations and preferences.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Antimicrobial Resistance; Infectious Diseases; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9578

Abstract Type Breakout

Abstract Title Small State, Big Collaboration: Creation of New Hampshire's First Statewide Antibigram Guides Stewardship Efforts

Abstract

BACKGROUND: Antibiotic resistant infections have been identified as an urgent national health threat. In response, the New Hampshire Division of Public Health Services (DPHS) sought to develop a system for tracking antibiotic resistance statewide through use of hospital antibiograms to 1) proactively monitor resistance trends over time and geographic region, 2) promote antimicrobial stewardship in NH healthcare facilities, and 3) provide a tool for providers to help guide appropriate antibiotic prescribing. Combining antibiogram data at the state level is a powerful tool to provide insight into antibiotic resistance trends, focus stewardship efforts, and aid providers in antibiotic prescribing.

METHODS: Through statutory administrative authority, DPHS requires hospital laboratories to report antibiogram data annually. DPHS formed an advisory group, consisting of infectious disease, medical and pharmacy subject matter experts to develop a standardized data collection tool to be used for 2016 as well as subsequent years. DPHS validated reported data to confirm accuracy, and clarify aberrant data by comparing the susceptibilities among all hospitals for each organism and antibiotic combination. Any questionable data were verified with the respective laboratory. The combined data were reviewed by the clinical advisory group and recommendations were created from the antibiogram data to highlight appropriate antibiotic prescribing key messages and the need for coordinated stewardship. The antibiogram and clinical recommendations were disseminated widely throughout the state as a "Call to Action to Prevent Emergence and Spread of Antibiotic Resistant Infections".

RESULTS: All 26 hospitals in New Hampshire submitted data, but three were excluded from the aggregated analysis due to inability to report in the requested format. From the 23 hospitals, 42,519 and 21,306 bacteria were cultured from urine and non-urine sources, respectively. The clinical advisory group's recommendations included interpretations for common clinical syndromes: uncomplicated urinary tract infections, community acquired pneumonia, skin and soft tissue infections, intra-abdominal infections, and healthcare-associated gram negative aerobic infections. Dissemination was accomplished through a health alert, partnership with a state working group of stakeholders, widespread email communication and online publication.

CONCLUSIONS: The small size of New Hampshire, centralized public health structure, and close working relationships with all hospitals allowed for efficient collection of this data. Our process may serve as a model for other states. Lessons learned will inform more accurate, comprehensive antibiotic resistance surveillance. The creation of this antibiogram is the launch for a larger statewide public health antibiotic stewardship campaign and coincides with national efforts around antibiotic stewardship and resistance surveillance.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Hospital Data; Antimicrobial Resistance; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9809

Abstract Type Poster

Abstract Title A Collaborative Approach to Promote Antimicrobial Stewardship in Pennsylvania

Abstract

BACKGROUND: Antimicrobial resistance poses a significant challenge to global public health. Inappropriate use of antibiotics in clinical settings, including prescriptions for acute upper respiratory infections, exacerbate the emergence of drug-resistant bacterial pathogens. Equally important is the overuse of antimicrobial drugs in agricultural settings.

METHODS: During 2005-2017, we implemented activities to promote antimicrobial stewardship in collaboration with the CDC, FDA and academic partners. We organized program components through focused initiatives, developed specific interventions, and designed implementation and evaluation methods. Beginning in 2012, we trained and engaged public health interns in the implementation of specific initiatives in collaboration with state-based partners, pharmacy schools, pediatric clinics, and childcare centers for quality improvement. In 2015, stewardship activities expanded through integration of data coming from surveillance programs, community interventions, and surveys of the public about knowledge and perceptions about antibiotics including use of these drugs in food production. Increased coordination with healthcare-associated infection programs and collaboration with a whole genome sequencing academic laboratory has strengthened our One Health approach.

RESULTS: During the past twelve years, we developed antimicrobial stewardship initiatives to promote the appropriate use of antibiotics in diverse healthcare settings, including ambulatory care practices and over 700 long-term care facilities. Using data from the program, we developed a summary report, *"Practical Considerations in Implementation of Model Sick-Child Exclusion Policy in Childcare Settings"* in 2014. We created a web portal in 2013, and began an annual art competition to engage children 12 years and younger in promoting vaccinations and antimicrobial stewardship. In 2016, we introduced an award ceremony for art competition winners, and this year, 12-18 year old students were invited to submit videos to promote prevention and increase antibiotic awareness. Annual surveys of consumers in community pharmacies in western Pennsylvania assessed knowledge and attitudes towards antibiotics and a statewide random survey of over 6,800 residents was conducted in 2016. Of all respondents, 41% reported that they had been prescribed antibiotics and 6% of these reported that they persuaded providers to prescribe them these drugs. A preference for antibiotics-free meat was noted by 42% of all Pennsylvanians surveyed.

CONCLUSIONS: We implemented, expanded and maintained efforts to promote antimicrobial stewardship through collaboration with federal, academic, and community partners. Focused initiatives such as training of pharmacy students and engagement of target audiences through art and video competitions contributed to increased visibility and success. Our experience suggests that creativity and diverse collaboration in program design can enhance efforts to promote antimicrobial stewardship.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10026

Abstract Type Poster

Abstract Title Antibiotic Stewardship Progress: A Longitudinal Assessment of Long-Term Care Facilities in Maine

Abstract

BACKGROUND: In 2016, the Centers for Medicare and Medicaid Services (CMS) released updated regulations long-term care facilities must meet to participate in Medicare and Medicaid funded programs. One of the notable requirements was that facilities must have an Antibiotic Stewardship Program in place by November 28, 2017. In October 2016, the Maine Center for Disease Control and Prevention (CDC) sent out an online survey to all nursing homes in the state to develop a baseline assessment of each facility's progress towards meeting all seven core elements of an Antibiotic Stewardship Program. This same survey was sent out again in January 2018 to measure progress over time.

METHODS: An online Typeform survey was sent to 103 nursing homes throughout the state of Maine in October 2016 and again in January 2018 to measure progress towards meeting the Antibiotic Stewardship Program requirement. The seven core elements assessed follow the CDC Core Elements of Antibiotic Stewardship for Nursing Homes. These elements were Leadership Commitment, Accountability, Drug Expertise, Action, Tracking, Reporting, and Education.

RESULTS: In total, 68 facilities responded to the 2016 survey resulting in a 66% response rate. Of the facilities that responded, 19 (28%) met all seven core elements. Given the low number of facilities meeting all the core elements in the year preceding the effective CMS requirement date, the Healthcare Associated Infections/Antibiotic Resistance (HAI/AR) program at the Maine CDC provided regional trainings on infection control and Antibiotic Stewardship in the summer of 2017. It is anticipated that the January 2018 survey will show an increased number of facilities meeting all seven core elements given the training and additional support provided by the Maine CDC, in addition to the CMS program requirement date having recently passed.

CONCLUSIONS: The CMS Antibiotic Stewardship Program is a new requirement for long-term care facilities throughout the nation. Based on the data acquired during the 2016 Maine nursing home survey of the core elements, it was clear that facilities needed assistance meeting this requirement. By providing training and direct assistance along with the requirement deadline date having recently passed, it is anticipated that there will be a substantial increase in the number of facilities meeting all seven core elements. Gaps identified in the 2018 Maine nursing home survey will be used to target additional needs of long-term care facilities in Maine meeting infection control and antibiotic stewardship requirements of participation.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Health Care; Healthcare Associated Infections (HAI); Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9006

Abstract Type Poster

Abstract Title Antimicrobial Resistance Among Enteric Pathogens from Humans in the United States – Data from the National Antimicrobial Resistance Monitoring System (NARMS)

Abstract

BACKGROUND: *Salmonella* , *Shigella* , and *Campylobacter* have been estimated to cause nearly half a million antibiotic-resistant infections in the United States annually. Antibiotic-resistant infections are a serious concern because they can be more severe and difficult to treat. Surveillance is critical to understanding and preventing the transmission of resistant infections. NARMS at CDC is a collaboration with state and local public health departments that track resistance among enteric pathogens from humans. We describe trends and findings from the most recent NARMS surveillance data.

METHODS: Participating health departments submitted a sample of nontyphoidal *Salmonella* (NTS), *Campylobacter* , and *Shigella* to CDC NARMS for antimicrobial susceptibility testing (AST). We defined multidrug resistance (MDR) as resistance to ≥ 3 antibiotic classes and decreased susceptibility to ciprofloxacin (DSC) as minimum inhibitory concentration ≥ 0.12 $\mu\text{g/ml}$. We used logistic regression to compare the prevalence of resistance among isolates tested in 2015 with the average prevalence from two reference periods, 2004–2008 and 2010–2014. For NTS collected in 2014 and 2015, we screened whole genome sequencing (WGS) data to determine resistance mechanisms and compared the predicted resistance pattern to AST results.

RESULTS: In 2015, we tested 2,364 NTS isolates, 1,118 *Campylobacter* isolates, and 569 *Shigella* isolates. Among NTS, the percentage of isolates with MDR (12.4%) and DSC (5.8%) were significantly higher in 2015 compared with 2004–2008 (MDR 11.1%; DSC 2.4%) and 2010–2014 (MDR 9.4%; DSC 3.4%). Ceftriaxone resistance (2.7%) was not significantly different (2004–2008: 3.2%; 2010–2014: 2.6%). In 2015, eight (0.34%) NTS isolates had azithromycin resistance, the largest proportion since testing began in 2011. Seven of them were also resistant to other agents; five had DSC, but none were resistant to ceftriaxone. Among *Campylobacter* , the percentage of isolates with ciprofloxacin resistance in 2015 was significantly higher in both *jejuni* (25.3%) and *coli* (39.8%) compared with 2004–2008 (21.0% and 28.0%, respectively). Among *Shigella* , the percentage of isolates with DSC was significantly higher in 2015 (9.8%) compared with both reference periods (1.7% and 5.8%, respectively). Among sequenced NTS isolates, predicted resistance from WGS data had a sensitivity of 93.0% (95% CI: 91.4%–94.4%) in 2014 and 92.1% (95% CI: 90.7%–93.4%) in 2015.

CONCLUSIONS: Resistance trends varied by pathogen. We found concerning increases in resistance to first-line antibiotics used to treat enteric infections, such as ciprofloxacin and azithromycin, as well as an increase in MDR. WGS was predictive of AST results and can be used to enhance surveillance for resistance.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Enteric Infectious Diseases; Surveillance; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9870
Abstract Type	Poster
Abstract Title	Antimicrobial Stewardship in Ambulatory Care: A Comprehensive Approach to Education and Toolkit Development By the Washington State Department of Health
Abstract	BACKGROUND: Antibiotic use is the key driver of antibiotic resistance. Higher use of antibiotics is associated with more antibiotic resistance in individuals, in hospitals, and in communities. Antibiotics are also associated with adverse events in humans such as allergic reactions, and <i>Clostridium difficile</i> infections. Modern medicine is threatened by increasing antibiotic resistance due to overuse of antibiotics. Most use in humans occurs in ambulatory settings. In fact, 30-50% of outpatient antibiotic prescriptions are considered inappropriate or unnecessary. These essential medications should be used only when necessary to preserve their effectiveness. Antimicrobial stewardship (AMS) is used to accomplish this by increasing appropriate use of antimicrobials, including antibiotics, decreasing resistance and spread of multi-drug resistant organisms, and increasing patient outcomes. The goals of the Washington State Department of Health (DOH) are to (1) assist prescribers in identifying situations when antibiotics are needed, (2) provide communication strategies to use with patients when antibiotics are not needed, (3) disseminate this information across the state through an AMS toolkit, and (4) increase the general public's knowledge of AMS importance. METHODS: Surveys were conducted and evidence-based research was used to guide the creation and development of resources in the toolkit. Expert advice from AMS leaders in WA State and nationally was solicited and used. Multiple formats, print and online, were utilized to increase access to the toolkit. Collaborations were developed with other public health partners and institutions to increase awareness and visibility of the projects undertaken. Communication campaigns were conducted to increase the general public's awareness along with the creation of public service announcement style videos targeting this population. RESULTS: Reactions to the toolkit and other projects have been positive. Collaborations with partner organizations have been fostered and made stronger. The toolkit contains a quick start to stewardship workbook, eLearning module for healthcare providers that can be accessed free online, clinical practice guidelines, which have been tapped for potential national use, and leadership and provider commitment posters. CONCLUSIONS: There is a need in Washington State for better practices surrounding AMS. DOH has created a toolkit for health care providers and targeted education for the general public to fill this need.
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Community Health; Antimicrobial Resistance
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9935

Abstract Type Poster

Abstract Title Art and Video Competition: An Innovative Approach to Engage Children in Antimicrobial Stewardship and Increase Website/Social Media Traffic in Pennsylvania

Abstract

BACKGROUND: Every year in the United States an estimated 154 million antibiotic prescriptions are prescribed in emergency rooms and doctor's offices. However, almost 50 percent of these antibiotic prescriptions are unnecessary or inappropriate. This overuse of antibiotics drove the start of the Get Smart program, a CDC initiative to combat antimicrobial resistance in a variety of settings. In Pennsylvania, several organizations have collaborated to build and maintain a website to promote antimicrobial stewardship to the public.

METHODS: Up-to-date information promoting stewardship has been available to the public at www.knowwhentosayno.org since 2012. One major goal for the website was to reach and educate older children and their parents about infection prevention and antimicrobial stewardship. To this end, we established a drawing competition for elementary-aged children in 2012 and a video competition for high school students in 2017. These activities were promoted through the website and advertised on Facebook. To evaluate the impact of these efforts, three months of Google website traffic data were obtained for the years from 2013-2016 (2017 data are still pending). Facebook ad analytics were obtained for October 5th-15th, 2017 (the peak time for competition participation).

RESULTS: From 2013-2016 there were a total of 878 entries into the art competition. In all years, visual inspection of Google data showed that website traffic increased during major competition announcements (e.g. start of competition, entries due, winner announcement). Of the 781 competition entries with complete information, most participants were from the southcentral (n=424) and northwestern (n=216) regions of the state. Facebook ad analytics showed that over ten days our ad reached 1,332 people. Seventy-three percent of viewers were women. Among both men and women, the ad was viewed most frequently by persons aged 25-34 years compared to other 10-year age groups (25% of female viewers [244/979] and 30% of male viewers [107/373]). Regional data in Facebook analytics showed that our ad was viewed by persons in every state in the continental U.S., with the highest number of views in PA, NY, VA, and GA.

CONCLUSIONS: The increase in website traffic associated with competition announcements and Facebook views suggest that online measures can be used to engage the public with antibiotics stewardship messages, particularly in a demographic likely to include young parents (age 25-34 years). Future projects will explore how to expand the impact of our public-facing programs.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10230

Abstract Type Poster

Abstract Title Association between Attending the Illinois Summit on Antimicrobial Stewardship and Meeting the Core Elements of Hospital Antibiotic Stewardship

Abstract

BACKGROUND: The Illinois Department of Public Health (IDPH) has hosted the annual Illinois Summit on Antimicrobial Stewardship since 2013. This statewide event convenes professionals across healthcare settings to discuss best practices and lessons learned around antibiotic stewardship. Summits have addressed antibiotic stewardship implementation in specific care settings, metrics for monitoring antibiotic use and stewardship, and summarized relevant national and local policy updates. IDPH evaluated the association between summit attendance and implementation of the Centers for Disease Control and Prevention's (CDC) Core Elements of Hospital Antibiotic Stewardship as reported on the National Healthcare Safety Network's (NHSN) annual hospital survey.

METHODS: Data was obtained using the attendee lists from the 2013, 2015, and 2016 summits and from the NHSN annual hospital survey. Chi-square tests and log binomial regression models were used to assess the relationship between summit attendance and implementing all seven core elements. Data was stratified by year, bed size, and medical school affiliation.

RESULTS: From 2013-2016, there was an increase in the number of Illinois acute care hospitals that attended the annual summit and reported meeting all seven core elements. In 2014, 39% of the 180 Illinois acute care hospitals reported meeting all core elements and this increased to 48% in 2015, and 71% in 2016. Hospitals that attended at least one summit were 37% more likely to report implementing all core elements compared to hospitals that did not attend (Rate ratio (RR) =1.37, p=0.0002). When adjusting for bed size, hospitals that attended the summit were 16% more likely to have met all seven core elements (RR=1.1625, p=0.0471). Similarly, when adjusting for medical school affiliation, those that attended the summit were 22% more likely to implement all seven core elements in comparison to hospitals that did not attend (RR=1.2209, p=0.0088).

CONCLUSIONS: Hospital participation in the Illinois Summit on Antimicrobial Stewardship was significantly associated with implementation of CDC's Core Elements of Hospital Antibiotic Stewardship as reported on the NHSN annual hospital survey. Limitations include the use of self-reported data and that the evaluation did not take into consideration other factors that may have affected stewardship implementation. The results suggest that such in-person trainings with peer-to-peer sharing can help propel implementation of antibiotic stewardship programs. IDPH will continue to offer this annual training and evaluate its impact in other care settings.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Evaluation; Disease Prevention; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10340

Abstract Type Poster

Abstract Title Caause Progress: Maryland's Statewide Antibiotic Stewardship Collaborative

Abstract

BACKGROUND: Improving antibiotic use and slowing the emergence of antibiotic resistance (AR) is a critical patient safety and public health issue. The Maryland Campaign for Appropriate Antibiotic Use (CAAUSE) is a statewide collaborative led by the Maryland Department of Health (MDH) that aims to assist facilities across the healthcare continuum with meeting antibiotic stewardship (AS) requirements while reducing the emergence of AR. Formed in January 2016, membership includes physicians, pharmacists, nurses, epidemiologists and healthcare administrators who represent public health, patient safety organizations, academic and community hospitals, and long-term care (LTC) facilities. Monthly meetings are held in person and via teleconference with both didactic and collaborative agenda components.

METHODS: Through discussion, CAAUSE facilities have conveyed a strong interest in conferring group validation for specific antimicrobial interventions and achieving even footing regarding AS program strategies via an open discussion forum. Stewardship interventions developed by CAAUSE subcommittees include protocols for asymptomatic bacteriuria management, targeted 48-72 hour antibiotic hold/review, and vancomycin toxicity prevention. Surveys were conducted using SurveyMonkey, and have included assessments of AU metrics, electronic medical record (EMR) AS capacity, and AS needs, including *Clostridium difficile* prevention.

RESULTS: Survey results showed that facilities have adopted a wide range of interventions, including: antibiotic reviews/consults, antibiotic timeouts/restrictions, pharmacy dosing/monitoring, and post-prescription reviews. A survey of EMR capacity for AS revealed that there were at least 8 EMR systems in use in 2017, just over half of which had built-in AS capacity (such as parenteral-oral switch, antibiotic timeout, automatic stop and/or restriction orders). Over 2/3 of respondents felt EMR systems enhanced offline stewardship activities, fit with AS workflow, but were labor intensive. Regarding AU metrics, over 2/3 of EMR could assist in quantifying all patients on antibiotics. Facilities used a variety of AU metrics, most commonly: days of therapy, purchasing data and defined daily dose, as well as other administrative data. Over 90% of responding facilities expressed interest in implementing AS to prevent *Clostridium difficile*.

CONCLUSIONS: The Maryland CAAUSE Collaborative has provided a forum to consolidate AS expertise and resources and to stimulate innovation in AS across the healthcare continuum, resulting in networking and relationship strengthening among its diverse members statewide. Notably, the valuable perspectives of infectious disease pharmacists and LTC quality experts have enriched this collaborative. As Centers for Medicare & Medicaid Services (CMS) and Joint Commission standards become mandated, Maryland aims to have its acute and LTC facilities actively prepared for full participation and compliance.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Infectious Diseases; Health Care; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10169

Abstract Type Poster

Abstract Title Carbapenem-Resistant *Enterobacteriaceae* in Maryland: 2015–2017

Abstract

BACKGROUND: In 2013 the CDC named carbapenem-resistant *Enterobacteriaceae* (CRE) as an urgent drug-resistant threat to the United States. Since 2015 any *Enterobacteriaceae* species isolated from any body site that is resistant to any carbapenem, including ertapenem, is required to be reported to the Maryland Department of Health (MDH). Isolates must be submitted to the Maryland Public Health Laboratory. Comprehensive testing of all isolates for carbapenemase genes by polymerase chain reaction (PCR) began in July 2016.

METHODS: Incident CRE cases were classified according to CSTE’s 2015 guidance (15-ID-05). Most analyses include all cases isolated at laboratories located in Maryland, including CRE isolated from out-of-state patients; however, these cases were excluded when calculating rates of CRE per 100,000 residents for five Maryland regions. Only one isolate per organism was included for each patient in analyses of molecular testing data.

RESULTS: During 2015–2017, laboratories serving Maryland healthcare facilities detected between 826 and 901 incident cases of CRE annually, representing 737–771 unique CRE patients each year. Maryland’s overall rate of CRE declined slightly over time from 13.6 to 12.8 cases per 100,000 residents, but regional variations were identified. Of 2,612 total incident CRE cases identified, 1,092 were identified as *Klebsiella pneumoniae* (41.8%), and 643 were *Enterobacter cloacae* (24.6%). As a proportion of all CRE, urine isolates increased over the three-year period from 47.9% in 2015 to 57.0% in 2017. CRE from sterile sites decreased from 9.8% of all isolates in 2015 to 6.9% in 2017. During July 2016–December 2017, 48.8% of CRE isolates tested were positive for carbapenemase genes by PCR; most were positive for the *Klebsiella pneumoniae* carbapenemase (KPC) gene (95%). Nine isolates were positive for a New Delhi metallo-beta-lactamase (NDM) gene, 8 for an oxacillinase (OXA)-48-like gene, and 2 for a Verona integron-encoded metallo-beta-lactamase (VIM) gene. The 326 KPC-positive isolates included 239 *Klebsiella spp* (73%), 40 *Enterobacter spp* (12%), 23 *E. coli* (7%), and 25 organisms from “non-big 3” genera (8%).

CONCLUSIONS: CRE incidence has been consistently high in Maryland between 2015 and 2017 compared to other states for which similar data exists, although a slight decrease in CRE from sterile sites is encouraging. The high proportion of carbapenemase-producing CRE in Maryland is concerning; more rapid detection and isolation of case patients in Maryland healthcare facilities is needed. Metallo-beta-lactamase-producing CRE remain rare in Maryland and present an opportunity for containment via continued partnership between clinical laboratories, acute and long term care infection prevention, and public health.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Surveillance; Healthcare Associated Infections (HAI); Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10309
Abstract Type	Poster
Abstract Title	Characterizing Candida Species Identification Isolate Submission to the Southeast Antibiotic Resistance Network (ARLN) Laboratory

Abstract

BACKGROUND: *Candida auris* is an emerging multi-drug resistant fungal pathogen found in healthcare settings. Unlike other fungal species found in healthcare settings, *Candida auris* persists in the environment and is easily spread from patient to patient. Identification of *Candida auris* in a timely manner is critical to prevent the spread of this organism. Timely identification in clinical laboratories is hindered by misidentification of *Candida auris* as other *Candida* species by commercial systems. The Southeast ARLN is one of the regional ARLN laboratories approved to perform confirmatory identification and susceptibility testing of *Candida auris* isolates as well as species identification of *Candida* isolates submitted as suspect *Candida auris*. Characterizing *Candida* isolates submitted to the Southeast ARLN helps inform guidance to laboratories and provides situational awareness of common machine misidentifications in the region.

METHODS: *Candida* isolates submitted to the Southeast ARLN regional laboratory from February through November were included for analysis. Species identification of isolates submitted was confirmed by Bruker Biotyper brand matrix assisted laser desorption-ionization time of flight (MALDI-TOF) software version 4.1. Data were obtained from the laboratory information management system (STARLIMS) and cleaned and aggregated into a comma separated values (.csv) file using R. Data was visualized and summarized using Tableau.

RESULTS: From February to November of 2017 42 *Candida* isolates were submitted to the Southeast ARLN for confirmatory testing. Isolates came from 15 clinical laboratories in 6 states representing patients from 7 states. Isolates were predominately submitted by Tennessee (50%) and Florida (42%) facilities. Regional isolate submission was visualized using maps of isolate submission by public health laboratory as well as patient state of origin. Submitting clinical laboratory identification methods were API 20C, MALDI-TOF, Microscan, Phoenix, Rapid Yeast-ID and Vitek-2. Vitek-2 and MALDI-TOF were the two most frequently used identification methods characterizing 57.1 and 26.2 percent of isolates, respectively. Of the 11 isolates tested by clinical laboratories using MALDI-TOF 4 (36%) clinical species did not match the ARLN species. For Vitek-2, of 24 isolates tested 20 (83%) did not match the ARLN species including 5 isolates from one patient that were identified by the clinical laboratory as *Candida haemulonii* but confirmed at the ARLN as *Candida auris*.

CONCLUSIONS: Situational awareness of *Candida* identification methods used in clinical laboratories can help identify gaps and improve recommendations to rapidly identify and prevent the spread of *C. auris*. Laboratory instruments should use up to date software and associated databases should include *Candida auris*.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Epi / Lab Capacity (ELC); Healthcare Associated Infections (HAI); Emerging Infections
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10320
Abstract Type	Poster
Abstract Title	Characterizing <i>Neisseria Gonorrhoeae</i> Susceptibilities for Isolates Submitted to the Antibiotic Resistance Laboratory Network (ARLN)

Abstract

BACKGROUND: Emerging antibiotic resistance in *Neisseria gonorrhoeae* was identified as a public health threat by the National Action Plan for Combating Antibiotic Resistant Bacteria (CARB). The antibiotic resistance laboratory network (ARLN), a system of laboratories used to characterize antibiotic threats identified by the National Action Plan for CARB currently tests *Neisseria gonorrhoeae* isolates in four regional laboratories including the Southeast regional laboratory. Information obtained from testing is used to characterize emerging resistance in *Neisseria gonorrhoeae* in the United States and inform treatment recommendations.

METHODS: Viable *Neisseria gonorrhoeae* isolates submitted to the Southeast ARLN regional laboratory from April to November (n=1495) from sentinel Gonococcal Isolate Surveillance Project (GISP) and (Strengthening the United States Response to Resistant Gonorrhea) SURRG sites were included for analysis in WHONET. Confirmatory species identification was done using matrix assisted laser desorption-ionization time of flight (MALDI-TOF). Minimum inhibitory concentrations (MIC) of penicillin, ciprofloxacin, cefixime, gentamicin, ceftriaxone, azithromycin and tetracycline were obtained using agar dilution. Data obtained from the Southeast ARLN laboratory information management system (STARLIMS) was cleaned using R and converted to WHONET files. WHONET files were used to create a WHONET laboratory in which data analysis could be performed. WHONET analysis included determining the percent of isolates resistant, susceptible or intermediate to antibiotics tested, MIC distributions of each antibiotic used and scatterplots to determine interactions of key drugs used for treatment of *Neisseria gonorrhoeae*. 69 isolates met ARLN alert criteria: Azithromycin MIC ≥ 2.0 ug/mL (n=64), Cefixime MIC ≥ 0.25 ug/mL (n=1), and Ceftriaxone MIC ≥ 0.125 ug/mL (n=4). Azithromycin alert organisms were subset for scatterplot analysis.

RESULTS: MIC distributions for each antibiotic tested followed a normal distribution with the exception of ciprofloxacin which had a bimodal distribution. Isolates had the highest percentage of resistance to Ciprofloxacin (26%) and Tetracycline (14%). 100% of isolates were sensitive to Ceftriaxone and Cefixime. Most isolates were susceptible to Azithromycin (99%) and Ciprofloxacin (71.1%). Scatterplot analysis identified that 99% of isolates were susceptible to both Ceftriaxone and Azithromycin and to both Cefixime and Azithromycin. Only 70.3% were susceptible to both Ciprofloxacin and Azithromycin. Analysis of the 64 isolates meeting the Azithromycin alert value revealed that no isolates also had resistance or non-susceptibility to Cefixime or Ceftriaxone.

CONCLUSIONS: *Neisseria gonorrhoeae* susceptibility testing assists in identifying emerging resistance and provides valuable information to develop treatment guidelines.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Surveillance; Antimicrobial Resistance; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
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Affiliation	State Public Health Agency

Submission Type Breakout/Quick/Lightning/Poster

ID 10143

Abstract Type Poster

Abstract Title Community Antibiotic Stewardship Programs Demonstrate Lower *Clostridium Difficile* Infections

Abstract

BACKGROUND: Antibiotic stewardship programs improve facility-level prescribing of antibiotic therapies and enhance surveillance of drug-resistant threats. When replicated at the community level, benefits such as reductions in infectious outcomes may be observed. In Louisiana, healthcare settings in 3 of 9 geographic regions with shared patient populations have organized to develop community antibiotic stewardship programs (CASPs) through inter-facility collaboration. Hospital-onset *Clostridium difficile* (CDIFF) infections may be reduced through antibiotic stewardship. The aim of this study is to determine if regions with CASPs experience fewer hospital-onset CDIFF than regions without CASPs.

METHODS: Regions 2, 4, and 9 were identified as having CASPs that were in effect during the study period. Acute care hospital CDIFF data from January 1, 2016 to June 30, 2017 were extracted from the Louisiana National Healthcare Safety Network (NHSN) Data Use Agreement Group and stratified by region. Incidence density rates (IDR) were summed and calculated as number of infections divided by patient-days. Regional IDR were compared to the referent overall Louisiana experience for the time period and tested for statistical significance at the 95% confidence level. Data were analyzed with the NHSN Statistics Calculator's Comparison of Two IDRs function.

RESULTS: The overall Louisiana CDIFF IDR was 5.42 per 10,000 patient-days. Regions 2 and 9 had significantly lower IDR with 4.68 per 10,000 ($p=0.04$) and 2.62 per 10,000 ($p<0.0001$), respectively. Region 4 had a lower CDIFF IDR than the overall experience; however, the result of 4.94 per 10,000 was non-significant ($p=0.22$). Two regions (1 and 7) had significantly higher IDR with 6.63 per 10,000 ($p=0.0001$) and 6.52 per 10,000 ($p=0.0031$), respectively.

CONCLUSIONS: Regions with CASPs have lower CDIFF outcomes than those without CASPs. CASPs in Louisiana have enacted stewardship policies, collaborative education, and have engaged facility leadership with their patient safety initiatives. While only regions 2 and 9 experienced CDIFF rates that were significantly lower than the state's experience, region 4's IDR was lower than the overall Louisiana IDR. Best practices from these CASPs should be compiled and distributed for replication across the state.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Healthcare Associated Infections (HAI); Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10334

Abstract Type Poster

Abstract Title Ensuring Antimicrobial Stewardship Expertise for Critical Access Hospitals in Washington

Abstract

BACKGROUND: Hospital antimicrobial stewardship programs (ASP) can improve judicious use of antibiotics in patients and are key for combating antibiotic resistance and other antibiotic-associated harms. In 2016, CMS proposed new rules requiring all hospitals to have an ASP. Many smaller hospitals lack ASP leaders with appropriate expertise. An academic university established a tele-antimicrobial stewardship program (TASP) to provide antimicrobial stewardship expertise via video-conference sessions. The state department of health has prioritized CDC ELC funding for this effort to support establishment and success of ASPs in small, rural hospitals.

METHODS: Critical access hospitals (CAH) were recruited to participate in weekly TASP sessions led by stewardship experts representing infectious disease, microbiology, and pharmacy. Topics covered include antibiograms, allergies, behavior change, clinical practice guidelines/order sets, formulary, metrics, reporting, and specific infectious syndromes. Participating CAHs are encouraged to present challenging situations for consultation. Hospital staff were asked to complete a baseline survey at the beginning of the program documenting hospital resources for antimicrobial stewardship. Additional data sources about hospital stewardship efforts and capabilities include CDC Infection Control, Assessment and Response on-site surveys and the CDC National Healthcare Safety Network (NHSN) Hospital Survey.

RESULTS: Over 2017, the number of CAHs actively participating in TASP ranged from 11-15, out of a total of 39 CAHs in the state. According to the baseline survey completed by 11 participating CAHs, gaps included: no ASP (10%); no stewardship team (37%); no pharmacist leader (37%); no physician leader (73%); no stewardship education for staff (37%), and no antibiotic treatment guidelines (37%). Before TASP began, the NHSN Hospital Survey demonstrated improvements in the percent of CAH meeting all 7 core elements of hospital stewardship rising from 21% to 29% to 50%, from 2014, to 2015 to 2016, respectively. We will compare improvements in ASP between CAH participating in TASP to those not with the 2017 and 2018 NHSN hospital surveys.

CONCLUSIONS: Tele-antimicrobial stewardship can provide ASP expertise to remote hospitals. Benefits of the program include enhancing stewardship across the state, improving regulatory compliance, and developing a community of support for small hospitals. Challenges include maintenance of stable funding, engaging remote area physicians in TASP, establishing trust at a distance, and identifying staff and resources in CAHs able to participate. By supporting antimicrobial stewardship expertise for rural areas we hope to improve judicious use of antibiotics in CAHs.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Rural Health; Antimicrobial Resistance; Epi / Lab Capacity (ELC)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9485

Abstract Type Poster

Abstract Title Trends in Antibiotic Treatment of Urinary Tract Infections in Older Populations, Massachusetts 2009-2012

Abstract

BACKGROUND: Urinary tract infection (UTI) is one of the most common diagnoses leading to an antibiotic prescription for older adults in both inpatient and outpatient settings. We sought to assess adherence to antibiotic prescription guidelines for UTI over time to optimize antibiotic use and stewardship efforts.

METHODS: Medicare claims data from 2009 to 2012 identified 38,391 Massachusetts residents, 65 years of age and older, without comorbidities who were diagnosed with a UTI (ICD-9/10: 599.0/N39.0 (UTI not otherwise specified) or 791.9/R82.90 (Bacteriuria with and without UTI)). We excluded claims that covered more than one day in order to exclude inpatient treatment. Initial antibiotic selection and duration of treatment was compared to Infectious Diseases Society of America (IDSA) treatment guidelines for uncomplicated UTIs (Y/N): duration of treatment for women of 3 days (7 days for nitrofurantoin) and duration of treatment for men of 7-14 days. Nitrofurantoin is recommended as a first line treatment, trimethoprim-sulfamethoxazole (TMP-SMZ) is recommended as a second line treatment, and fluoroquinolones and β -Lactams (some cephalosporins) as the last option for treatment. We also examined changes in antibiotic prescribing practices over time.

RESULTS: Fluoroquinolones were used as the primary treatment option (>40% of yearly prescriptions) for uncomplicated UTIs. The average duration (in days) of treatment for uncomplicated UTIs was 7 days for females and 9 days for males. Over 80% (n=32,459) of prescriptions written between 2009 and 2012 for uncomplicated UTIs among older populations were not consistent with IDSA guidelines.

CONCLUSIONS: Despite FDA black box warnings released in 2008, fluoroquinolones were the most often prescribed antibiotic for UTI in those 65 years of age and older from 2009-2012. The majority of antibiotic prescriptions for older adults with uncomplicated UTI did not adhere to IDSA treatment guidelines. Medicare claims data provide supplemental antibiotic use data to target stewardship efforts.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Antimicrobial Resistance; Evaluation

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10084
Abstract Type	Quick
Abstract Title	Antibiotic Use: An Assessment of Knowledge, Attitudes, and Practices of Parents at Federally Qualified Health Centers in Hawaii

Abstract

BACKGROUND: Inappropriate prescribing of antibiotics for upper respiratory tract infections (URI), especially in the pediatric setting, contributes to the increase of antibiotic resistance worldwide. Previous research indicates perceived parent pressures may contribute to the inappropriate prescription of antibiotics by physicians. Our assessment aimed to evaluate parents' perceptions of antibiotics to better understand potential barriers to judicious antibiotic use for URIs in Hawaii and inform efforts to reduce antibiotic resistance.

METHODS: Using a cross-sectional design, anonymous structured questionnaires were disseminated over a three-month period in 2017 to parents and guardians presenting at four Federally Qualified Health Centers (FQHCs) comprising five clinics across Hawaii. The survey contained questions on perceptions, knowledge, and practices related to antibiotics as well as demographic information. Descriptive statistics were used to report participant responses. Multivariable linear regression was performed to identify factors influencing incorrect perceptions related to antibiotic use for URI, defined as influenza and the common cold.

RESULTS: Completed surveys were submitted by 145 respondents spanning three islands, with 47% identifying as Pacific Islander or Native Hawaiian (PI/NH). Compared with all other races, PI/NH respondents were more likely to believe antibiotics were needed for URI (OR: 7.23; 95% CI: 3-20). After adjusting for race, lack of post-secondary education (OR: 3.07; 95% CI: 1-8) and classification as low income (OR: 5.30; 95% CI: 1-20) were also significantly associated with incorrect perceptions regarding antibiotic use for URI. Almost half (45%) of respondents reported directly requesting antibiotics from their medical provider. Individuals who reported direct request for antibiotics were more likely to believe they were necessary for treatment of URI (OR: 3.51; 95% CI: 1-9) as compared with respondents who did not report directly requesting antibiotics. Most (73%) respondents reported receiving the majority of their information on antibiotics from their medical provider.

CONCLUSIONS: Race, education level, and income were associated with incorrect perceptions regarding antibiotic necessity for URIs. As almost half of respondents reported directly requesting antibiotics from their physicians, parents and guardians presenting at FQHCs in Hawaii may benefit from culturally and linguistically appropriate education on the proper use of antibiotics. Public health may support clinicians in drafting appropriate language to discuss correct indications for antibiotics and the importance of only prescribing when clinically necessary.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Social Determinants; Antimicrobial Resistance; Maternal and Child Health
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9281

Abstract Type Quick

Abstract Title Capturing Multidrug-Resistant Organisms in Massachusetts Using Maven

Abstract

BACKGROUND: Emerging antimicrobial-resistant pathogens such as *Candida auris* and carbapenem-resistant *Enterobacteriaceae* (CRE), and resistance mechanisms including novel carbapenemases and mobilized colistin resistance (*mcr*) now challenge public health departments to capture vital information on individuals infected or colonized with these pathogens and their contacts to maintain a surveillance and case management system.

METHODS: In April 2016, the Massachusetts Department of Public Health (MDPH) created a multidrug-resistant organism (MDRO) product code within the Massachusetts Virtual Epidemiologic Network (MAVEN), the fully integrated infectious disease surveillance system utilized by MDPH epidemiologists in order to manage reported “cases” in a single database. The MDRO product code allows for the capture of electronic laboratory reports and manual data entry of cases reported by clinical laboratories and the state public health laboratory in Massachusetts. Within each case record, an epidemiologist classifies the event as a CRE or other MDRO, and then selects the organism and carbapenemase (KPC, OXA-48, NDM, VIM, or IMP) or other resistance mechanism (*mcr*) from dropdown menus based on the laboratory information available. If the case requires further follow-up, an epidemiologist will then collect and enter information on the case, such as symptoms, travel history, previous healthcare exposure(s), place of current/past residence, and whether contact precautions were implemented (if indicated). If a case is determined to be part of an outbreak investigation, an MDRO cluster event can be created to link case and contact events, allowing for the capture of colonization screening test results.

RESULTS: As of December 2017, MDPH has captured 471 MDRO events in MAVEN since implementation, which includes 6 cases of *Candida auris*, 61 contacts of patient(s) with *Candida auris*, 4 cases of isolates carrying the *mcr-1* gene element, 29 contacts of a patient with an *mcr-1* isolate, 273 cases of CRE, and 5 contacts of patient(s) with a novel carbapenemase-producing CRE.

CONCLUSIONS: The MDRO event in MAVEN has streamlined the collection of data related to antimicrobial-resistant pathogens in Massachusetts by allowing epidemiologists to easily track the number and types of MDRO cases and outbreaks reported by healthcare facilities. The system will also allow for a simplified reporting process to CDC in the future as these conditions become part of the National Notifiable Disease Surveillance System.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Surveillance; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9015

Abstract Type Quick

Abstract Title Enhanced Surveillance for Highly-Concerning Antimicrobial Resistance and the Emergence of *Mcr* Genes Among Foodborne Pathogens in the United States

Abstract

BACKGROUND: Certain resistance determinants present in enteric pathogens pose an urgent public health threat due to their ability to compromise treatment of severe infections or to spread to other bacteria via plasmids. Widespread use of whole genome sequencing (WGS) by state public health departments (SPHDs) has provided new opportunities to identify these highly-concerning resistance determinants in near-real time. We describe the public health experience with enhanced surveillance (the collection of additional laboratory and epidemiological information) for enteric pathogens carrying *mcr* genes, which confer transferable resistance to the antibiotic colistin, an agent that is used to treat severe multidrug-resistant infections but that is not included in broth microdilution testing performed by CDC's National Antimicrobial Resistance Monitoring System (NARMS).

METHODS: SPHDs (or in some cases, CDC) performed WGS on nontyphoidal *Salmonella* and Shiga toxin-producing *E. coli* clinical isolates and made sequences publicly available through the National Center for Biotechnology Information (NCBI). Since 2014, CDC has screened sequenced public health isolates for plasmids and resistance determinants using ResFinder 3.0. Isolates with *mcr* genes were submitted to CDC for confirmation, and isolates sharing a serotype were compared via whole genome multilocus sequence typing (wgMLST). SPHDs provided epidemiological information from patient interviews.

RESULTS: We identified nine patients with NTS containing *mcr-1*, two patients with NTS containing *mcr-3*, and one patient with STEC containing *mcr-1*. All 12 patients traveled internationally in the 10 days before illness onset. Six patients whose NTS isolates contained *mcr-1* traveled to the Dominican Republic, five (three with *mcr-1* and two with *mcr-3* containing isolates) traveled to Southeast Asia, and one patient whose STEC isolate contained *mcr-1* traveled to Peru. The isolates from the travelers to the Dominican Republic shared an identical IncX4 plasmid but were not highly related by wgMLST (range 6–20 alleles).

CONCLUSIONS: Using WGS, we detected 12 patients who were returning international travelers with enteric pathogens harboring *mcr* genes, which would likely not have been identified by routine antimicrobial susceptibility testing. Enhanced surveillance allowed the linkage of important epidemiological and molecular features, including the presence of a common plasmid among isolates from patients with a shared travel history to the Dominican Republic. Information obtained by enhanced surveillance may help to inform public health recommendations in affected states and countries. Enhanced surveillance for important resistance determinants may detect early introduction of new and emerging resistance and help to prevent spread in communities and healthcare settings.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Antimicrobial Resistance; Foodborne Disease; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9499

Abstract Type Quick

Abstract Title Examining the Epidemiology of Carbapenemase-Producing Carbapenem-Resistant Enterobacteriaceae in Indiana

Abstract

BACKGROUND: Carbapenemase-producing carbapenem-resistant *Enterobacteriaceae* (CP-CRE) are a recognized public health threat due to extensive drug-resistance and increased mortality and transmissibility. In response, a position statement was created at the 2017 CSTE Annual Conference that recommended public health reporting and national notification of CP-CRE. However, the position statement only focuses on the three most common genera of CP-CRE, often colloquially referred to as the “big three”: *Escherichia coli*, *Klebsiella* species, and *Enterobacter* species. The Indiana State Department of Health (ISDH) mandated reporting for all CP-CRE on December 25, 2016.

Indiana’s updated reporting rule, as well as expanded laboratory capacity for CP-CRE detection, allowed ISDH to conduct surveillance for all carbapenemase-producing *Enterobacteriaceae*. The distribution of CP-CRE cases in Indiana is described in this study to inform public health professionals of the epidemiology of CP-CRE in Indiana and to compare to the recommendations of the CSTE position statement.

METHODS: The epidemiology of reported CP-CRE cases in Indiana from January through December 2017 was analyzed. Descriptive statistics were used to assess the distribution of CP-CRE cases by organism.

RESULTS: A total of 354 cases of CP-CRE were reported to the ISDH in 2016 and 249 cases were (preliminarily) reported in 2017, resulting in 603 total CP-CRE cases identified during the study. Case counts of the “big three” causative agents are: *Klebsiella pneumoniae* (475, 78.8%), *Escherichia coli* (33, 5.5%), *Enterobacter cloacae* complex (27, 4.5%), *Klebsiella oxytoca* (4, 0.6%), and *Enterobacter aerogenes* (2, 0.3%). The “non-big three” causative agents include: *Serratia marcescens* (39, 6.4%), *Citrobacter freundii* complex (14, 2.3%), *Proteus mirabilis* (3, 0.5%), *Citrobacter koseri* (3, 0.5%), *Morganella morganii* (1, 0.2%), *Providencia rettgeri* (1, 0.2%) and *Citrobacter amalonaticus* (1, 0.2%). Collectively, the “big three” organisms account for 89.7% of total CP-CRE cases, while the “non-big three” organisms account for 10.3% of total CP-CRE cases.

CONCLUSIONS: These data suggest that 10.3% of cases likely occur nationally that would be unreported in states that have not mandated expanded surveillance definitions for CP-CRE. Based on the recommendations of the current position statement, the results of the study demonstrate the need for recommending public health reporting and national notification for all CP-CRE.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Healthcare Associated Infections (HAI); Infectious Diseases; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9951
Abstract Type	Quick
Abstract Title	Expansion of Precious Drugs & Scary Bugs Campaign: Assessment of Knowledge, Attitudes, and Antibiotic Prescribing Behaviors of Illinois Dentists
Abstract	BACKGROUND: Up to 50% of antibiotics prescribed in the outpatient setting are inappropriate or unnecessary. Dentists have been identified as a high prescribing group; in 2011 nationwide, general dentists prescribed 10% (24.5 million prescriptions) of antibiotics in the community setting. To promote judicious antibiotic prescribing among dental providers and identify opportunities for improvement, the Illinois Department of Public Health (IDPH) expanded the statewide Precious Drugs & Scary Bugs Campaign to include dentists. Campaign participation includes completing a survey, returning a commitment statement, and implementing stewardship activities outlined in a toolkit customized for dental providers. IDPH assessed dental provider's knowledge, attitudes, and antibiotic prescribing behavior to guide the implementation of future dental antibiotic stewardship efforts. METHODS: IDPH worked with a multi-stakeholder antibiotic stewardship workgroup, including the Illinois State Dental Society, to develop a dental provider toolkit and survey. The toolkit adapts the CDC Core Elements of Outpatient Antibiotic Stewardship for dental providers and includes treatment guidelines for antibiotic use in dental settings and patient education resources. Dentists were invited to participate in the campaign through a mailed packet that included an invitation letter, a statement of commitment form, a survey, and the toolkit. IDPH provided a postage paid envelope to return both the survey and commitment form. RESULTS: In November 2017, IDPH mailed 331 packets to licensed dentists in four Illinois counties. As of December 2017, 47 dentists have completed the survey. The majority of respondents were general dentists who have been in practice for over 20 years. Over 65% of respondents agreed that antibiotics are overprescribed in Illinois, however, only six percent agreed that they prescribe antibiotics more than they should. Over 70% percent of providers agreed that they were concerned about antibiotic resistance in the community when prescribing antibiotics. For high risk patients, most respondents reported that they would recommend prophylactic antibiotics for dental extractions (73%), dental implant placement (67%), or periodontal procedures (62%). Respondents (24%) indicated that patients pressured them for antibiotics for oral infections. Respondents reported several challenges with making decisions about antibiotic prescribing, including being unclear about the best guidelines to reference, conflicting scientific evidence, and the need for more information on antibiotic selection and potential risks of antibiotic use. CONCLUSIONS: Dental providers in Illinois recognize that antibiotic overuse is a problem but need additional support and guidance. IDPH will collaborate with stakeholders to provide dentists with education and resources on antibiotic prescribing and best practices for antibiotic stewardship.
Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Evaluation; Disease Prevention
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9640

Abstract Type Quick

Abstract Title Impact of Ertapenem on Detection of Carbapenemase-Producing Enterobacteriaceae in Tennessee

Abstract

BACKGROUND: Carbapenem-resistant Enterobacteriaceae (CRE) are reportable in Tennessee; isolates must be sent to the State Public Health Laboratory (SPHL) for carbapenemase-production (CP-CRE) detection and for resistance mechanism testing. In 2015, the Council of State and Territorial Epidemiologists (CSTE) changed the CRE case definition to include resistance to ertapenem, known to have high sensitivity but lower specificity for CP-CRE detection. We aim to describe the role ertapenem plays in statewide surveillance.

METHODS: CRE were defined as *E.coli*, *Klebsiella*, and *Enterobacter* species isolated from any clinical specimen and resistant to doripenem, meropenem, imipenem (minimum inhibitory concentrations [MIC] of ≥ 4 $\mu\text{g/ml}$) or ertapenem (MIC ≥ 2 $\mu\text{g/ml}$), or demonstrated production of a carbapenemase. We aggregated CRE surveillance data from Jan. 1st, 2016 thru Nov. 30th, 2017. We grouped isolates into an 'ertapenem only' group, based on resistance to ertapenem alone, and an 'other carbapenems' group, based on resistance to at least one other carbapenem (i.e. meropenem, doripenem, imipenem) regardless of ertapenem resistance. We used clinical laboratory susceptibilities. Statistical analyses were conducted using SAS V9.4.

RESULTS: Among 1,410 cases reported, 1,043 cases (74%) had isolates submitted to the SPHL with susceptibilities. Out of these 1,043 cases, 401 (38%) were CP-CRE. There were 412 (40%) cases in the 'ertapenem only' group and 631 (60%) in the 'other carbapenems' group. Within each group, 22 (5%) of the ertapenem group were CP-CRE and 379 (60%) of the 'other carbapenem' group were CP-CRE. By univariate logistic regression, the odds of detecting a CP-CRE were 26 times higher when an isolate was resistant to at least one of meropenem, doripenem, or imipenem when compared to the isolates resistant to only ertapenem (OR=26.7, 95% CI 16.9--42.2). Within the 'ertapenem only' group, out of all the *Enterobacter spp.*, *E. coli*, and *Klebsiella spp.* sent to the SPHL, 5%, 2%, and 11% were CP-CRE compared to 67%, 21%, and 71% of the 'other carbapenems' group, respectively.

CONCLUSIONS: Including ertapenem in the case definition detected additional CP-CRE cases and may be important if ertapenem is the only carbapenem tested. However, the likelihood of detecting CP-CRE was much lower compared to other carbapenems. These findings should be taken into account if resources are limited (e.g., to perform additional characterization of CRE, or a limited number of isolation rooms). Additionally, we suggest including at least one non-ertapenem carbapenem when performing susceptibility testing.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Surveillance; Antimicrobial Resistance; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9284

Abstract Type Quick

Abstract Title Mapping Hospital Antibigram Data in Massachusetts Using Healthmap

Abstract

BACKGROUND: The need to understand the burden and geographic spread of emerging resistant pathogens such as carbapenem-resistant Enterobacteriaceae (CRE) has become increasingly important. The Massachusetts Department of Public Health (MDPH) has been collecting aggregate hospital antibiogram data since 1999 for feedback to providers in healthcare settings. We sought to develop an online tool for analyzing temporal and geographic trends in antibiotic resistance prevalence across the state of Massachusetts using these data.

METHODS: We used an existing online platform for antibiotic resistance surveillance, www.resistanceopen.com, to house aggregate antibiogram data for the calendar years 2013-2015. This cloud-based, mobile-compatible, web platform was developed by an academic research group specializing in infectious diseases mapping, HealthMap. It is housed on an Amazon EC2 instance, and allows user restricted visualization of antibiotic resistance surveillance data, along with front-facing public antibiotic resistance data visualization. We adapted existing tools within the web-based platform to allow us to view temporal (annual) and geographic trends (facility, county, and state) in resistance for commonly used antibiotics for Gram-positive and Gram-negative organisms.

RESULTS: Aggregate geographic resistance data exists on the online platform, representing 72 clinical laboratories in Massachusetts, 11 bacterial species, and relevant antibiotics. These visualizations are generated in real-time using uploaded data, and are modular and expandable across antibiotic, region (county), bacterium, and time.

CONCLUSIONS: This approach will allow both internal evaluations of trends in emerging pathogens, such as CRE, and antibiotic susceptibility by facility, as well as facilitate public-facing data access to garner public interest regarding the growing challenge of antibiotic resistance. Additionally, with this resistance data readily available for prescribers, it might be expected to support antibiotic decision-making.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Surveillance; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9861

Abstract Type Quick

Abstract Title Perceptions and Behaviors Regarding Antibiotic Use Among Pediatric and Family Physicians in Hawaii

Abstract

BACKGROUND: Antibiotic resistance is one of our most serious public health threats. According to CDC, roughly 30% of US prescriptions in the outpatient setting are unnecessary. In Hawaii, little is known about factors contributing to inappropriate prescribing of antibiotics. Our study aimed to better understand perceptions of antibiotic overuse and reasons for inappropriate prescribing among family physicians and pediatricians in outpatient settings across Hawaii.

METHODS: An online survey was created using Epi Info™ and disseminated to members of the relevant professional medical societies across the state (N=485). Questions included topics on provider perception of antibiotic overuse, parent expectations, and confidence in prescribing, as well as behaviors related to antibiotic prescribing and receipt of antibiotic education. Descriptive statistics were calculated for perceptions of antibiotic overuse and prescriber confidence. Logistic regression was used to estimate odds ratios (OR's) for factors contributing to inappropriate prescribing practices. When appropriate, results were stratified by gender.

RESULTS: Completed surveys were collected from 100 physicians (21% response rate). While 90% of responding physicians agreed or strongly agreed antibiotics were overused in Hawaii, only 21% stated the same within their practice. Most physicians (93%) reported feeling confident or very confident in their ability to choose the correct antibiotic or to decide against prescribing an antibiotic when deemed unnecessary. Self-identified inappropriate prescribing was significantly associated with perceived parent pressures. Male physicians who reported experiencing parent pressure for antibiotics in the 30 days before taking the survey were more likely (OR: 3.9; 95% CI: 1-14) to report potentially inappropriate prescribing. This relationship was not seen among female providers. Physicians who reported changing treatment based on parent pressure were more likely (OR: 4.1; 95% CI: 1-13) to report uncertainty in their choice to prescribe antibiotics, regardless of gender. No relationship was found between inappropriate prescribing and physician confidence, cost to patient or facility, risk of missing an infection, or recent receipt of education on antimicrobials.

CONCLUSIONS: While most physicians in Hawaii agree antibiotics are overused across the state, few believe overprescribing is occurring within their practice. Point prevalence estimates on appropriateness of antibiotic prescribing at the practice level may help elucidate true rates of antibiotic overuse across the state. Perceived parent pressures were the strongest indicators of inappropriate prescribing among responding physicians. Responding physicians were confident in their prescribing abilities, but may benefit from support in effective dialogue with parents on antibiotic stewardship and the harms of inappropriate prescribing.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Antimicrobial Resistance; Healthcare Associated Infections (HAI); Prevention

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9233

Abstract Type Quick

Abstract Title The Reality and Usefulness of Generating a County-Wide Antibigram

Abstract

BACKGROUND: National surveillance of antimicrobial resistance (AR) is hampered by limited geographic sampling, low numbers of participating hospitals, and small numbers of isolates. National surveillance cannot estimate local AR burden. US hospitals are required to generate an annual report of AR: the antibiogram. Combining facility-level antibiograms into a regional antibiogram provides an opportunity to track multi-drug resistant organism (MDRO) burden and identify new MDRO public health threats.

METHODS: The Los Angeles County (LAC) Department of Public Health (DPH) conducted a cross-sectional, voluntary survey of 2015 annual facility-level antibiograms. Isolates from sterile sources were pooled. Susceptibility was aggregated and percent susceptible was calculated when all isolates were routinely tested (i.e. no reflex testing). Duplicate data entry was used, and discordance was mediated by consensus. The LAC Healthcare-Associated Infections (HAI) and AR Committee reviewed results and collaboratively generated the final report, which included organism-specific feedback on testing, analysis and reporting methodologies to improve future antibiograms. This report was posted online, and shared directly with all clinical microbiology directors in LAC.

RESULTS: Antibiograms were submitted by 77 (84%) acute care hospitals (ACH) and 9 (100%) long-term ACHs (LTACHs). Carbapenem-resistance (CR) among *Escherichia coli* was rarer than expected, with 0.1% prevalence in the county (range 0-1%). CR among *Pseudomonas aeruginosa* was found to be much more prevalent at 19.3% in the county (range of 3-36%). Clindamycin resistance among group B streptococcus was surprisingly high at 79.3% (range 12-100%). Four (5%) ACHs erroneously reported susceptibility results for beta-lactam antibiotics to which *Stenotrophomonas maltophilia* are intrinsically resistant. Thirty-four (44%) of ACHs reported on species for which there were less than 30 isolates tested.

CONCLUSIONS: Generation of a regional antibiogram allowed LACDPH to better characterize local AR burden, and identified a potentially novel public health threat that has initiated further investigation. Examination of facility-level antibiograms also provided an opportunity to offer specific feedback on analyzing and reporting antibiogram data, i.e. reporting results for species that have data from at least 30 isolates. As of February 2017, annual antibiograms are reportable to LACDPH. LACDPH will generate regional antibiograms annually to track local AR trends over time, identify emerging public health threats, and in turn target intervention and prevention efforts as needed.

Committee Infectious Disease

Topic Antimicrobial Resistance

Keywords Hospital Data; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type	Roundtable
ID	9497
Abstract Type	Roundtable
Abstract Title	Antibiotic Resistance Is Shore to Stay: How HAI Programs Are Using the Antibiotic Resistance Laboratory Network to Effect Change

Abstract

Key Objectives:

Roundtable participants will discuss the impact the Antibiotic Resistance Laboratory Network has had on state and local health departments and share successful strategies for utilizing new antibiotic resistance data to guide public health action.

Brief Summary:

The Centers for Disease Control and Prevention (CDC) has recognized antibiotic resistance as one of today's most serious public health threats. Detection of current and emerging antibiotic resistant pathogens, such as carbapenemase-producing carbapenem-resistant *Enterobacteriaceae* and multidrug-resistant *Candida auris*, require strong public health laboratory capacity. As such, the CDC has dedicated Epidemiology and Laboratory Capacity (ELC) funding to facilitate the growth of state and local health department healthcare-associated infections epidemiology capacity as well as the expansion of state public health laboratories. CDC ELC funding dedicated to state public health laboratories allows for increased detection of antibiotic resistant threats. In addition to expanded state public health laboratory capacity, CDC ELC funding was allocated to seven state laboratories to create regional laboratories across the country known as the Antibiotic Resistance Laboratory Network (ARLN). The ARLN aims to provide stronger detection, better data for prevention, an increased antimicrobial resistance isolate bank for innovative research, and increased laboratory data to inform epidemiologic response. Enhanced capacity provided by the ARLN has allowed state and local public health departments to efficiently and rapidly respond to antimicrobial resistant threats. This roundtable will provide participants the opportunity to discuss how their jurisdictions have used the ARLN as a tool to change public health intervention; the true value of the ARLN for state and local epidemiologists; and share success stories. Topics to be discussed include jurisdiction implementation and utilization of the ARLN, protocols for epidemiologic response, and procedural tools developed to aid local and state health departments in responding to antibiotic resistant threats. The goal of this roundtable is to facilitate dialogue between state and local health departments and encourage participants to share their experiences in order to improve the antibiotic resistance epidemiologic response across the nation.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Healthcare Associated Infections (HAI); Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9766
Abstract Type	Roundtable
Abstract Title	Antimicrobial Resistance (AR) Surveillance – Collecting and Utilizing AR Data to Enhance Stewardship Efforts

Abstract

Key Objectives:

- Discuss state and local health department efforts to conduct antibiotic resistance surveillance through statewide or regional antibiograms.
- Share New Hampshire's successes and challenges with creation of a statewide antibiogram as a tool for promoting antibiotic stewardship and tracking antibiotic resistance patterns.
- Discuss future use of antibiograms and how individual state efforts can contribute to reducing antimicrobial resistance nationally.

Brief Summary:

Antimicrobial resistance (AR) is among our nation's most significant growing global public health concerns and poses a major threat to individual and population health. The Centers for Disease Control and Prevention (CDC) reported that each year in the United States, at least 2 million people become infected with bacteria that are resistant to antibiotics and at least 23,000 people die each year as a direct result of these infections[i]. Improved local, state, and national AR surveillance is needed to proactively respond to new and emerging antimicrobial resistant threats. Collecting and disseminating AR data can serve as a useful clinical and public health tool to promote antibiotic stewardship and reduce resistance. The New Hampshire Division of Public Health Services (DPHS) is addressing antimicrobial resistance by enhancing surveillance and partnering with subject matter experts throughout the state to provide additional guidance. In November 2016, the NH reportable disease administrative rules (He-P 301) were amended to require hospitals to submit antibiogram data annually. In December 2017, the first statewide antibiogram was published with the guidance of a clinical advisory group of infectious disease medical and pharmacy experts. NH DPHS is currently discussing future iterations of the statewide antibiogram and planning to assess state and regional trends annually in order to guide continued antimicrobial stewardship efforts. State, as well as local and county level jurisdictions would benefit from discussions about utility and future directions of antibiogram data; particularly validity, comparisons, data collection methods, limitations, and presentation. While coordination of national AR surveillance is an issue being addressed through the CSTE/CDC/APHL co-led national AR Task Force, it is also important for individual jurisdictions to share experiences and best practice specific to public health use of antibiogram data. This roundtable would provide a forum for collaboration and sharing of ideas and has potential to inform future antimicrobial resistance surveillance efforts.

[i] <https://www.cdc.gov/drugresistance/index.html>

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance; Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9982
Abstract Type	Roundtable
Abstract Title	Collaborative Approaches to Promote Antimicrobial Stewardship across the One Health Spectrum

Abstract

Key Objectives:

- Describe lessons learned from the New York State Department of Health 'Be Antibiotics Aware' outpatient antibiotic stewardship campaign including:
 - NYS Medicaid data analysis to evaluate county-level antibiotic prescribing trends to target intervention and outreach
 - Development of an evidence-based 'Smart Use' commitment poster for healthcare providers
 - Production of adult/pediatric distilled antibiotic prescribing guidelines pocket card
 - Development of a training video on healthcare provider communication regarding smart use of antibiotics and a patient-oriented video on antibiotic use
- Review successes and lessons learned in the implementation of antimicrobial stewardship in state health departments including Pennsylvania and Minnesota and review the development of a statewide educational art and video competition and development of a One Health approach to antibiotic stewardship, respectively.
- Discuss novel resources, approaches, and opportunities in antimicrobial stewardship with federal public health partners.
- Engage roundtable participants in discussion about best practices regarding a One Health approach to antibiotic stewardship.

Brief Summary:

Antimicrobial resistance poses a significant challenge that undermines progress in public health globally. Inappropriate use of antibiotics in clinical settings, including prescriptions for acute upper respiratory infections, exacerbates the emergence of drug-resistant bacterial pathogens. Equally important is the overuse and misuse of antimicrobial drugs in agriculture settings. As part of the overview, this panel will highlight sources of data and tools that can be used to promote antimicrobial stewardship in the spirit of a One Health approach. The session will include presentations on lessons learned in selected public health jurisdictions and examples of planned expansion of the 'Be Antibiotics Aware' program will be discussed as will be opportunities for new collaborative initiatives.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10020
Abstract Type	Roundtable
Abstract Title	Minnesota One Health Antibiotic Stewardship Collaborative: Working across Health Disciplines to Improve Antibiotic Use

Abstract

Key Objectives:

In this roundtable discussion, we will describe Minnesota's approach to impact antibiotic resistance (AR) emergence in healthcare facilities, communities, farms, and the natural environment by coordinated improvement of antibiotic use (antibiotic stewardship, AS). We will discuss the origin and startup of the Minnesota One Health AS Collaborative (MOHASC), operational logistics, challenges, and activities that have been carried out to date. With the panelists from New York and Pennsylvania, we will also highlight the multistate approach to One Health antibiotic stewardship ongoing since early 2017.

Brief Summary:

AR is a local, national, and global problem with considerable implications for human health. Antibiotic use (AU), a chief driver of AR, is a major part of healthcare and animal health. AU also contributes to antibiotic contamination of the natural environment. "One Health" is the recognition that human, animal, and environmental health is interconnected. AR and AU exemplify this concept. State leaders in public health, healthcare, veterinary medicine, agriculture, and academia have formed the MOHASC to meet goals of a Minnesota AS Five-Year Strategic Plan. Qualitative data collected at a statewide Antibiotic Summit in January 2016 show similar AU "wants" and "fears" among human, animal, and environmental health fields. These attitudes informed Minnesota's Strategic Plan goals: advance healthcare and animal AS, understand the environmental impact of antibiotics, and promote the one health concept of AS to professionals and the public. Strategic plan goals are met by activities developed and implemented by four voluntary work groups, each comprised of professionals from all health disciplines and led by a chair person. Overall OHASC direction and action are guided by a Director of One Health Antibiotic Stewardship, housed in Minnesota Department of Health's Executive Office. Key elements of MOHASC include sharing AS needs and challenges among health fields; acknowledging that all fields can improve; developing setting-specific priorities and goals; engaging with industry; and garnering support in state government. Understanding can improve transparency and trust among disciplines, both which are essential to track and communicate AU and AR data in meaningful ways. In turn, trust and measurement are both critical to maintain the forward momentum of change. All or parts of the approach used in Minnesota might be replicable in other states.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Healthcare Associated Infections (HAI); Antimicrobial Resistance; One Health
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9049
Abstract Type	Roundtable
Abstract Title	NARMS Roundtable

Abstract

Key Objectives:

1. Discuss changes to the National Antimicrobial Resistance Monitoring System (NARMS) in response to increased use of whole genome sequencing by federal, state, and large urban health department laboratories. 2. Discuss plans to develop an enhanced national surveillance program in collaboration with federal, state, and local partners to better track and respond to emerging or highly-concerning resistance.

Brief Summary:

Infections caused by antimicrobial-resistant enteric pathogens are a serious public health threat. NARMS, a collaboration among federal, state, and large urban health departments, identifies and tracks trends in antimicrobial resistance among *Salmonella*, Shiga toxin-producing *E. coli*, *Shigella*, *Campylobacter*, and non-cholera *Vibrio* species. State and large urban health departments submit a subset of patient isolates (1 in 20 for most pathogens) to CDC for antimicrobial susceptibility testing (AST). The 2015 National Action Plan for Combatting Antibiotic-Resistant Bacteria (CARB) was introduced to address a growing national threat. In response, 54 state and large urban health departments have received funding to perform whole genome sequencing (WGS) of bacterial isolates. The NARMS team is now able to use WGS information to screen isolate genomes for resistance determinants, and to predict the corresponding resistance pattern of sequenced isolates. Use of genotypic data has expedited the identification of the resistance profile of strains causing outbreaks and made it possible to detect emerging resistance in near-real time. Discussion will address the changes to NARMS surveillance that have resulted from the incorporation of genotypic resistance data including the correlation between phenotypic and genotypic resistance, plans to enhance surveillance to better assess the emergence and spread of highly resistant infections, and opportunities for partner collaboration on projects.

Committee	Infectious Disease
Topic	Antimicrobial Resistance
Keywords	Antimicrobial Resistance
Consider for Different Presentation?	No
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9462
Abstract Type	Breakout
Abstract Title	Association between Rurality, Social Determinants of Health and Non-Typhoidal Salmonella and Campylobacter Infections, Pennsylvania, 2001-2015
Abstract	BACKGROUND: The importance of social determinants of health have not been widely characterized with respect to enteric diseases, but they may play an important role, 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 both <i>Salmonella</i> and <i>Campylobacter</i>, but other social determinants have not been studied in Pennsylvania. The purpose of this study was to evaluate the relationship between social determinants of health and county <i>Salmonella</i> and <i>Campylobacter</i> rates, and determine if these relationships differ in rural and urban Pennsylvania counties. METHODS: Annual county rates/100,000 population of <i>Salmonella</i> and <i>Campylobacter</i> in Pennsylvania during 2001-2015 were analyzed (stratified by pathogen). Social determinants (county level) included rurality (urban/rural), median household income, percent living below the poverty level, percent with high school education or less, percent uninsured, percent receiving Supplemental Nutrition Assistance Program (SNAP) benefits, percent farmland, and percent of census tracts within the county with low supermarket access. Poisson regression (SAS v9.4) was used to determine if any social determinant was associated with either <i>Salmonella</i> or <i>Campylobacter</i> rates statewide or stratified by rurality. RESULTS: Rates of <i>Salmonella</i> and <i>Campylobacter</i> were significantly higher in rural counties than urban counties (<i>Salmonella</i>: 32% higher; statewide=13.8 cases/100,000, urban=12.1, rural=16.0; <i>Campylobacter</i>: 75% higher; statewide=16.3 cases/100,000, urban=12.7, rural=22.0) in. A \$10,000/year median income increase was associated with 10% lower <i>Campylobacter</i> rates (95% CI: 3.2-16%). A 10% increase in uninsured residents was associated with 62% higher <i>Salmonella</i> (95% CI: 18-122%) or 229% higher <i>Campylobacter</i> (95% CI: 150-332%) rates. A 10% farmland increase was associated with 8% higher <i>Salmonella</i> (95% CI: 3-13%) or 15% higher <i>Campylobacter</i> (95% CI: 10-20%) rates. Among rural counties, a 10% increase in residents with high school education or less was associated with 24% higher <i>Salmonella</i> (95% CI: 2-51%) or 64% higher <i>Campylobacter</i> (95% CI: 39-93%) rates. Among urban counties, a 10% increase in households receiving SNAP was associated with 32% lower <i>Campylobacter</i> rates (95% CI: 12-47%), and a 10% increase in the percent of low supermarket access census tracts was associated with 3% higher <i>Salmonella</i> (95% CI: 0-6%) or 6% higher <i>Campylobacter</i> (95% CI: 3-9%) rates. CONCLUSIONS: Multiple social determinants appeared associated with <i>Salmonella</i> or <i>Campylobacter</i> at the ecological/county level, but associations differed by pathogen and rurality. These results suggest public health programs to prevent enteric illness should be tailored for urban and rural communities. Programs targeting income inequality, education and food access could consider adding a food safety/education component.
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Epidemiologic Methods; Rural Health
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9517
Abstract Type	Breakout
Abstract Title	Comparing Outbreaks Associated with Meat and Poultry Products Reported to the National Outbreak Reporting System and the USDA, Food Safety and Inspection Service
Abstract	BACKGROUND: The National Outbreak Reporting System (NORS) is a platform for local, state, territorial health departments and the Centers for Disease Control and Prevention (CDC) to report outbreaks transmitted through food, water, or animal contact. The United States Department of Agriculture, Food Safety and Inspection Service (FSIS) also receives reports from partner agencies of outbreaks associated with meat and poultry products; FSIS responds to these outbreaks to protect public health. Comparing outbreaks reported to NORS and FSIS can help identify potential reporting gaps. METHODS: Outbreaks caused by <i>Salmonella</i> , Shiga toxin–producing <i>E. coli</i> (STEC), <i>Campylobacter</i> , and <i>Listeria Monocytogenes</i> , with evidence of linkage to meat and poultry, and reported to NORS and FSIS during 2010–2014, were identified and compared by etiology, number of states reporting illnesses, implicated vehicle, and investigation outcomes RESULTS: During 2010–2014, 197 meat and poultry-associated outbreaks caused by the four pathogens listed above were reported to NORS. During the same time period, 118 outbreaks were reported to FSIS. Of the 197 NORS outbreaks, 159 (80.7%) were not reported to FSIS, and 80 outbreaks reported to FSIS were not reported to NORS. A significant proportion of NORS-only outbreaks involved a single-state compared to FSIS-only outbreaks (94.3% vs 23.7%, respectively; $P < 0.01$). With respect to etiology, proportionally more NORS-only outbreaks involved <i>Salmonella</i> than did FSIS-only outbreaks (80.1% vs 37.5%, respectively; $P < 0.01$). NORS-only outbreaks were more frequently linked to chicken (39.6%) and pork (24.5%) than were FSIS-only outbreaks (20.0% and 3.8%, respectively; $P < 0.01$). Of the 80 FSIS-only-reported outbreaks, 37(46.3%) were caused by STEC and 26 of 37(70.3%) were linked to beef products. Fifteen of 159 (9.4%) NORS-only outbreaks were caused by STEC and 8 of 15 (53.3%) were linked to beef products. CONCLUSIONS: Approximately 80% of meat-or-poultry products associated NORS outbreaks were not reported to FSIS, especially single-state outbreaks and outbreaks associated with chicken and pork products. Multi-state, STEC, and beef-associated outbreaks were more likely reported to FSIS. Thirty-eight outbreaks were reported both NORS and FSIS, 14 resulted in FSIS recalls. The reporting gap between NORS and FSIS limits the ability of FSIS to rapidly respond to outbreaks and take appropriate measures to protect public health. State and federal partners should enhance information sharing to ensure early detection and coordinated efforts to prevent foodborne illness.
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Outbreaks; NORS (National Outbreak Reporting System)
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10043

Abstract Type Breakout

Abstract Title Culture-Independent Diagnostic Testing for Vibriosis: Preliminary 2017 National Surveillance

Abstract

BACKGROUND: The Cholera and Other *Vibrio* Illness Surveillance (COVIS) system collects data on domestic foodborne and non-foodborne *Vibrio* infections. Foodborne *Vibrio* infections are usually associated with seafood consumption, particularly raw shellfish, and can cause gastrointestinal illness or septicemia. In 2017, the vibriosis national case definition expanded to classify cases detected by culture-independent diagnostic tests (CIDs) as probable cases due to increased CIDT use for enteric pathogen diagnosis.

METHODS: CDC collected national case data using a questionnaire revised to accommodate CIDT-detected cases. We reviewed cases identified in 2017 by isolation or detection of *Vibrio* in stool. We summarized CIDT-positive *Vibrio* infections and reported seafood exposures and clinical features among patients with infections identified by culture only (Cx+ only), CIDT not confirmed by culture or culture negative (CIDT+ only), or both (Cx+/CIDT+).

RESULTS: In 2017, states reported 502 *Vibrio* infections identified from stool. Among these, 281 (56%) specimens were identified as positive for *Vibrio* by CIDT; the remaining infections were Cx+ only. Infections identified by CIDT, which can include multiple assays for *Vibrio* in one panel, were reported as *Vibrio*, species not identified (n=223, 79%); *V. cholerae* (n=36, 13%); *V. cholerae* with *Vibrio*, species not identified (n=15, 5%); and *V. parahaemolyticus* (n=7, 2%). Among CIDT-positive specimens, 74% were CIDT+ only (38% with negative culture and 36% not cultured) and 26% were Cx+/CIDT+. Among Cx+/CIDT+ infections, 47% were determined to be *V. parahaemolyticus* by culture. Non-*Vibrio* pathogens were identified by culture or CIDT in 8% of Cx+ only, 17% of Cx+/CIDT+, and 18% of CIDT+ only infections. Raw shellfish consumption was reported by 53% of patients with Cx+ only infections, 51% of patients with Cx+/CIDT+ infections, and 14% of patients with CIDT+ only infections. Frequently reported symptoms for Cx+ only, Cx+/CIDT+, and CIDT+ only infections were diarrhea (90%, 92%, and 84%, respectively), abdominal cramps (69%, 74%, and 63%, respectively), and vomiting (30%, 32%, and 36%, respectively).

CONCLUSIONS: CIDs were commonly used to detect *Vibrio* in 2017 and often do not identify species. Most specimens in which *Vibrio* were detected by CIDT were never cultured or had a negative culture. Detection of non-*Vibrio* pathogens is more common when CIDs are used. Fewer patients with infections identified only by CIDT reported consuming raw shellfish, suggesting that some infections detected only by CIDT may be false-positives. Current shellfish regulations that depend on culture confirmation and *Vibrio* species identification may warrant reconsideration as CIDT use increases.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Enteric Infectious Diseases; Foodborne Disease; Surveillance

Consider for Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9616

Abstract Type Breakout

Abstract Title Cyclosporiasis Outbreak Among Patrons at a Restaurant in Texas, 2017

Abstract

BACKGROUND: Outbreaks of cyclosporiasis, a gastrointestinal illness caused by the protozoan *Cyclospora cayetanensis*, have occurred in Texas during the past five summers. Outbreak cases in 2012–2015 were associated with consumption of fresh cilantro imported from Puebla, Mexico. In July 2017, epidemiologists with the Texas Department of State Health Services (DSHS) noted an increase in cases of *Cyclospora* infection in diners at one of four locations of Restaurant A. To identify the potential source, DSHS requested assistance from the Centers for Disease Control and Prevention (CDC) to conduct an investigation with the cooperation of City of Houston Health Department, Harris County Public Health, Fort Bend County Health and Human Services, and Brazoria County Health Department.

METHODS: Since cyclosporiasis has previously been associated with fresh produce, a menu-specific questionnaire was designed to focus on fresh produce items served at Restaurant A, a Mediterranean-style restaurant with multiple locations. A confirmed case was defined as laboratory-confirmed infection in a person who had clinically compatible symptoms within two weeks of eating at one of four restaurant locations on or after May 28 and who did not report international travel within that same two week-period. A probable case was defined in the same way, but without laboratory confirmation. Controls were defined as diners at Restaurant A on or after May 28, who did not have symptoms of cyclosporiasis (watery diarrhea, nausea, fatigue, abdominal cramps, weight loss). Case-patients and controls were matched on dining date and restaurant location. Bivariate logistic regression was used to determine associations between food exposures and illness, and to calculate matched odds ratios (mORs) and 95% confidence intervals (CIs).

RESULTS: Twenty-four case patients (16 confirmed; 8 probable) and 70 controls were interviewed using the menu-specific questionnaire; of those, 22 case patients were matched with 66 controls. In menu-item analyses, consumption of tabouli was associated with illness (mOR = 8.0; 95% CI 2.1–44.5). In ingredient-level analyses, green onions -- consumed by 18 case-patients (81.8 %), including 15 who ate tabouli -- were associated with cyclosporiasis (mOR = 11.3; 95% CI 2.6–104.7).

CONCLUSIONS: To our knowledge, green onions have not previously been epidemiologically linked to cyclosporiasis outbreaks in the United States. Although traceback investigations were initiated to determine the source(s) of green onions, this effort was delayed due to public health response to hurricanes and was ultimately unsuccessful. This investigation illustrates the need for timely and thorough epidemiologic investigations to prevent future cyclosporiasis outbreaks.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Epidemiology; Foodborne Disease; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9561

Abstract Type Breakout

Abstract Title Epidemiologic Lessons Learned from the Investigation of a Multistate Cluster of Multidrug Resistant *Shigella Sonnei* Infection Among Men, United States, 2017.

Abstract

BACKGROUND: In August 2017, CDC and state health departments initiated an investigation of a cluster of multidrug resistant (MDR) shigellosis identified through PulseNet.

METHODS: A case was defined as infection in an individual with a clinical specimen culture *Shigella sonnei* isolate with a matching pulsed field gel electrophoresis pattern in PulseNet and illness onset after June 2, 2017. Study isolates underwent antimicrobial susceptibility testing (AST) and whole-genome sequencing (WGS) to identify genetic determinants of resistance and assess isolate relatedness. Case-patients were interviewed using a supplemental questionnaire, which asked about demographic characteristics, treatment, and exposures. Risk factors assessed 7 days before illness onset included water, person-to-person contact and sexual activities. Other questions explored health promotion materials received.

RESULTS: There were 67 cases in 14 states and Washington, D.C. Case patient median age was 49 years (range 21-73), and 97% were male. WGS for 19 clinical isolates showed that all were closely related. AST for two isolates, and genetic analysis of 31 isolates, showed resistance to six classes of antibiotics. Of 67 case-patients, 24 (37%) had completed supplemental questionnaires. Of these, 100% were male, 87% were white, and 90% described their sexual orientation as gay or bisexual. Median duration of illness was 8.3 days (range 3-21 days); 39% of case-patients were hospitalized (median 3 days; range 0-6 days). Antibiotics were commonly prescribed (88%); however, 5 (23%) case-patients reported treatment failure. In the week before symptom onset, 3 (14%) case-patients swam in the ocean, 4 (21%) swam in a pool, 8 (44%) attended social gatherings, 12 (54%) traveled domestically, and 14 (70%) had sexual contact with another person. All 14 case-patients reporting sexual contact had male partners, and described a variety of sexual behaviors. Over half (53%) of case-patients providing sexual health information had ever been diagnosed with a sexually transmitted infection (STI), and 40% were HIV positive. Only 22% of case-patients had heard of shigellosis before their illness, and 33% wanted more information about shigellosis beyond what they had received.

CONCLUSIONS: The use of a supplemental questionnaire in this investigation identified several potential exposures to infection, including through sexual activity. Additionally, self-identified gay or bisexual males with a history of STIs may be particularly vulnerable. This investigation highlighted the utility of supplemental questionnaires to enhance our understanding of MDR shigellosis among men who have sex with men, and to identify future prevention and control opportunities for this population.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Emerging Infections; Enteric Infectious Diseases; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9882

Abstract Type Breakout

Abstract Title Epidemiology of Enterotoxigenic *Escherichia coli* Infections in Minnesota, 2015-2016

Abstract

BACKGROUND: Enterotoxigenic *Escherichia coli* (ETEC) is a reportable pathogen in Minnesota. It is a well-established cause of traveler's diarrhea and occasionally causes domestic foodborne outbreaks via imported produce, but it is not detected by conventional stool culture. Increasingly, clinical laboratories are adopting commercially available culture-independent diagnostic tests (CIDTs) which can detect ETEC. This study used the corresponding increase in reported ETEC cases during 2015-16 to describe the epidemiology of ETEC infections in Minnesota.

METHODS: Clinical materials for ETEC-positive specimens are submitted to the Minnesota Department of Health (MDH) Public Health Laboratory (PHL). The PHL uses polymerase chain reaction to test for heat-labile (LT) and heat-stable (ST) toxin genes to confirm that ETEC are present. Cases are interviewed regarding illness and potential exposures. All ETEC cases from September 2015 through December 2016 were included in the analysis.

RESULTS: Among the five clinical laboratories in Minnesota that adopted CIDT methods prior to 2016, ETEC accounted for 8.6% (n=73) of all bacterial enteric pathogen cases reported to MDH in 2016; only *Campylobacter* (27.4% of reported pathogen cases), enteroaggregative *E. coli* (EAEC) (20.7%), *Salmonella* (12.8%), and Shiga toxin-producing *E. coli* (11.7%) were reported more frequently than ETEC. In total, 105 specimens were positive for ETEC at a clinical laboratory during the study period. Fifty-three (51%) cases were confirmed as ETEC at the PHL. ST and LT were both detected in 27% of confirmed cases, ST only in 56%, and LT only in 17%. Among confirmed cases, nearly all reported diarrhea (98%), 89% reported cramps, 49% reported fever, 18% reported vomiting, and 16% reported bloody stools; 15% of cases were hospitalized and none died. Median illness duration was 9 days. Only 45% of cases traveled internationally. Most (69%) domestically acquired cases occurred in summer or fall. Thirty-five (67%) cases tested positive for additional pathogens at the clinical laboratory, including EAEC (n=22) and/or enteropathogenic *E. coli* (n=20). In a case-case comparison study of confirmed ETEC and contemporaneous *Salmonella* cases, ETEC cases were significantly more likely to have traveled internationally and to have eaten cucumbers. *Salmonella* cases were significantly more likely to have eaten at a restaurant.

CONCLUSIONS: ETEC are commonly detected when CIDTs are used. International travel was a risk factor, but a majority of infections were domestically acquired, providing evidence that ETEC infection is an underestimated source of domestically acquired foodborne illness. ETEC frequently were detected along with other diarrheagenic *E. coli*.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Surveillance; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9329

Abstract Type Breakout

Abstract Title Estimating the Burden of Waterborne Disease in the United States

Abstract

BACKGROUND: The magnitude of waterborne disease in the United States has not been well quantified, and an estimate of this burden, or the total number of illnesses, hospitalizations, and deaths due to waterborne diseases is needed to direct prevention activities and set public health goals. A comprehensive estimate that encompasses all water exposures (i.e., drinking, recreational, environmental, and undetermined) is needed for succinct and impactful decision-making and communication, similar to the foodborne disease estimate that 48 million Americans are sickened annually.

METHODS: We defined waterborne disease as illness where water was the proximate vehicle for an infectious pathogen. We chose 21 diseases for which surveillance data, administrative billing data, or literature estimates indicated domestic waterborne transmission was plausible, the disease was likely to cause substantial illness or death, and health outcome data were available. We adapted methods previously applied to foodborne estimates. Briefly, we used a series of pathogen-specific multipliers to adjust the reported/documented number of cases of each disease or syndrome, for under-reporting and under-diagnosis, domestically acquired transmission, and waterborne transmission. Sources for multipliers included surveillance data, population studies, and expert judgment when no other data were available. A distribution instead of a point estimate was used to account for the uncertainty in each input and multiplier. This allowed the calculation of uncertainty intervals for each outcome. We estimated the number of illnesses, emergency department visits, hospitalizations and deaths, and quantified the direct healthcare costs of emergency department visits and hospitalizations due to waterborne disease transmitted in the United States in 2014.

RESULTS: The most common causes of domestic waterborne illness and emergency department visits in 2014 included otitis externa, norovirus, and acute gastrointestinal illness from agents not well captured by surveillance systems. The most common, and costly, causes of waterborne hospitalizations in 2014 were infections with organisms associated with premise plumbing systems (non-tuberculous mycobacterial infections, *Pseudomonas* pneumonia and septicemia, and Legionnaires' disease), at an annual cost above \$2 billion.

CONCLUSIONS: These results represent the first estimate of the burden of waterborne disease in the United States that encompasses all water exposures. Results are already informing CDC's waterborne disease prevention efforts. For example, recognition of the substantial burden of emergency department and physicians' office visits for otitis externa has led to the creation of specific prevention materials for the public and guidance for physicians. The results of this estimate will be vital in prioritizing resources and informing policy makers.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Infectious Diseases; Water; Waterborne Disease

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10325
Abstract Type	Breakout
Abstract Title	Foodborne Illness Source Attribution Estimates for 2013 Using Multi-Year Outbreak Surveillance Data, United States

Abstract

BACKGROUND: The Interagency Food Safety Analytics Collaboration (IFSAC), established in 2011 by the Centers for Disease Control and Prevention, Food and Drug Administration, and the Food Safety and Inspection Service, works to improve U.S. foodborne illness source attribution estimates. We present IFSAC's new harmonized attribution estimates for *Salmonella*, *E. coli* O157, *Listeria monocytogenes*, and *Campylobacter* for 2013, based on multi-year outbreak data.

METHODS: We analyzed 1998-2013 outbreaks from CDC's Foodborne Disease Outbreak Surveillance System (FDOSS) where one of the four pathogens was the confirmed or suspected etiology and the implicated food was assignable to one of the 17 IFSAC food categories. Pathogen-specific analysis of variance (ANOVA) models were developed to mitigate the influence of large outbreaks and to control for epidemiological factors. We exponentially down-weighted outbreaks before 2009 because we considered more recently implicated foods to be more relevant for estimating current attribution. For each pathogen, we calculated the percentage of illnesses attributable to each food category based on the down-weighted model-estimated illnesses.

RESULTS: Of the 1,043 outbreaks included in this analysis, *Salmonella* illnesses were broadly attributed, with 75% of illnesses attributed to seven food categories: Seeded Vegetables (e.g., tomatoes), Eggs, Chicken, Other Produce (e.g., nuts), Pork, Beef, and Fruits. Eighty percent of *E. coli* O157 illnesses were linked to just two categories: Vegetable Row Crops (e.g., leafy greens) and Beef. Similarly, 86% of illnesses due to *L. monocytogenes* were attributed to two categories, Fruits and Dairy, though the rarity of these outbreaks makes these estimates less reliable than those for other pathogens. Almost 80% of non-Dairy *Campylobacter* illnesses were attributed to Chicken, Other Seafood (e.g., shellfish), Seeded Vegetables, Vegetable Row Crops, and Other Meat/Poultry (e.g., lamb, duck). Though most foodborne *Campylobacter* outbreaks were associated with unpasteurized milk, a high-risk product not widely consumed by the general population, other evidence suggests that these outbreaks over-represent Dairy as a source of *Campylobacter* illness; thus, we excluded Dairy from the *Campylobacter* estimates.

CONCLUSIONS: IFSAC's work to provide a harmonized analytic approach for estimating foodborne illness source attribution from outbreak data can provide consistency in the use and interpretation of estimates across agencies. Taken together with other scientific data, these results can support evidence-based food safety decision-making. As more data become available and methods evolve, updates to these estimates will enhance IFSAC's efforts to inform agencies and engage stakeholders, and further the ability to assess whether food safety prevention measures are working.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Food Safety; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10261

Abstract Type Breakout

Abstract Title Illness Outbreaks Linked to Unpasteurized Milk— United States, 2015–2016

Abstract

BACKGROUND: Infection with enteric pathogens, such as *Campylobacter* and *Salmonella*, after consumption of unpasteurized milk has resulted in severe illness and death in the United States. Although interstate sale of unpasteurized milk is illegal in the United States, laws regarding intrastate sale of unpasteurized milk differ by state. Legislation has recently been proposed in some states that would facilitate intrastate sale of unpasteurized milk. We conducted an analysis to: i) describe characteristics of 2015 and 2016 outbreaks; ii) determine if there was a change in the number of outbreaks per year during 2010–2016; and iii) assess whether outbreaks continue to occur at higher frequencies in states where the sale of unpasteurized milk is legal.

METHODS: We analyzed data from the Foodborne Disease Outbreak Surveillance System (FDOSS), a component of the National Outbreak Reporting System (NORS). FDOSS collects data on disease outbreaks from state, local, and territorial health departments on agents, foods, and settings responsible for foodborne illness. To assess changes in the number of outbreaks per year, we defined proportions of outbreaks (PO) as the number of outbreaks that occurred each year over the total number of outbreaks that occurred during the time period. A chi-square test of significance was performed. Legal status of unpasteurized milk sales in each state was determined through a review of state and federal regulations.

RESULTS: In 2015 and 2016, there were 25 outbreaks in 13 states linked to unpasteurized milk from several pathogens, including *Campylobacter* (13), *Salmonella* (5), *Escherichia coli* (4), and *Cryptosporidium* (3). In 16 (64%) of the 25 outbreaks, severe outcomes were noted, including 34 hospitalizations and two patients who developed Guillain-Barré syndrome. The PO did not vary significantly from year to year between 2010 and 2016 ($p=0.82$). Between 2010–2016, 102 of 107 (95%) of outbreaks occurred in states where the sale of unpasteurized milk is legal, either through herdshares, on-farm sales, or retail sales. Of the 25 outbreaks in 2015 and 2016, none occurred in states where sale of unpasteurized milk was illegal.

CONCLUSIONS: Outbreaks linked to unpasteurized milk continue to occur in the United States and result in severe patient outcomes. Our finding that outbreaks linked to unpasteurized milk occur more frequently in states where sale of unpasteurized milk is legal is consistent with other studies. Changes in regulations that result in increased availability of unpasteurized milk might result in an increase in outbreaks from this source.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Outbreaks; Enteric Infectious Diseases; Foodborne Disease

**Consider for
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Submission Type Breakout/Quick/Lightning/Poster

ID 10154

Abstract Type Breakout

Abstract Title Multi-Pathogen Foodborne Outbreak Investigation of Home-Prepared Fundraiser Meal in Louisiana

Abstract

BACKGROUND: In October 2017, Louisiana Office of Public Health (OPH) Infectious Disease Epidemiology Section (IDEpi) was notified by several hospitals that patients were presenting with gastrointestinal illness after eating jambalaya meals served the previous day as a fundraiser for a local school sports team. OPH investigated the outbreak with consultation from Centers for Disease Control (CDC) and United States Department of Agriculture (USDA) Food Safety and Inspection Service (FSIS).

METHODS: In conducting the epidemiologic investigation, IDEpi attempted to identify and interview everyone who ate the fundraiser meal. The person who prepared the meal provided a partial list of purchasers. During initial interviews, epidemiologists requested information regarding additional people who ate the meal. IDEpi also conducted active surveillance with local healthcare providers to identify cases. A case was defined as any person reporting diarrhea within 96 hours of consuming the meal. An environmental investigation was conducted by OPH Sanitarian Services and meal preparation was thoroughly reviewed. Stool and food samples were collected and submitted to OPH laboratory for testing.

RESULTS: IDEpi identified 142 people who ate the fundraiser meal, 118 reported illness (83% attack rate). 82 (69%) cases were female, and ages ranged from 5 to 82 years with a mean of 38. People ages 20-39 had the highest attack rate (96%). 118 (100%) cases reported diarrhea, 69 (58%) reported vomiting, and 102 (86%) reported fever. Incubation periods ranged from 2.25 to 70 hours, with a median of 23 hours. Reports of symptom duration ranged from 1 to 6 days. 45 cases were hospitalized. None of the food items had a relative risk greater than 1. The OPH lab identified *Salmonella subspecies I, serotype 4,5,12:i:-* with matching PFGE patterns in 44 stool samples from 31 cases and 14 food samples including jambalaya, corn, and bread. 10 of 11 stool samples tested for *Clostridium perfringens enterotoxin* were positive. Food and stool samples were forwarded to CDC for additional testing and results are pending. The environmental investigation found that food was prepped and partially cooked in a household the day before the fundraiser and cooking was completed the next day at another location. No obvious violations were noted but possible inadequate cooling overnight may have allowed proliferation.

CONCLUSIONS: This was a confirmed foodborne outbreak due to *Salmonella* and *Clostridium perfringens*. Paying close attention to food safety is crucial at all points of food preparation, holding and serving to prevent contamination and proliferation of harmful bacteria in food.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Outbreaks; Food Safety

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9214
Abstract Type	Breakout
Abstract Title	Multi-Provincial Outbreak Investigation of <i>E. coli</i> O121 Infections Associated with Flour in Canada, November 2016 to May 2017

Abstract

BACKGROUND: In January 2017 a national outbreak investigation was initiated to investigate the first multi-provincial cluster of *E. coli* non-O157 cases identified in Canada.

METHODS: A case was defined as a resident or visitor to Canada with one of the outbreak PFGE strains of *E. coli* non-O157 or closely related by whole genome sequencing (WGS) with symptom onset on or after November 1, 2016. Initial hypothesis generating methods included: case interview with hypothesis generating and focused questionnaires, grocery purchase record review, informational traceback and product sampling from case homes. When these methods did not point to a common source, cases were centrally re-interviewed using an open-ended approach. Clinical isolate serotype and PFGE analyses were performed by provincial laboratories and WGS was performed by the National Microbiological Laboratory.

RESULTS: Thirty cases in six provinces and one visitor to Canada were identified with onset dates from November 13, 2016 to April 3, 2017. Case ages ranged from 2 to 79 years (median = 24) and 50% were female. Eight cases were hospitalized, one case developed haemolytic uremic syndrome and no deaths were reported. Multiple hypotheses were considered during the investigation, but no convergence was identified. An open sample of Brand X flour from a case home and a closed sample collected at retail of the same brand and production date tested positive for the outbreak strain of *E. coli*. Seventy-percent (16/23) of cases reported that Brand X flour was used or probably was used in the home during their exposure period and 75% of these cases reported eating or probably eating raw dough during their exposure period. All cases were serotyped as *E. coli* O121 with matching or similar PFGE patterns and all cases and flour samples were related by WGS.

CONCLUSIONS: This was the first Canadian *E. coli* outbreak linked to flour. A concurrent *E. coli* O121 outbreak was identified in British Columbia that was associated with a different brand of flour. In 2015/2016 the US CDC investigated an outbreak of *E. coli* O121 also linked to flour. These outbreaks suggest that flour is an emerging vehicle for *E. coli* infections and should be considered as a potential source in all *E. coli* outbreak investigations. Open-ended interviewing and product sampling from case homes proved to be successful hypothesis generation methods and should be considered for investigating outbreaks where no source emerges through routine interviewing or when an ingredient is suspected.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9263

Abstract Type Breakout

Abstract Title Multi-Provincial Outbreak Investigation of Hepatitis A Associated with Frozen Berries in Canada, 2016

Abstract

BACKGROUND: Two local health units identified three locally acquired cases of Hepatitis A (HAV) who reported consuming frozen berries from a single retailer. Subsequently, other provinces reported HAV cases with frozen berry consumption and a national outbreak investigation was conducted in collaboration with provincial and federal partners.

METHODS: A case was defined as a resident or visitor to Canada with lab-confirmed HAV infection likely acquired in Canada, with the outbreak genotype and RNA fingerprint, with illness onset on or after January 1, 2016. Case interviews and review of purchase histories were conducted. Sequencing determined the genotype and RNA fingerprint of clinical isolates. Traceback of inputs and trace forward of the implicated product were conducted. Closed samples and input ingredients were collected for testing.

RESULTS: A total of 25 cases were identified with illness onsets ranging from February 26 to May 16, 2016 (ten hospitalizations, no deaths reported). The median age of cases was 48 years (range 10 – 70 years) and 14 cases (56%) were male. Sixteen cases were genotype 1B with a matching RNA fingerprint, 5 cases were genotype 1A with a nearly identical RNA fingerprint. A single brand of a frozen berry blend was consumed by 23 of 25 cases (92%). A closed sample collected from retail, an open sample from a case home, and an input of blackberries tested positive for the presence of HAV. The product was recalled on April 15, 2016. Consumers who had purchased the product were contacted by the retailer to advise of the recall and to offer post-exposure prophylaxis to those who had consumed the product within the previous two weeks. More than 9400 people were vaccinated at the retailer clinics, and more than 2500 people were vaccinated by local health units in provinces where the recalled product was sold. In September 2016, a new cluster matching the outbreak strain was identified. Case follow-up confirmed that the index case consumed the recalled product, despite efforts to remove the product from consumer homes and the marketplace.

CONCLUSIONS: Rapid detection by the local health unit, detailed epidemiologic and loyalty card information, traceback evidence and active engagement of the retail chain resulted in the rapid identification and recall of the implicated product. The subsequent post-exposure prophylaxis campaign likely prevented further illnesses. The second outbreak associated with consumption of recalled product highlights the importance of broad consumer communications, as recall notices may not reach all consumers.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Outbreaks; Foodborne Disease; Food Safety

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9878

Abstract Type Breakout

Abstract Title Multistate Outbreaks of *Salmonella* Infections Linked to Maradol Papayas Imported from Mexico — United States, May – September, 2017

Abstract

BACKGROUND: Foodborne salmonellosis causes approximately 1 million illnesses and 400 deaths annually in the United States (US). In June 2017, PulseNet, the national laboratory network for foodborne disease surveillance, detected a cluster of 13 *Salmonella* Kiambu 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 infection with an outbreak strain of *Salmonella* occurring during May 17–October 4, 2017. Case-patients were identified in PulseNet and interviewed to determine common exposures. Investigators conducted traceback to determine the source of reported foods and tested product samples for *Salmonella*. FDA also conducted increased sampling of imported produce. Selected clinical and food isolates were further characterized by whole-genome sequencing (WGS).

RESULTS: Early interviews indicated that papayas were an exposure of interest, so investigators from Maryland, Virginia, and the FDA collected papayas from points of service, distributors, and at import for testing. Several strains of *Salmonella* were isolated from papayas sourced from Farm A in Mexico, including *Salmonella* Agona, Gaminara, Kiambu, Thompson, and Senftenberg. We identified 220 cases from 23 states. The median case-patient age was 40 years (range <1–95); 62% were female. Sixty-eight (40%) case-patients were hospitalized; one death was reported. 113 (67%) of 169 case-patients were of Hispanic ethnicity. Seventy-nine (54%) of 145 case-patients interviewed reported eating papayas, significantly higher than 22% reported in a survey of healthy Hispanic persons ($p<0.05$). Traceback from two points of service associated with illness sub-clusters in two states identified Farm A as a common source of papayas, and three voluntary recalls of Farm A papayas were issued. During the investigation, we identified two other, concurrent outbreaks of salmonellosis associated with papayas that involved different *Salmonella* strains from two additional Mexican farms. These two additional outbreaks resulted in 11 illnesses. Selected clinical and food isolates within all different serotypes associated with these three outbreaks were closely related genetically by WGS.

CONCLUSIONS: Our investigations implicated imported papayas from Mexico as the source of three multistate *Salmonella* outbreaks in the summer of 2017, one of which was the largest papaya-associated outbreak identified in the United States. FDA's increased testing of papayas from Mexico during this outbreak assisted in the identification of additional papaya-associated illnesses and outbreaks of salmonellosis. Increased testing of imported foods may help identify sources of illnesses in the future.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Enteric Infectious Diseases; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9322

Abstract Type Breakout

Abstract Title Outbreak of Campylobacteriosis Linked to Contaminated Water in a Small Rural Municipality—Nebraska, February–March 2017

Abstract

BACKGROUND: During March 2017, 5 campylobacteriosis cases were identified in City A, a Nebraska community (population <1,000) previously averaging <1 case/year. Anecdotal reports suggested dairy farm waste lagoon runoff had collected in a road ditch near two City A wells. In response, Nebraska Department of Health and Human Services (NDHHS) and Southwest Nebraska Public Health Department investigated to identify the outbreak's cause and institute preventive measures.

METHODS: A site visit was conducted on March 15, 2017 to investigate poultry and ground beef distribution/handling procedures in City A's two restaurants and single grocery store, interview city officials, identify well locations, and collect recent water pumping and testing records. Over the following two days, environmental health officials inspected the untreated municipal water supply and the dairy's waste water handling. An Internet-based questionnaire was shared via social media for City A residents and visitors to provide contact information; demographics; food/animal exposures; and drinking water source(s) including personal treatment of tap water. Probable cases were defined as illness with diarrhea (≥ 2 days) and ≥ 1 additional symptom (i.e., nausea, vomiting, fever, chills, headache) among City A residents with onset during February 28–March 23, 2017. Confirmed cases were defined as probable cases with either stool culture or PCR-positive results for *Campylobacter*, or lab-confirmed probable illness among non-residents who worked, dined, or shopped for groceries in City A.

RESULTS: Of 94 questionnaires, 39 (41%) campylobacteriosis cases (six confirmed, 33 probable) were identified (25 [64%] females; 14 [36%] males); median age was 34.5 years (range, 1.5–85). Of these, 12 (31%) sought medical care; three (8%) were hospitalized. No deaths were reported. Consumption of untreated City A tap water was significantly associated with illness (OR=7.84 [95% CI, 1.69–36.36]). Environmental investigations confirmed the dairy pumped 612,000 gallons of lagoon waste water through a malfunctioning irrigation system that collected from February 22–25, 2017 in a road ditch within 15 feet of two untreated, shallow City A groundwater wells (pumping depth 25–26 feet). Both wells had been used until March 8; coliform tests were negative. After both were permanently removed from service on March 16, no additional illnesses were reported.

CONCLUSIONS: Our findings indicate that this campylobacteriosis outbreak was likely caused by exposure to untreated municipal water contaminated by waste water run-off from an adjacent dairy farm. Under the direction of NDHHS environmental health officials, City A opted to replace these two wells with a single deep higher capacity groundwater well.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Waterborne Disease; Enteric Infectious Diseases; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10091

Abstract Type Breakout

Abstract Title Recurring Outbreaks of Salmonella Thompson Associated with a Restaurant – Connecticut, 2015 - 2017

Abstract

BACKGROUND: S. Thompson is the 10th most common *Salmonella* serotype in Connecticut (CT), with a median of 8 cases reported annually. During 2015 – 2017, CT investigated 1 unsolved cluster and 3 outbreaks of S. Thompson linked to a common food service establishment (Restaurant X). Previous to these investigations, there had been no prior documented outbreaks of S. Thompson in CT.

METHODS: Clusters were identified and investigated when 2 or more isolates within a 60-day period were indistinguishable by pulsed-field gel electrophoresis (PFGE). Whole genome sequencing (WGS) was also conducted. Cases were interviewed to determine linkage to Restaurant X and foods consumed. Public notification and active case-finding was conducted through a press release during outbreak #3. Food workers were interviewed and tested, and food and environmental samples were collected and tested during each outbreak investigation.

RESULTS: The one unsolved cluster and 3 outbreaks occurred between May 2015 and June 2017, with each event occurring approximately 6 months apart. A total of 30 (21 culture-confirmed, 9 probable) cases were identified; 2 were hospitalized and there were no deaths. The median number of cases per cluster/outbreak was 5 (range 3-17). All clinical isolates were closely related within 0-9 single nucleotide polymorphisms (SNPs). No specific food vehicle was implicated. One food worker tested positive during outbreak #3. One food sample (cut cucumbers) collected during outbreak #1 and two environmental swabs (floor of meat cooler and cutting board mat) collected during outbreak #3 tested positive for S. Thompson with PFGE patterns indistinguishable from the clinical isolates. Environmental assessment during outbreak #3 identified lack of washing and sanitizing of cutting boards and mats.

CONCLUSIONS: Despite epidemiologic, laboratory, and environmental investigation and control efforts, recurring outbreaks of S. Thompson occurred at a restaurant in CT over a 2-year period. Epidemiologic evidence and WGS were valuable in establishing a strong link between cases across the different outbreaks. The original source of the outbreak remains unknown. However, introduction of S. Thompson and its likely persistent environmental presence, coupled with lack of proper cleaning and sanitization likely led to repeated cross-contamination of foods served to patrons. All identified clusters should be investigated rigorously. Aggressive pursuit of sampling of food, food workers, and the environment is important for source identification and establishing possible routes of contamination, especially in the context of recurring *Salmonella* outbreaks.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Food Safety; Foodborne Disease; Outbreaks

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9739
Abstract Type	Breakout
Abstract Title	Source Attribution of Illnesses Transmitted Commonly By Food and Water in the United States Using Structured Expert Judgment

Abstract

BACKGROUND: Illnesses transmitted commonly by food and water are the cause of a major disease burden in the United States. In addition to food and water, these illnesses may be transmitted by other pathways: person-to-person, animal contact, or through the environment. Limited data are available to estimate the proportion of disease attributable to each of these modes of transmission. We report findings from a structured expert judgment (SEJ) study to provide such estimates.

METHODS: Forty-eight experts were assigned to one or more of 15 panels based on publication records and self-evaluation of professional interest and experience with each of 33 pathogens. Including subdivisions by serotypes, age, and clinical manifestations for some pathogens, a total of 47 target questions for the annual percentage of domestic illnesses that are transmitted through each pathway were elicited. Before providing estimates, experts attended on-line and in-person training and answered 14 separate calibration questions from which performance weights were derived. Experts provided estimates representing their judgments of the uncertainty distribution (5th, 50th, and 95th percentile) for each question. Cooke's Classical Model, aggregated with equal and performance based weighting, was used to synthesize the panels' collective judgments. Robustness analysis and out-of-sample validation showed that the panels each comprised a satisfactory number of both accurate and informative experts.

RESULTS: Estimates for *Salmonella enterica* across the modes of transmission were 66% foodborne, 6% waterborne, 7% person-to-person, 11% animal to person, and 10% environmental. Estimates for norovirus were 19% foodborne, 6% waterborne, 70% person-to-person, 0% animal to person, and 5% environmental. Estimates for *Cryptosporidium* were 8% foodborne, 43% waterborne, 20% person-to-person, 21% animal to person, and 8% environmental.

CONCLUSIONS: This is the first study to estimate attributable proportions of disease in the United States across all modes of transmission. For most pathogens, a lower proportion of disease was attributed to foodborne transmission compared with previous estimates. Rather than considering only one pathway, as in previous studies, our findings may provide a more balanced understanding by allowing internal comparison across modes of transmission. For example, while norovirus is primarily transmitted person-to-person, transmission through food, water, and the environment can still occur. Our findings can be applied to estimates of the incidence and burden caused by these pathogens in the United States and support appropriate targeting of resources to prevent and control these diseases by all pathways.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Waterborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9538
Abstract Type	Breakout
Abstract Title	Use of an Incubation-Driven Case Definition to Identify the Causative Organism during a Foodborne Outbreak Investigation at a Large Catered Event in Alabama, October 2017
Abstract	BACKGROUND: Foodborne outbreak investigations rely on multiple tools, including patient interviews and laboratory testing to classify cases and correctly identify the causative agent. Reported symptoms or laboratory results may not always be straightforward, especially when multiple organisms are involved. This study describes the use of an incubation-driven case definition to successfully investigate a foodborne outbreak associated with a large catered event. METHODS: Demographic, exposure, and clinical data for cases and controls were collected via REDCap™ and analyzed using SAS® 9.4. Three case definitions were developed and employed over the course of the investigation as potential etiologies were considered: 1. Any symptom; 2. Diarrhea within 9-72 hours; and, 3. Diarrhea within 6-24 hours. Clinical specimens (CS), food samples, and environmental swabs were submitted to the State Public Health Laboratory (SPHL) for testing. RESULTS: Among 1,500 attendees, 90 reported illness after attending the catered event. Among those, complete data were collected from 38 ill and 40 non-ill persons. While CS testing was pending, the case definition of any symptom was used. The top five symptoms reported by the ill were diarrhea (100%), abdominal cramps (71%), nausea (58%), vomiting (37%), and headache (26%) with a median incubation of 14.5 hours (range: 4-115) and duration of 2 days (range: 1-4). While SPHL detected ETEC/EPEC in two CS, most reported incubations were more consistent with <i>Clostridium perfringens</i>. Given the small number of CS submitted and lack of capacity at SPHL to test for these pathogens, new case definitions were developed to tease these apart while confirmatory testing at CDC was pending. Ten cases met the definition of diarrhea within 9-72 hours. The median incubation was 17.5 hours (range: 12-22). No exposures were statistically significant. Seventeen cases met the definition of diarrhea within 6-24 hours. The median incubation was 13.0 hours (range: 6-22). Cases experienced a wider range of symptoms including body/muscle aches and sweats. Significant exposures included pulled chicken (OR: 10.9; p-value: 0.017) and to-go plates (OR: 6.3; p-value: 0.041). CDC detected ETEC in one CS and <i>C. perfringens</i> in three CS. No pathogens were detected on the environmental swabs. Food samples were not tested. CONCLUSIONS: Use of an incubation-driven case definition was supported by the detection of <i>C. perfringens</i>, which is more commonly associated with large catered events than ETEC/EPEC. The development of case definitions based on symptoms or incubation periods may provide an alternative approach when investigating outbreaks with limited or conflicting laboratory evidence.
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiologic Methods; Outbreaks; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10201

Abstract Type Breakout

Abstract Title Use of Whole Genome Sequencing for *Salmonella* Typhimurium Surveillance in Minnesota

Abstract

BACKGROUND: *Salmonella* Typhimurium is one of the most common *Salmonella* serotypes in the United States. We determined how *S. Typhimurium* cases cluster by whole genome sequencing (WGS) versus pulsed-field gel electrophoresis (PFGE), and evaluated parameters for outbreak detection.

METHODS: Forty-two isolates from 13 outbreaks from 2000-2012 and all 188 isolates from 2017 were subtyped by PFGE and sequenced on the Illumina MiSeq (analyzed with reference strain LT2 using a whole genome hq-SNP pipeline Lyve-SET v1.1.4f). A cluster was defined as ≥ 2 cases from different households with isolates with indistinguishable PFGE patterns within 30 days or 0-5 single nucleotide polymorphisms (SNPs) apart by WGS within 60 days.

RESULTS: Retrospective outbreak analysis, 2000-2012 In 10 outbreaks, isolates varied by 0-2 SNPs by WGS. In three outbreaks, isolates varied by 0-5, 5, and 6-33 SNPs. Three outbreaks shared the same PFGE subtype. Two of these outbreaks occurred in different years at restaurants that shared the same egg supplier. The third outbreak occurred right after the second outbreak, but eggs were not suspected. By WGS, isolates from the first two outbreaks were 2-3 SNPs apart, but differed from the third outbreak by 126-128 SNPs. Prospective analysis, 2017 In 2017, 24 PFGE clusters and 17 WGS clusters were identified. PFGE clusters had a median of 2 cases (range, 2-8). WGS clusters had a median of 3 cases (range, 2-6). Five outbreaks were identified. Within each of the 5 outbreaks, isolates varied by 0-6 SNPs. In three outbreaks, PFGE and WGS were concordant. In the fourth outbreak, WGS identified a cluster of 2 cases with isolates that differed by PFGE. In the fifth outbreak, 2 cases associated with a restaurant had identical isolates by WGS; a third isolate matched by PFGE and was 1 SNP different by WGS but was epidemiologically unrelated to the outbreak. WGS also identified 2 additional unsolved small clusters in which all of the case-isolates had different PFGE patterns. An emerging common PFGE subtype of monophasic Typhimurium had 2 long-term clusters (8 cases and 6 cases). By WGS, 2 smaller clusters (3 cases and 2 cases) involving this PFGE pattern were identified.

CONCLUSIONS: Most *S. Typhimurium* outbreak isolates fall within 2 SNPs by WGS, but more variation can occur. WGS identified 30% fewer clusters than PFGE; several small PFGE clusters were not clusters by WGS. Conversely, WGS identified clusters of isolates with different PFGE subtypes. WGS may save time by focusing investigations on cases that are truly related.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Outbreaks; Epidemiology; Foodborne Disease

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9275
Abstract Type	Lightning
Abstract Title	An Outbreak of Human Cases of Campylobacteriosis Linked to Puppies from a National Pet Store Chain – Orange County, Florida, July 2017

Abstract

BACKGROUND: In July 2017, the Florida Department of Health in Orange County (DOH-Orange) initially investigated a cluster of human campylobacteriosis with a common exposure to two locations of a national pet store chain. Six cases were culture confirmed (*Campylobacter jejuni*) and two were polymerase chain reaction (PCR) confirmed (*Campylobacter* spp.). The probable case-patient is a symptomatic household contact of a confirmed case with exposure to an adopted puppy from the same pet store.

METHODS: Statewide notification was sent to local health departments on July 18, 2017. A national EPI-X notification to was subsequently sent on August 8, 2017. DOH-Orange collaborated with the Florida Department of Agriculture and Consumer Services (FDACS) to conduct multiple site visits between July 25-August 8 at the two pet store locations. Both locations were also surveyed regarding hand hygiene, ill puppy policy, and current infection control practices.

RESULTS: Case-patients had onsets of illness ranging from April 6 to December 2, 2017. Four of the nine (44.4%) were employees and five (55.6%) were patrons of the pet store. During the onsite visit, multiple symptomatic puppies from both locations were observed with either diarrhea or loose stools. Twenty-three total stool specimens from puppies at both pet store locations were collected. Eight (35%) of the 23 were culture positive for *Campylobacter jejuni*. Multiple lapses in infection control and prevention practices were observed during the onsite visits, including, improper hand hygiene after contact with fecal material, minimal and improper use of personal protective equipment (PPE), and reported consumption of food and beverages by employees in the kennel area.

CONCLUSIONS: *Campylobacter* is prevalent in puppies less than six months old, and can be transmitted to humans via the fecal-oral route. Bacterial shedding in symptomatic and asymptomatic puppies might contribute to outbreak occurrence and be perpetuated in pet stores with inadequately enforced infection prevention programs. Evidence of campylobacteriosis cases associated with exposure to pet stores is limited. Information about such exposures is not routinely captured during routine surveillance investigations. Public health officials should be vigilant for clusters of cases linked to common exposure locations. Public education should stress that vigilant hand hygiene after handling any animals is the most effective way to prevent illness from animal contact.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Zoonotic Diseases; Enteric Infectious Diseases; Veterinary Public Health
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9934
Abstract Type	Lightning
Abstract Title	Assessing the Impact of Multiplex Polymerase Chain Reaction Assays on the Number of People with Coinfections of Selected Reportable Enteric Pathogens in Florida
Abstract	BACKGROUND: Use of culture-independent diagnostic testing (CIDT) to detect enteric pathogens has increased rapidly following FDA approval of multiplex nucleic acid tests in 2014. Use of multiplex polymerase chain reaction (PCR) assays (MPAs) became popular because they test for multiple pathogens concurrently, produce results faster, and cost less than traditional culture and microscopy methods. To assess the impact of MPAs on the number of people with reportable enteric coinfections, selected reportable disease case and laboratory data for Florida were reviewed. METHODS: All campylobacteriosis, cryptosporidiosis, giardiasis, listeriosis, paratyphoid fever, salmonellosis, Shiga toxin-producing <i>Escherichia coli</i> infection, shigellosis, typhoid fever, and vibriosis cases reported from 2013 to 2017 were reviewed. Coinfection was defined as a person with more than one type of enteric pathogen case reported in the same year and whose cases had event dates, specimen collection dates, or specimen accession numbers that matched. CIDT was defined as antigen detection, enzyme immunoassay, immunochromatographic assay and PCR tests. CIDT was further divided into PCR and non-PCR tests. RESULTS: From January 1 to December 8, 2017, 264 coinfections were identified among 2017 cases. Of the 210 coinfections with CIDT, 100 (48%) had non-PCR CIDT only, 23 (11%) had both PCR and non-PCR CIDT, and 87 (41%) had PCR CIDT only. Of the 110 coinfections with PCR CIDT, 81 (74%) had PCR CIDT on all concurrent cases due to MPAs. Of the 83 coinfections with PCR CIDT in 2016; 57 (69%) had PCR CIDT on all concurrent cases due to MPAs. Assessment of the laboratories utilizing MPAs and 2013-2017 trend data will be presented. Final analysis will include remaining data for 2017 not currently available. CONCLUSIONS: Use of MPAs has increased the number of coinfections from 208 in 2016 to 264 in 2017. These estimates underrepresent the number of enteric coinfections as the analysis does not include common, non-reportable pathogens such as norovirus and <i>Clostridium difficile</i>. MPAs make it difficult to identify the etiology of an acute enteric illness when co-detections occur and cause multiple reportable enteric disease cases due to classification of CIDT in national case definitions. Co-detections from MPAs will continue to challenge how public health counts enteric illnesses and manages infections in sensitive situations as exclusion and re-admittance criteria can differ by pathogen. Future investigations into ways to better quantify MPA detections that would allow clearer assessments for pathogen attribution to acute enteric illnesses would be useful.
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Waterborne Disease; Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9604

Abstract Type Lightning

Abstract Title Detection of Various Norovirus Strains, Including Emerging GII.4 Recombinant, in Multiple Outbreaks—U.S. Virgin Islands, December 2016-January 2017

Abstract

BACKGROUND: Four distinct outbreaks of acute gastroenteritis were reported in the U.S. Virgin Islands from December 2016-January 2017. Outbreaks occurred at a government facility in Saint Croix (Location A), an elementary school in Saint Thomas (Location B), and two events located in same hotel facility in Saint Thomas—baby shower and government interagency meeting (Location C).

METHODS: A case was defined as confirmed if it met the laboratory criteria for diagnosis, while a probable case was defined as clinical diagnosis compatibility and was epidemiologically linked to a confirmed case. On-site visits to locations were performed and stool specimens were collected. A paper based survey was completed for Location B, while an electronic survey was distributed for Location C events to identify infection risk factors and to encourage stool specimen submission. Stool specimens were collected for all events, and specimens were submitted for laboratory diagnosis.

RESULTS: In Location A, a total of 6 stool samples were collected, 6 cases met the confirmed case definition, and 1 case met the probable case definition, and. All Location A specimens were positive for a novel GII.4 recombinant, GII.P16-GII.4 Sydney. In Location B, 2 cases met the confirmed case criteria, 11 cases met the probable case criteria, and 5 (38%) stool samples were collected. Two (40%) samples tested positive for norovirus genotype GII.Pg-GII.1. For Location C, a total of 63 individuals responded to the survey. Eight (13%) cases met the confirmed case criteria, thirty-eight (60%) responses met the probable case definition and 13 (21%) specimens were collected. In Location C, one sample was collected for baby shower attendees, which tested positive for norovirus genotype GII.Pg-GII.1, while 7 (64%) samples collected from the government interagency meeting tested positive for norovirus genotype GI.P7-GI.7. Across all locations, 83 individuals were interviewed for symptoms; the most commonly reported symptoms were diarrhea (52%) and vomiting (48%).

CONCLUSIONS: We identified 2 genogroup II strains and 1 genogroup I strain in a 60 day period, including an emerging GII.4 recombinant. GII.4 strains mutate by genetic drift, which is likely driven by rising population immunity and, generally, new norovirus strains emerge about every 2 to 4 years. Recommendations based on guidance from the U.S. Centers for Disease Control and Prevention for infection control of acute viral gastroenteritis outbreaks were provided. Location C implemented an intensified cleaning regimen to address potential hot spots and provided employee training.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Waterborne Disease; Food Safety

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9929

Abstract Type Lightning

Abstract Title Not a Winner Turkey Dinner: Outbreak of *Clostridium Perfringens* at a Thanksgiving Dinner

Abstract

BACKGROUND: In November 2017, the New Hampshire (NH) Department of Health and Human Services and the Manchester Health Department investigated an outbreak of *Clostridium perfringens* following a Thanksgiving dinner at Veteran's service organization (VSO) in Manchester, NH after several attendees reported diarrheal illness and abdominal cramping. Twenty-five cases were identified in meal attendees.

METHODS: All meal attendees at the VSO were interviewed using an outbreak-specific questionnaire. Ill attendees were also asked about clinical illness, and clinical specimens were requested from ill individuals. A case was defined as any individual who ate the Thanksgiving dinner and had diarrhea and/or abdominal cramping after the meal. Environmental assessments of the VSO kitchen were conducted to assess food service practices and collect leftover food specimens for laboratory testing.

RESULTS: Twenty-five cases were identified from New Hampshire, Maine, and Massachusetts. The most common symptoms among cases were diarrhea (92%), abdominal cramps (41%), and fatigue (33%). No cases were hospitalized or died as a result of their illness. One stool specimen was obtained from an ill person and tested. Twenty-four of 25 food histories were obtained, and no statistically significant associations between illness and food consumption were identified. Environmental assessments identified a lack of managerial controls, using homemade foods, and several improper cooling, reheating and hot-holding issues at the VSO kitchen. Turkey stock that was used in multiple dishes, including stuffing and turkey, was obtained during the kitchen inspection. Both the stool and turkey stock tested positive for *Clostridium perfringens*. Remediation and education was conducted with the group that performed the cooking at the VSO to prevent future incidents.

CONCLUSIONS: Consumption of foods contaminated with *C. perfringens* was the source of this outbreak. Several temperature-related issues were identified during the preparation and holding of foods served at this dinner, which created an environment where *C. perfringens* could proliferate. Foods should be heated to the specified time and temperature according to the FDA Food Code, or reheated to 165°F and held at or above 135°F. Proper cooling of hot foods, cooling to from 140°F or above to 70°F within 2 hours and to below 41°F within an additional 4 hours, is a requirement for foods that are going to be reheated to prevent pathogen or toxin growth.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Enteric Infectious Diseases; Food Safety; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9842

Abstract Type Lightning

Abstract Title Outbreak of Enteroinvasive *Escherichia coli* Associated with an Elementary School—Kansas, August 2017

Abstract

BACKGROUND: Enteroinvasive *Escherichia coli* (EIEC) bacteria are human enteric pathogens and identified outbreaks of EIEC are rare in the United States. On August 30, 2017, a local health department (LHD) notified the Kansas Department of Health and Environment (KDHE) of two students within the same grade at an elementary school that had been hospitalized, reportedly for shigellosis. An investigation was initiated by KDHE and the LHD.

METHODS: Ill students or their guardians were interviewed with a disease-specific or outbreak-specific questionnaire, dependent upon testing status, by telephone. Staff were emailed a survey link to complete the outbreak-specific questionnaire. Stool specimens were tested using the FilmArray GI Panel®, a culture-independent diagnostic test (CIDT), privately and at Kansas Health Environmental Laboratories (KHEL), and culture at KHEL. In addition, CIDT, colony PCR for identification of the invasion plasmid antigen H gene (*ipaH*), pulsed-field gel electrophoresis (PFGE), and whole genome sequencing (WGS) were performed at the Minnesota Department of Health Public Health Laboratory (MDH). An outbreak case was defined as isolation of EIEC O124 with an indistinguishable PFGE pattern or diarrhea or vomiting in a person with epidemiologic linkage to the school.

RESULTS: Questionnaires were completed by 9 students, 4 household members, and 37 staff. Fourteen persons met the outbreak case definition. Median age was 10 years (range: 4-43 years). Of those who reported symptoms, 11/13 (84.6%) experienced diarrhea and 9/14 (64.3%) had vomiting. Three (21.4%) persons were hospitalized for their illness. Eight ill persons were tested by CIDT either privately or at KHEL; six were positive for *Shigella* /EIEC. KHEL performed culture on the six positive specimens; *Shigella* was not isolated. MDH confirmed presence of *Shigella* /EIEC in the six specimens, five of which were positive for the *ipaH* gene. Of those, EIEC O124 was isolated from three specimens which were indistinguishable by PFGE.

CONCLUSIONS: The causative etiologic agent of this outbreak was EIEC, not *Shigella*. Symptoms caused by EIEC infection are similar to those of *Shigella* infection and this outbreak highlights that EIEC has the capacity to cause severe gastrointestinal illness. Increasingly, laboratories are utilizing CIDTs, but because the *ipaH* gene is present in *Shigella* and EIEC, CIDTs cannot differentiate between the two pathogens. EIEC should be considered as a potential pathogen in enteric outbreaks especially when *Shigella* is not able to be isolated from specimens positive for *Shigella* /EIEC by CIDT.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Enteric Infectious Diseases; Epi / Lab Capacity (ELC); Outbreaks

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9778
Abstract Type	Poster
Abstract Title	<i>Listeria Monocytogenes</i> Outbreak Spanning Multiple Years in Erie County, New York: How Whole Genome Sequencing Helped Identify and Solve
Abstract	BACKGROUND: Listeriosis is a rare but serious foodborne illness with an average of three lab-confirmed cases reported to Erie County annually and outbreaks infrequently recognized. <i>Listeria monocytogenes</i> can survive in the environment for extended periods of time and contaminate food and settings where meals are prepared and served. Pulsed-field gel electrophoresis (PFGE) and whole-genome sequencing (WGS) analysis are essential for outbreak detection. Erie County Department of Health (ECDOH) and New York State Department of Health (NYSDOH) utilized PFGE and WGS and epidemiologic data to link seven listeriosis cases occurring in Erie County residents from 2014-2017. METHODS: ECDOH investigated positive <i>Listeria</i> laboratory reports utilizing a standard questionnaire that captures demographic, clinical, exposure, and testing information. Clinical laboratories submitted patient isolates to the NYSDOH Public Health Laboratory, Wadsworth Center (WC), for PFGE and WGS. WC compared PFGE and WGS results to national databases and reported case matches to NYSDOH and ECDOH, prompting further epidemiologic and environmental investigation. RESULTS: ECDOH investigated 15 listeriosis cases between 2014-2017. A cluster of seven cases was identified. Isolates from the seven cases had an indistinguishable PFGE pattern combination (GX6A16.0677/GX6A12.0770), and were highly-related by WGS, differing by 0-4 alleles; no other closely related isolates were identified by WGS elsewhere in the nation. The seven cases had a median age at onset of 81 years and reported multiple comorbidities. Five cases (71%) were male, six (86%) were hospitalized, and three (43%) died. During follow-up interviews six cases reported eating food prepared at and delivered by a single establishment. <i>Listeria</i> was not identified in initial environmental samples collected from the establishment. Using methodologies recommended by the NYS Integrated Food Safety Center of Excellence and NYS Department of Agriculture and Markets, 40 non-food contact surface environmental samples were collected at the establishment and tested at WC. <i>Listeria monocytogenes</i> isolated from four (10%) samples shared an indistinguishable PFGE pattern with the seven cases and were highly-related by WGS, differing by 1-6 alleles. The establishment voluntarily agreed to cease production, hired a consultant, conducted remediation and resampled. CONCLUSIONS: This outbreak underscores the significant role of WGS in identifying related cases. Environmental results suggested persistent contamination in the establishment. Collaboration with partners to assist with environmental sampling helped focus areas for concern in the establishment. Without these public health activities, a food establishment may not have been identified and implicated, nor would control measures have been implemented to prevent further transmission.
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Food Safety; Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9574

Abstract Type Poster

Abstract Title *Salmonella* Serotype Javiana Outbreak Associated with a Restaurant in Kentucky, 2017

Abstract

BACKGROUND: In August and September 2017, the Kentucky Department for Public Health (KDPH) and the Purchase District Health Department (PDHD) investigated a *Salmonella* Javiana outbreak in western Kentucky. Cases reported dining at or being associated with a restaurant (Restaurant A) prior to illness onset.

METHODS: A case was defined as: Any individual or close contact of an individual who dined at Restaurant A from August 10 through August 28, 2017 and exhibited signs or symptoms of *Salmonella* infection and/or had positive laboratory tests for *Salmonella* Javiana. Cases were initially interviewed with the Kentucky Foodborne/Waterborne Illness Investigation Form. Once the restaurant was identified as a common exposure among cases, investigations of restaurant staff and practices were conducted. The Kentucky Division of Laboratory Services (DLS) serotyped and performed pulsed-field gel electrophoresis (PFGE) analysis on all clinical isolates. Whole genome sequencing (WGS) was performed on all eight clinical isolates. Environmental assessments were conducted and yielded five stool specimens from other restaurant employees, but no food samples were collected.

RESULTS: Eleven cases (eight culture-confirmed and three probable) were identified as part of the outbreak, including five individuals associated with Restaurant A (three employees and two of their family members). All but two of the cases reported dining at Restaurant A prior to illness onset; one was a close contact of ill restaurant employees, and one had no reported associations with the restaurant or its employees. *Salmonella* Javiana, pattern JGGX01.0131, was identified as the outbreak strain. All isolates were identified as closely related by WGS, including the individual without other associations. All subsequent stool specimens collected from restaurant employees tested negative for *Salmonella* infection. Although no critical violations were noted, environmental assessments identified some improper holding temperatures for several food items.

CONCLUSIONS: Although this outbreak was linked to Restaurant A, investigations were unable to identify the outbreak source. WGS helped link the individual without associations to Restaurant A. It is unknown whether the identified restaurant employees were the cause of the outbreak.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Outbreaks; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10051

Abstract Type Poster

Abstract Title Antimicrobial Resistance of Nontyphoidal Salmonella Isolates in Kentucky, 2004-2016

Abstract

BACKGROUND: Nontyphoidal *Salmonella* (NTS) causes an infection characterized by diarrhea, fever, and nausea typically lasting for several days. The pathogen is responsible for an average of 600 confirmed cases and 3 outbreaks a year in Kentucky. Although data from the National Antimicrobial Resistance Monitoring System (NARMS) have revealed that antimicrobial resistance in NTS is common, data from Kentucky's isolates submitted to NARMS have never been reviewed by state personnel.

METHODS: NTS isolates were sent to the NARMS laboratory for antimicrobial susceptibility testing using broth micro dilution to determine the minimum inhibitory concentrations for each of the 15 antimicrobial agents on the NARMS panel. Antimicrobial resistance data for Kentucky were downloaded from the NARMS website and were analyzed using IBM SPSS Statistics. Kentucky data were compared to national data obtained from the 2014 *NARMS Annual Human Isolates Report*.

RESULTS: A total of 370 human NTS isolates from Kentucky were sent to the NARMS laboratory from 2004-2016. The majority of isolates displayed resistance to Streptomycin (64.3%) and Ampicillin (84.5%). Approximately one fifth of isolates were resistant to Sulfisoxazole (16.7%) and Trimethoprim-Sulfamethoxazole (21.4%). A minority of isolates displayed resistance to Amoxicillin-clavulanic acid (1.2%), Chloramphenicol (1.2%) and Tetracycline (3.6%). These results are comparable to national data, in which 81.9% of isolates were resistant to Streptomycin, 52.9% to Ampicillin, and 1.6% to Chloramphenicol. In contrast, a much higher percentage of isolates from the national database displayed resistance to Sulfisoxazole (33.1%), Trimethoprim-Sulfamethoxazole (41.4%), and Tetracycline (24.2%). Of the Kentucky isolates, 6.0% were pan-susceptible to all antimicrobials on the NARMS panel, 36.9% were resistant to only one class of antimicrobials, and 57.2% were resistant to more than one class of antimicrobials. These data are comparable to the national database in which 4.2% were pan-susceptible, 32.7% were resistant to one class of antimicrobials, and 63.1% were resistant to more than one class of antimicrobials.

CONCLUSIONS: Although NTS isolates from Kentucky generally displayed less antimicrobial resistance than those from the national database, the vast majority was still resistant to at least one class of antimicrobials. This is concerning because drug resistance combined with high transmissibility increases the likelihood that future *Shigella* outbreaks will be larger, occur more frequently, and be more difficult to treat. Continued antimicrobial resistance testing of *Shigella* isolates is critical to monitor changes in antimicrobial sensitivity and to ensure appropriate antimicrobial treatment.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Infectious Diseases; Antimicrobial Resistance; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9704

Abstract Type Poster

Abstract Title Case-Case Analysis of Campylobacter and Salmonella – Using Surveillance Data for Outbreak Investigations and Monitoring Routine Risk Factors

Abstract

BACKGROUND: Case-case analyses are a useful tool to generate hypotheses during an outbreak investigation or to track changing trends in disease patterns over time within a population. Baseline exposure information can be determined at a more reduced cost and time period than a traditional case-control design. Utilizing routine surveillance data, this study presents a method for generating a baseline comparison that can be used in future foodborne outbreak investigations.

METHODS: *Salmonella* and *Campylobacter* cases (2012-2015) from Maricopa County, AZ were compared to determine differences in risk factors, symptoms and demographics. The University of Arizona's student team interviewed the majority of cases. Following extensive data cleaning to account for variations in coding over time, a merged dataset was created to make comparisons by pathogen. For foods and other risk factors, adjusted odds ratios were developed using *Campylobacter* as the reference. Comparisons were also made for three major *Salmonella* subtypes, Typhimurium, Enteritidis and Poona as compared to *Campylobacter*. A sensitivity analysis was conducted to determine differences based on the inclusion or exclusion of outbreak cases.

RESULTS: A total of 2,980 patients were included in the analyses (1,027 *Campylobacter* cases and 1,953 *Salmonella* cases). *Salmonella* cases were younger with 43.6% of these cases under 20 years old. A higher proportion of *Campylobacter* cases were Hispanic and female. The odds of reporting exposure to food items was higher in *Campylobacter* cases for all items included in the multivariable models. However, only peppers, sprouts, poultry, queso fresco, eggs, and raw nuts were statistically significant. The odds of reporting visiting a petting zoo and contact with a reptile was higher among *Salmonella* cases, whereas *Campylobacter* cases had higher odds of reporting contact with animal products, birds, visiting a farm or dairy, owning a pet, a sick pet, swimming in untreated water or handling multiple raw meats. There were significant variations by *Salmonella* subtype in both foods and exposures. The sensitivity analysis found few significant differences when only non-outbreak cases were included.

CONCLUSIONS: This study generated a baseline comparison that can be used in future outbreaks of *Salmonella* where the source is unknown. We recommend departments conduct this analysis on a yearly basis, and when the data permits, create a running average of relevant odds ratios to be used for comparison. This can decrease the resources needed to determine the outbreak source allowing staff to focus on trace-back of contaminated food items earlier in the investigation.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Surveillance; Food Safety; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9645

Abstract Type Poster

Abstract Title Comparative Epidemiology of O157 Versus Non-O157 Shiga Toxin-Producing *E. coli* in Georgia, 2011-2017

Abstract

BACKGROUND: Nationally, non-O157 Shiga toxin-producing *E. coli* (STEC) infections have increased relative to O157 STEC. Georgia Department of Public Health (DPH) has received a higher proportion of non-O157 STEC reports than O157 in the past several years but these infections and exposures have not been characterized. Identifying commonalities among case-patients may lead to prevention measures. We sought to understand the epidemiology of non-O157 STEC compared to O157 and describe non-O157 serotypes in Georgia.

METHODS: DPH conducts active laboratory-based surveillance through the Foodborne Disease Active Surveillance Network (FoodNet). STEC surveillance data between 2011 and 2017 were queried from our State Electronic Notifiable Disease Surveillance System. Only case-patients with cultures confirmed at a state public health laboratory were included in the analysis. Differences among age groups, race, ethnicity, hospitalization, and travel within 7 days of illness onset were compared between O157 and non-O157 serotypes and a descriptive analysis of the top non-O157 serotypes was conducted. Comparative and descriptive analyses were performed using SAS 9.3.

RESULTS: During 2011-2017, 824 confirmed STEC infections were identified in Georgia. Of these infections, 603 were non-O157 STEC (73.2%). The top five non-O157 (comprising 70.2% of all non-O157 STEC) serotypes were O103 (22.4.9%), O26 (17.9%), O111 (14.3%), O118 (9.0%) and O186 (6.6%). Among non-O157 reports, children less than five years of age accounted for the highest percentage (35.2%) while ages 10-19 accounted for the highest percentage among O157 (25.3%; p: 0.0091). Most non-O157 (73.0%) and O157 (70.6%) case-patients were White. More non-O157 case-patients were Hispanic (16.6%) compared to O157 (5.0%; p: 0.0001). Hospitalization was more common among O157 case-patients (35.3%) than non-O157 (11.3%). Non-O157 case-patients reported more international travel (16.3%) compared to O157 (0.9%; p<0.0001); with the highest percent travel among O186-infected patients (31.6%). Among the top 5 non-O157 serotypes, 35.6% reported international travel to Mexico.

CONCLUSIONS: Non-O157 STEC infections in Georgia were more commonly reported than O157 and less likely to result in hospitalization. Young children, Hispanics, and international travelers were disproportionately affected. While serotype O186 accounted for the smallest percentage of non-O157 serotypes, it represented the highest percentage of international-travel associated case-patients. Further analysis should focus on the epidemiologic characteristics of specific non-O157 serotypes and the relationship between Hispanic ethnicity and international travel. Prevention messages should be targeted to families with children, as well as travelers.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Epidemiology; Foodborne Disease

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9686
Abstract Type	Poster
Abstract Title	Culture-Independent Diagnostic Testing As Predictor of <i>Vibrio</i> Case Confirmation in Oregon in 2017

Abstract

BACKGROUND: Starting in 2017, culture-independent diagnostic testing (CIDT) became an indicator of “probable” (rather than “suspect”) vibriosis case status in the National Notifiable Diseases Surveillance System. Laboratory criteria were expanded, in part, to address the lack of evidence of validity of these methods even as they are increasingly adopted among private laboratories. Oregon vibriosis case investigation requires a significant amount of work, predominantly for local public health staff. Nevertheless, the public health benefit of CIDT testing for *Vibrio* is unclear. Therefore, at the end of 2017, Oregon reviewed CIDT-identified *Vibrio* cases to determine the extent to which patterns of reported cases differed from 2016 to 2017; whether CIDT cases were then confirmed by culture; and the extent to which these cases had epidemiological risks consistent with vibriosis.

METHODS: Number of laboratory reports by primary test (culture vs CIDT) were compared from 2016 to 2017 to determine whether reports differed by test type. Next, final case status (probable vs. confirmed) was compared, by CIDT technique. Among cases first tested by CIDT, plausibility of exposure (broadly defined as contact with natural bodies of water or consumption of any seafood) was evaluated by test type. All comparisons were made using two-tailed Fisher exact tests.

RESULTS: The number of non-outbreak *Vibrio* case reports increased significantly from 24 in 2016 (including suspect cases) to 31 in 2017 ($p=0.05$). Final case status differed by initial CIDT. Of the two types of CIDT for *Vibrio* in Oregon, none of the case-patients initially identified by the BioFire FilmArray Gastrointestinal Panel (BioFire Diagnostics, Salt Lake City, UT) was confirmed by culture, while 6 (55%) of the 11 cases initially identified by the Nanosphere Verigene enteric pathogen test (Nanosphere, Inc., Northbrook, IL) test were confirmed ($p=0.01$). Among case-patients first identified by CIDT, two-thirds of those identified by the BioFire test had no risk of disease (no contact with bodies of water, consumption of raw or any seafood). All patients first identified by the Nanosphere test or culture reported typical risks for vibriosis ($p<0.0001$).

CONCLUSIONS: In 2017, Oregon saw a significant increase in numbers of *Vibrio* cases first identified by CIDT. Only 30% of BioFire cases were confirmed by culture, and none proved to have exposures typically associated with *Vibrio* infection. In contrast, 6 (55%) cases identified by Nanosphere were confirmed by culture, and all had typical *Vibrio* exposures.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiology; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9316

Abstract Type Poster

Abstract Title Differences in Exposures between *Cryptosporidium* Species and Genotypes, Cryptonet, 2016

Abstract

BACKGROUND: Existing literature suggests exposures leading to human illness can differ among *Cryptosporidium* species. In 2010, CDC and states formally began to collaborate on CryptoNet, the first combined epidemiological and molecular-based surveillance system for a parasitic disease in the United States, in response to a >3-fold rise in *Cryptosporidium* incidence since 2004. CryptoNet systematically collected both epidemiologic exposure and molecular genotyping information for the first time in 2016.

METHODS: In 2015, a standardized reporting form for CryptoNet was developed with state partners. In addition to demographic information, the CryptoNet form asks about exposures related to food consumption, drinking water, recreational water, person-to-person exposures (e.g., daycare attendance and diapering activities), and animal contact in the 14 days before illness onset. To facilitate timely collection of CryptoNet forms, CDC staff monitored when specimens were submitted to the CDC laboratory and worked with states to support completion and submission of forms. Frequency tables were used in the analysis to provide proportions for categorical variables, and Fisher's exact test was used to find significant differences in exposures between *C. parvum* and *C. hominis* cases.

RESULTS: In 2016, CDC's CryptoNet laboratory received 321 specimens for molecular subtyping from state partners. For these specimens, 233 (73%) CryptoNet forms were received. A majority of case-patients reported their race as white (76%); a majority of case-patients reported their ethnicity as non-Hispanic/Latino (75%); 56% of case-patients were female (n= 155). The median age was 21 years (range: > 1 – 78 years). Specimens were most commonly positive for *C. hominis* (n = 167; 52%) and *C. parvum* (n = 138; 43%). Additionally, 10 (3%) specimens were positive for *Cryptosporidium* chipmunk genotype I. *C. hominis* case-patients reported significantly higher levels of recreational water exposures (p< 0.01) and person-to-person exposures (p < 0.01), compared to *C. parvum* cases. , *C. parvum* case-patients reported significantly higher levels of animal exposure than *C. hominis* case-patients (p < 0.01).

CONCLUSIONS: CryptoNet surveillance for 2016 provides additional support to previous studies on *Cryptosporidium* exposures. As anticipated, *C. hominis* case-patients were more likely to report exposures connected with human activity whereas *C. parvum* cases were more likely to report exposures connected with animal activities. By integrating detailed epidemiologic data with molecular-based genotyping information, CryptoNet provides a continued evidence base for better understanding of *Cryptosporidium* epidemiology and transmission.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Surveillance; Waterborne Disease; Infectious Diseases

**Consider for
Different
Presentation?** Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10057
Abstract Type	Poster
Abstract Title	Do Foodborne Clusters Have an Expiration Date? Investigation of Multi-Year Salmonella Clusters Identified By Whole Genome Sequencing

Abstract

BACKGROUND: The traditional molecular subtyping method of Pulsed-Field Gel Electrophoresis (PFGE) has been used in Tennessee (TN) to identify clusters among cases occurring within 45 days of each other. With the advent of Whole Genome Sequencing (WGS), a replacement for PFGE, it is now more feasible to identify and review clusters across longer periods of time. We examined twenty-five WGS-linked clusters of *Salmonella* Enteritidis (SE) with cases spanning multiple years to determine if a common exposure source could be identified and if cluster review without time constraints is feasible in the era of WGS.

METHODS: WGS was performed at the Tennessee Department of Health in collaboration with the Wadsworth Center/New York State Department of Health Bioinformatics Core for SE pattern JEGX01.0004 and JEGX01.0005 isolates occurring between 2014 and 2017. Sequence data was assembled and single nucleotide polymorphisms (SNPs) were identified between sequenced isolates and a reference genome, SE sequence P125109. These data were used to construct a maximum-likelihood phylogenetic tree and heat map denoting pairwise SNP differences between each isolate in the data set. A threshold of ≤ 5 SNPs was used to establish clusters of related specimens. Multi-year clusters were identified and compared with epidemiological data collected through routine interviewing for exposure ascertainment.

RESULTS: Sequences for 381 unique isolates were analyzed. Sixty clusters were identified and 25 (42%) had collection dates that spanned multiple years. The median cluster size was 3 cases, with a range from 2 to 23. The amount of time between earliest collection date and latest collection date ranged from 184 to 1170 days with a median of 478 days. A suspected or confirmed vehicle or location was identified for one of 25 multi-year clusters to date.

CONCLUSIONS: As WGS becomes the standard subtyping method, the results may allow epidemiologists to respond to previously unrecognized multi-year outbreaks of ubiquitous *Salmonella* patterns. For WGS, expanding the 60 day PFGE cluster detection timeframe and using a ≤ 5 SNP threshold would be helpful in confirming all related cases are investigated. After reviewing 25 multi-year SE clusters with collection dates between 2014 and 2017, a common location or food item was only identified for one cluster (<1%). While it is possible and rewarding to find a source of illness for previously unsolved multi-year clusters, there are disadvantages to investigating clusters with cases that span several years, particularly the time and staff resources that are necessary to obtain meaningful exposure information.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiology; Foodborne Disease; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9632

Abstract Type Poster

Abstract Title Do You Know Your Clinical Labs? the Foodborne Diseases Active Surveillance Network's Clinical Laboratory Survey

Abstract

BACKGROUND: The increased development and availability of culture-independent diagnostic tests (CIDs) and uptake by clinical laboratories are changing the landscape of enteric pathogen detection. In 2012, the Foodborne Diseases Active Surveillance Network (FoodNet) expanded the case definition of laboratory-diagnosed enteric infections to include positive CIDs, and began conducting a bi-annual clinical laboratory survey to provide context to case surveillance data and interpretation of incidence trends.

METHODS: In spring 2012, FoodNet sites implemented a standardized, pathogen-specific questionnaire of clinical laboratories in FoodNet catchment via email, phone, or personal visit. Data are collected bi-annually (January–March and July–September) and entered into a central, web-based database. Survey questions include whether onsite testing for each pathogen is conducted, which methods were used for primary detection (culture, CID, or both), CID brand name, and specimen type submitted to the state public health laboratory.

RESULTS: During 2012 to 2017, FoodNet conducted 10 cycles with an average of 676 (range, 647–701) participating clinical laboratories per cycle. Comparing laboratories that tested for *Campylobacter* in 2012 with 2017, those exclusively using culture decreased from 90% to 66%, those exclusively using CIDs increased from 8% to 28%, and those using both remained similar (2% and 4%). Comparing the laboratories that tested for Shiga toxin-producing *Escherichia coli* (STEC) or Shiga toxin in 2012 with 2016, those exclusively using culture for O157 decreased from 47% to 20%, those exclusively using Shiga toxin-detecting CIDs increased from 16% to 35%, and those using culture for O157 with a test for Shiga toxin increased from 37% to 45%. Among the laboratories that tested for *Salmonella*, *Shigella*, *Vibrio*, or *Yersinia* in 2012 versus 2017, those using CIDs increased from ≤1% to 18%, 17%, 22% and 19% respectively. In October 2017, among clinical laboratories that test onsite, the percentage conducting reflex culture on CID-positive specimens varied by pathogen (*Shigella* 49%; *Salmonella* 48%; *Vibrio* 31%; Shiga toxin, 28%; *Yersinia* 24%; *Campylobacter* 17%).

CONCLUSIONS: The knowledge and partnerships gained through clinical laboratory surveys provides context to interpret state-specific illness trends, and early notification of new testing practices. Survey results help state health departments provide targeted and timely recommendations to clinical laboratories considering discontinuing culture, prepare for reporting differences due to the addition of multi-pathogen panels, and plan for increased demand for reflex culture at their state public health laboratory.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Enteric Infectious Diseases; Foodborne Disease; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10193

Abstract Type Poster

Abstract Title Epidemiology of Vibrio Infection in Texas, 2007-2016

Abstract

BACKGROUND: Vibriosis is an illness caused by bacteria of the *Vibrio* genus that are naturally found in salty and brackish waters. Such infections cause an estimated 80,000 illnesses and 100 deaths in the United States every year. Vibriosis was added to the list of nationally notifiable conditions in 2007; however, Gulf Coast states, including Texas, have been reporting *Vibrio* illness to the CDC since 1988. Accordingly, with the National Shellfish Sanitation Program (NSSP), Texas cases with history of seafood consumption are reported to state and federal partners who monitor shellfish harvest areas and illnesses associated with those areas.

METHODS: Reported vibriosis cases in Texas are dually reported through the National Notifiable Diseases Surveillance System (NNDSS) and to the CDC using the Cholera and Other Vibrio Illness Surveillance Report (COVIS) form. By Texas law, *Vibrio* species isolates must be submitted to the DSHS (Department of State Health Services) Laboratory. For this study, a review and descriptive epidemiological analysis of NNDSS, laboratory data, and COVIS form data between 2007 and 2016 were conducted. In Texas, vibriosis case exposures are further categorized by shellfish, water, and other/unknown types.

RESULTS: During the 10 year-period from 2007-2016, 773 cases of vibriosis, excluding *V. cholera*, were reported in Texas. Among these cases, 24.1 percent were due to *V. parahaemolyticus*, 30.4 percent *V. vulnificus*, and 45.5 percent to other species of *Vibrio*. The average number of vibriosis cases in Texas is 77 per year (range 54 to 102 cases). The majority of cases (43.7 percent) were associated with water contact, 25 percent with shellfish exposure, and 31.3 percent with unknown exposure. Seventy-three percent of all case patients were males and 64 percent of all cases occurring during the warmer months, May through August. The case fatality rate for the 10-year period was 9 percent (66 deaths), with most (86 percent, or 57 deaths) caused by *V. vulnificus*. Among the fatalities, shellfish exposure was associated with 58 percent, while water contact and unknown exposures each account for 21 percent of deaths.

CONCLUSIONS: Exposure to shellfish accounted for the majority of vibriosis deaths, highlighting the importance of not consuming raw or undercooked shellfish and other seafood, especially by immunocompromised persons. Since more than 43 percent of vibriosis cases were associated with water contact during warmer months, education and prevention messages are crucial. Improving vibriosis surveillance awareness and providing community education is necessary to reduce illnesses and deaths.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Infectious Diseases; Waterborne Disease; Disease Prevention

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10228

Abstract Type Poster

Abstract Title Escherichia coli O157:H7 Outbreak Linked to Locally Sourced Beef

Abstract

BACKGROUND: *Escherichia coli* causes ~265,000 infections annually in the United States, with ~ 1/3 due to Shiga-toxin producing *E. coli* (STEC) O157. Although *E. coli* O157:H7 is an adulterant of ground beef, outbreaks are commonly associated with undercooked beef. We identified an outbreak of STEC associated with a restaurant promoting local food products, and investigated to determine the source and implement control measures.

METHODS: In November 2015, an increase in STEC infections was detected through routine disease surveillance in Knox County, Tennessee. Four cases of STEC O157:H7 were identified among persons who reported eating at Restaurant A. The restaurant's reservation list and menu were used to identify patrons and conduct an unmatched case-control study. Descriptive, univariate, and bivariate analyses were performed using Microsoft Excel and Epi Info 7. A comprehensive environmental assessment was conducted. Restaurant invoices were used for trace-back and trace forward investigations. Food and clinical samples were collected in collaboration with United States Department of Agriculture Food Safety and Inspection Service and isolates underwent testing by pulsed field gel electrophoresis (PFGE).

RESULTS: Among 132 restaurant patrons contacted, 69 (52.3%) completed the survey and were enrolled in the case-control study. Several components of the hamburger entrée were significantly associated with illness including, ground beef (odds ratio [OR] 6.3, confidence interval [CI] 1.54-25.33), chutney (OR 6.11, CI 1.42-26.36), and artisan cheese (OR 8.8, CI 2.04-37.95). Temperatures below the USDA safe minimum of 160°F for ground beef were observed during the environmental assessment. Trace-back investigation identified a single local ground beef supplier for Restaurant A and three additional establishments (Restaurant B, Restaurant C and Store A). Stool specimens from four case patients with *E. coli* O157:H7 had a matching PFGE pattern. All six ground beef samples from Restaurant A tested positive for STEC by polymerase chain reaction; one was a novel *E. coli* strain (O117:H4). Among three unopened beef packages from Restaurant B, one contained *E. coli* O157:H7 with an identical PFGE pattern to the clinical isolates.

CONCLUSIONS: Detection of STEC from the local beef distributor demonstrates there is risk of foodborne disease from locally sourced beef. The identification of multiple strains of STEC in the same ground beef source stresses the importance of safe food handling practices and appropriate cooking temperatures. A multidisciplinary approach to this investigation allowed for expedited trace forward and trace-back of contaminated food products; ultimately resulting in a product recall and potential prevention of additional illnesses.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9385

Abstract Type Poster

Abstract Title Exposure Completeness for Shigellosis Cases, Kentucky, 2015

Abstract

BACKGROUND: Complete exposure information for enteric illness investigations facilitates accurate data analysis, timely discovery of a common exposure, and early intervention. Our objective was to determine the completeness of exposure reporting for suspected, probable, and confirmed Shigellosis cases in Kentucky in 2015.

METHODS: A case was any Kentucky resident who met the National Notifiable Diseases Surveillance System 2012 case definition for suspected, probable, or confirmed Shigellosis. Health department nurses, environmentalists, and epidemiologists conducted interviews using Kentucky's Foodborne/Waterborne Illness Investigation Form and recorded responses in NEDSS. Completeness was calculated based on responses to 59 variables related to food, occupation, water, and animal exposures; any non-blank response was considered a completed field. A questionnaire was considered incomplete if <50% of the exposure-related items were answered, acceptable if 50% - 75% were answered, and preferred if >75% were answered. Questions that assessed highly important risk factors were considered separately, including daycare association, food handler status, recreational water activity, recent travel, and attending a group or social event. Other important exposures are not included on the questionnaire, e.g. sexual behavior or were unable to be queried, e.g. close contacts with similar illness.

RESULTS: In 2015, Kentucky reported 490 Shigellosis cases. Of these, 417 were confirmed cases, 14 probable, and 59 suspected. Exposure information for 182 (37%), of all cases was considered preferred, 0 (0%) considered acceptable, and 308 (63%) considered incomplete. The average response rate for individual questionnaires was 45%. Highly important risk factors tended to have more complete information. 318 (65%) cases had preferred completeness for exposures of high importance; 14 (3%) cases had acceptable completeness. 158 (32%) cases were considered incomplete. The average response rate for important risk factors on individual questionnaires was 73%.

CONCLUSIONS: These results demonstrate the need to improve data collection. With incomplete exposure information for more than half of all cases, Kentucky has a limited capacity to intervene in the spread of disease and prevent future infections or outbreaks. The comparison with important risk factors indicates that the public health professionals conducting interviews are using their expertise to prioritize key questions; however, it should also be noted that exposures of high importance may not be the only source or spread of *Shigella*. To facilitate improved completeness, we suggest reviewing and tailoring the questionnaire, adding a question assessing sexual exposure, pursuing other formats for questionnaire administration such as online or after hours, and providing supplemental staff training.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Enteric Infectious Diseases; Epidemiology; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9967

Abstract Type Poster

Abstract Title Exposures to Fresh and Well Water Among Salmonella Cases in Georgia, 2007-2016

Abstract

BACKGROUND: *Salmonella* is often associated with consumption of contaminated food and exposure to animals, though it is also found in well water and fresh water. Since 2007, an average of 7.3% of *Salmonella* reports to the Georgia Department of Public Health (GDPH) included exposure to fresh or well water before illness onset. We characterized fresh and well water exposures and summarized associated case-patient demographics and serotype distribution.

METHODS: GDPH collects *Salmonella* case-patient demographic and exposure data in its State Electronic Notifiable Disease Surveillance System. *Salmonella* case-patient data from 2007 through 2016 were reviewed for fresh water exposure, well water exposure, or neither exposure within the 7 days before illness onset. Demographics, including residence location, and serotype were ascertained. Descriptive statistics were calculated in Microsoft Excel. Ninety-nine case-patients who reported exposure to both fresh and well water were excluded from analysis.

RESULTS: From 2007 through 2016, 24,489 *Salmonella* case-patients reported either no fresh or well water exposure [NOWATER] (22,596, 92.3%), exposure to well water [WELLONLY] (1282, 5.2%), or exposure to fresh water [FRESHONLY] (611, 2.5%). Of FRESHONLY case-patients, 50.9% were female and 34.0% were under the age of 5. WELLONLY and NOWATER case-patients had similar sex and ages. Whites more frequently reported exposure to fresh water (81.3%) than Blacks (9.2%), and percentages were similar among WELLONLY case-patients (86.7% White, 7.2% Black). In contrast, NOWATER case-patients had a significantly different racial breakdown than either the FRESHONLY group or the WELLONLY group, with 61.7% white and 21.4% black ($p < .0001$ for each comparison). The top 5 serotypes for each of the 3 water exposure groups were Javiana, Newport, Enteritidis, Muenchen, and Typhimurium. The greatest variation in serotype frequency across exposure groups was Enteritidis, which made up 17.0% of the FRESHONLY group, 9.5% of the NOWATER group, and 4.1% of the WELLONLY group. Approximately one third of the WELLONLY case-patients lived in southeast Georgia. In contrast, one third of the FRESHONLY case-patients lived in metro Atlanta.

CONCLUSIONS: A substantial number of Georgia residents infected with *Salmonella* reported exposure to fresh water or well water and these exposures may be a source of infection. Continued monitoring of trends in water exposure and examination of demographic, serotype, and geographical differences may provide input about possible sources of infection. Preventative measures may include ensuring proper well maintenance and practicing hand hygiene after fresh water exposures.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Epidemiology; Enteric Infectious Diseases; Environmental Exposures

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9989

Abstract Type Poster

Abstract Title Increased Incidence of Alabama *Vibrio* Cases Triggers Analysis of Demographic Factors and Indicators of Disease Severity, 2012-2016

Abstract

BACKGROUND: Species in the *Vibrionaceae* family are natural inhabitants of marine/estuarine environments. Whether exposure occurs through consumption of shellfish or participation in recreational water activities, the resulting illnesses can be of varying severity and include gastrointestinal symptoms, wound infections, and even death. In Alabama, there is opportunity for both foodborne and environmental exposure. Understanding state-specific characteristics of reported cases and health outcomes may inform targeted provider and community education and prevention efforts.

METHODS: Data for vibriosis cases reported to the Alabama Department of Public Health 2012 - 2016 were analyzed using SAS® 9.3. Descriptive analysis of case demographics, recreational water exposure, and outcomes was conducted. Logistic regression was performed to assess the association between gender, race, ethnicity, age group, and underlying conditions and indicators of illness severity (hospitalization, antibiotic therapy, and mortality); Firth's Penalized Likelihood method was utilized to reduce small sample bias. Outcomes were then compared to assess differences in indicators across species.

RESULTS: From 2012 to 2016, there were 108 cases of vibriosis reported in Alabama; complete species information was available for 107. There was an overall increase (63%) in cases reported between 2012 and 2016; 78% were male, 93% were non-Hispanic, 90% were Caucasian, and 65% reported at least one underlying condition. Ages ranged from 1 to 89 years, with a median of 58 years. Antibiotic therapy was received by 89% of the cases, 56% were hospitalized, and 6% were known to have died. Recreational water exposure in the 7 days before illness was reported by 48% of the cases; of these, 65% had ocean water exposure. *V. vulnificus* accounted for 34% of cases. It was found that females (p-value <0.05), those without underlying conditions (p-value <0.001), and those aged 1-10, 11-21, and 22-32 years (p-value_{1-10,11-21,22-32} ≤0.05) were significantly less likely to become hospitalized; differences in antibiotic therapy and mortality were not statistically significant. *Vibrio* species, including *V. parahaemolyticus*, non-*cholerae*, *V. alginolyticus*, *V. cholerae* (non-O1/O139), and *V. mimicus* (p-value_{all} <0.05) were less likely to be hospitalized compared to those infected with *V. vulnificus*. No significance was observed among other indicators.

CONCLUSIONS: Though this study had limitations, state-specific analyses of vibriosis case demographics, illness severity indicators, and predominant species may indicate the need for modification of education and intervention efforts. The addition of follow-up interviews or medical record review to the current investigation processes may provide additional information on case outcome and contributing factors required for more detailed analyses.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Waterborne Disease; Epidemiology; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10166

Abstract Type Poster

Abstract Title Multistate Salmonella Illness Outbreaks Linked to Live Poultry – United States, 2017

Abstract

BACKGROUND: Annual outbreaks of *Salmonella* illnesses linked to live poultry have increased in the United States (US) since 2008. In 2017, record numbers of *Salmonella* infections linked to live poultry were reported. In the US, most *Salmonella* infections from live poultry contact result from contact with backyard flocks. Twenty major hatcheries supply live poultry to feedstores for use in US backyard flocks. Investigating behaviors among ill people and conducting traceback on purchased poultry are important to understand risk factors for these outbreaks and identify prevention measures.

METHODS: Outbreak strains were identified through PulseNet. Ill people were interviewed with state-specific enteric and live poultry supplemental questionnaires. Feedstore and hatchery staff were interviewed to ascertain origin of poultry. Data were collected in the System for Enteric Disease Response, Investigation, and Coordination (SEDRIC) and Epi Info 7, and descriptive statistics were calculated using SAS 9.4.

RESULTS: In 2017, 1120 people in 48 states and the District of Columbia were infected with one of 20 *Salmonella* outbreak strains. Seventy-four percent (498/672) of ill people interviewed reported contact with live poultry prior to illness onset; of these, behaviors reported included touching poultry (72%), snuggling or kissing poultry (24%), touching cages (66%), and keeping poultry indoors (34%). Seventy-five percent (237/314) reported owning poultry and traceback identified forty different feedstores and 15 different hatcheries. Nine ill people reported occupational contact with live poultry. Forty-two percent of ill people reported they did not know about the connection between *Salmonella* and live poultry.

CONCLUSIONS: *Salmonella* illness outbreaks linked to US backyard flocks have continued to increase. In 2017, ill people engaged in behaviors that might have led to *Salmonella* transmission. Education of poultry owners and feedstore employees on the link between *Salmonella* and live poultry might prevent behaviors that can lead to illness. Encouraging identified hatcheries to reduce human disease-causing *Salmonella* strains in the hatchery environment might help further reduce the number of illness outbreaks.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Zoonotic Diseases; One Health; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9539
Abstract Type	Poster
Abstract Title	Outbreak of Co-Infection with Shiga-Toxin Producing <i>E. coli</i> and Norovirus at a Daycare Center in Miami-Dade County, March 2017

Abstract

BACKGROUND: In March 2017, the Florida Department of Health in Miami-Dade County (DOH-Miami-Dade), Epidemiology, Disease Control and Immunization Services (EDC-IS) was notified by DOH-Broward of a Broward resident positive for Shiga-toxin producing *E. coli* (STEC) attending a Miami-Dade daycare center as well as several ill contacts at the center. An investigation was initiated and a total of 19 ill attendees and staff were identified. Symptoms included vomiting, diarrhea and/or fever. Laboratory results revealed that the outbreak was caused by both STEC and Norovirus.

METHODS: An in-depth investigation was launched and consisted of interviews, an inspection and food assessment. EDC-IS immediately recommended that symptomatic attendees and staff be excluded from the daycare center based on the state's Guidelines for Control of Outbreaks of Enteric Disease in Child Care Settings. EDC-IS provided the facility with recommended environmental control measures. Stool collection kits were provided and samples were sent to the Bureau of Public Health Laboratories (BPHL). Two parent letters were provided to the facility alerting parents of the outbreak, control measures, and readmission requirements.

RESULTS: The inspection and food assessment showed no violations. Attack rates among ill attendees and staff were 15.0% (15/100) and 22.2% (4/18), respectively. Among ill attendees and staff, 73.7% reported vomiting, 63.2% reported diarrhea, and 15.8% reported fever. The earliest onset of symptoms was 2/22/17 and the latest onset was 3/13/17. Laboratory results indicated that 8/19 ill (5/15 attendees and 3/4 staff) were PCR (+) for STEC. Additionally, 4/19 ill were PCR (+) for Norovirus (3/15 attendees and 1/4 staff). Two of the eight individuals positive for STEC (one attendee and one staff) had a co-infection with Norovirus. All culture results were negative except for one attendee who was culture (+) for STEC serotype O123:H2. Ill attendees were from six different classrooms and ill staff were all front desk workers.

CONCLUSIONS: Variance in symptom onset suggests that the outbreak may have resulted from person-to-person transmission. This investigation highlights the importance of initiating timely control measures to prevent further disease spread. Due to the duration for culture results, daycare readmission criteria were modified after consultation with the Bureau of Epidemiology and BPHL from two consecutive negative stool cultures to two consecutive negative stool PCR results at least 24 hours apart and no sooner than 48 hours. Eighteen of the 19 ill attendees and staff were readmitted into the daycare center based on the modified criteria and one attendee no longer attends the center.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Children and Adolescents; Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9933

Abstract Type Poster

Abstract Title The Changing Epidemiology of Cryptosporidiosis in New Hampshire

Abstract

BACKGROUND: Cryptosporidiosis is a diarrheal illness caused by the parasite *Cryptosporidium* that is commonly associated with recreational water, farm animals, contact with infected individuals and consumption of raw fruits and vegetables. Approximately 46 cases are reported annually in New Hampshire, mostly in the summer. Enhanced standardized collection of exposure information from cryptosporidiosis cases was initiated in mid-2016 as part of CryptoNet activities. We analyzed data collected in 2016 and 2017 to identify emerging trends in cryptosporidiosis epidemiology in New Hampshire.

METHODS: Reported illnesses were evaluated using the national case definition and all confirmed or probable cases were interviewed using either the cryptosporidiosis-specific investigation form or a New Hampshire-specific enteric disease investigation form. Only cases that had a complete cryptosporidiosis-specific investigation form reported between June 1, 2016 to December 31, 2017 were included in this analysis. Reported exposure frequencies were calculated and compared between 2016 and 2017.

RESULTS: Of 66 cases reported in 2017, 49 (11 confirmed and 38 probable) were included in this analysis; all 19 cases that had completed the surveillance form from 2016 were included. The highest incidence of cases based on onset of illness occurred during May and September, both of which were significantly elevated above a historical 5-year baseline. The number of cases in June, July and August were below, but not significantly, the respective baselines. The most common exposures reported in 2017 were spending time outdoors (65%), spending time on a farm (59%), and having contact with cattle (42%). A significant difference between 2016 and 2017 was observed in the proportion of cases spending time on a farm (27% vs 59%; p-value 0.0082) and having exposure to any farm animal (27% vs 57%; p-value 0.0127). Two animal contact outbreaks resulting in 14 cases were identified in 2017.

CONCLUSIONS: Enhanced exposure assessment has identified increased reporting of animal contact exposures among New Hampshire cryptosporidiosis cases, including identification of two common source outbreaks associated with calves. This observation is consistent with the increased occurrence of cases in the spring (April and May) when calves are purchased, and the fall (September) during agricultural fair season. The decrease in reported cases in June through August 2017 was not expected and warrants ongoing surveillance to determine if this change in epidemiology will continue. The importance of animal contact exposures recognized in 2017 highlights the need for future cryptosporidiosis prevention and education efforts.

Committee Infectious Disease

Topic Enteric Diseases

Keywords One Health; Epidemiology; Sustainability

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9893

Abstract Type Quick

Abstract Title *Salmonella* Heidelberg Investigations Associated with a Catering Service, New York State, 2017

Abstract

BACKGROUND: In August 2017, the New York State (NYS) Department of Health and two local health departments investigated six *Salmonella* cases among individuals who attended two unrelated events. The events were held in different counties five days apart and were catered by the same establishment. The establishment had catered many events during the same time frame, but illness was only reported following these two events. An investigation was started to determine if a common source caused illness at both events. In NYS, all *Salmonella* isolates are submitted to Wadsworth Center for pulsed-field gel electrophoresis (PFGE) and whole genome sequencing (WGS).

METHODS: Menu items were obtained for both events from the establishment and a guest list from the second event was secured. Outbreak questionnaires were emailed to 64 guests of the second event to document symptoms and food exposures. Four food handlers from the catering service submitted stool specimens. Leftover food from the establishment was not available, but a guest's leftover roast beef was submitted for testing. An environmental health assessment was conducted at the catering company. Three isolates (food and one clinical from each event) were sent to the National Antimicrobial Resistance Monitoring System for Enteric Bacteria (NARMS) for resistance testing.

RESULTS: Of the 58 guests who completed questionnaires from the second event, 28 (48%) reported symptoms consistent with *Salmonella*. Four individuals from event one and two individuals and leftover roast beef from event two tested positive for *Salmonella* Heidelberg and matched via PFGE. The PFGE pattern identified was considered endemic in NYS. All food handlers tested negative for *Salmonella*. WGS analysis revealed the six clinical and one food sample were highly related. The three isolates sent to NARMS had matching resistance patterns with resistance to gentamicin, streptomycin and sulfisoxazole. No contributing factors were identified from the initial environmental health assessment, however, further follow-up identified that cross contamination could have occurred due to improper glove use.

CONCLUSIONS: *Salmonella* Heidelberg was considered the causative agent of this two-event outbreak. While food and clinical samples were highly related with WGS, it remains unclear at which step contamination occurred. No additional illnesses were associated with this establishment.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Local Epidemiology; Foodborne Disease; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10167

Abstract Type Quick

Abstract Title *Vibrio Vulnificus* Infections Associated with Handling of Tilapia from Live Retail Fish Market Tanks — King County, Washington, 2016–2017

Abstract

BACKGROUND: CDC estimates that 77 persons die annually from *Vibrio vulnificus* infections, making it the leading cause of seafood-related deaths in the United States. Two *V. vulnificus* wound infections were reported to Public Health — Seattle & King County (PHSKC) in 2016–2017; both sustained wounds while handling tilapia, a freshwater fish, purchased live from 2 retail fish markets before illness onset. Because *V. vulnificus* infections are typically associated with wound exposure to brackish water and associations with handling tilapia are rare, we investigated to identify contamination source and implement prevention measures.

METHODS: PHSKC inspected both retail fish markets where patients purchased live tilapia (Market A and Market B) and transport tanks from a common distributor (Distributor A). Fish specimens and swabs from fish tanks, utensils, and environmental surfaces were collected. Samples underwent polymerase chain reaction and culture; *V. vulnificus* isolates were compared with patient isolates using pulsed field-gel electrophoresis (PFGE).

RESULTS: *V. vulnificus* was identified from 2/2 fish and 7/7 environmental swabs collected from Market A where Patient A shopped, 2/2 fish and 6/8 environmental swabs from Market B where Patient B shopped, and 1/2 fish samples and 3/5 transport tanks from Distributor A. PFGE patterns differed between patients, but matched investigation isolates; 3 environmental isolates from Market A matched Patient A's isolate and all isolates from Market B and Distributor A matched Patient B's isolate.

CONCLUSIONS: We describe the first *V. vulnificus* wound infections associated with handling tilapia from retail market fish tanks in the United States. Live fish tanks should be properly cleaned and maintained, and retail fish market employees and consumers with underlying chronic diseases should be educated about *V. vulnificus* infection. Wearing thick rubber or cut resistant gloves when handling tilapia and other seafood products may help minimize risk for infection.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Enteric Infectious Diseases; Food Safety

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10260

Abstract Type Quick

Abstract Title A Never Ending Cycle of Poop: Can an Outbreak Become the New Baseline?

Abstract

BACKGROUND: *Shigella sonnei* is a relatively common and highly contagious bacterium that can be associated with outbreaks. Usually these outbreaks are quickly contained by taking appropriate prevention measures. However, New Mexico faced an unprecedented outbreak; both in size and duration. For over 17 months, New Mexico Department of Health (NMDOH) had seen 268 confirmed and probable cases of *Shigella* located in the southeastern portion of the state.

METHODS: On May 10, 2016, NMDOH was notified via electronic laboratory reporting (ELR) of a positive *Shigella* culture in a pregnant 17-year-old patient. After conducting an interview, it was determined that family members as well as foster children living at her residence were also symptomatic. This outbreak quickly became associated with multiple daycares and families. Robust prevention measures were put in place; including press releases, letters to daycares and schools, HANs, educational materials, conference calls and in-person meeting with local providers in partnership the CDC, and new protocols for middle and high school children were developed. However, this outbreak would continue to come in four waves and eventually maintain a consistent stream of cases for the final four months.

RESULTS: *Shigella sonnei* 1603ML16-1 was the primary PFGE associated with this outbreak. This strain of *Shigella* was linked with a multi-state outbreak and had not been seen in New Mexico previously. Determining the baseline for this outbreak became complicated when the hospitals in that region switched from culture testing to culture independent testing (CIDT) in July of 2016; it became unclear if NMDOH was seeing more cases of *Shigella* because of the outbreak or because of the more frequent use of CIDT. This outbreak was further complicated by the socio-economic status of the region, movement of foster children, and miscommunication between schools and daycares. In addition, the reluctance of providers to conduct testing and/or provide antibiotics to symptomatic children as well as providing notes to patients to return to work/school/daycare while still symptomatic helped to propagate the outbreak.

CONCLUSIONS: NMDOH identified an outbreak of *Shigella sonnei* that originated in a daycare with foster children that ultimately grew to become entrenched in several southeastern communities in New Mexico for over 17 months. This case study illustrated the challenges in containing an outbreak if not caught early enough, the complications that may arise from relying heavily on culture-independent testing, and the need to develop and maintain strong relationships within the communities and partner organizations.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Health Disparities; Outbreaks; Enteric Infectious Diseases

**Consider for
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Submission Type Breakout/Quick/Lightning/Poster

ID 9983

Abstract Type Quick

Abstract Title An Investigation of an Outbreak of Stec 0111 at a Daycare in Pennsylvania

Abstract

BACKGROUND: Shiga toxin-producing *E. coli*, or STEC, produce toxins which cause diarrhea (often bloody), Complications can include hemolytic uremic syndrome and kidney failure. Outbreaks of STEC in daycare settings are not common in Pennsylvania, with five identified since the year 2000. These five comprise 6% of all reported STEC outbreaks in PA. The most common STEC serogroup identified in North America is O157; however, most hospital and commercial labs are not equipped to identify non-O157 serogroups.

METHODS: In September 2017, a single case of STEC serogroup O111 in a child attending a daycare was reported to Pennsylvania's surveillance system. An investigation was initiated. A site visit was performed to identify additional cases and provide guidance to the daycare and the families on prevention and control measures, including exclusion requirements for cases and high-risk contacts. A confirmed case was defined as someone associated with the daycare (e.g. attendees, employees, siblings, or parents) between 8/8/2017 and 10/1/2017, and who had a positive shiga toxin stool test (by ELISA or PCR) or a culture positive for STEC O111. A probable case was defined as a person with diarrhea between 8/8/2017 and 10/1/2017, without any laboratory confirmation, who was epidemiologically linked to a confirmed case.

RESULTS: After completing the initial site visit, the Department conducted additional case finding by interviewing families and cross-referencing the daycare roster with PA's surveillance system. Two additional STEC O111 cases and four probable cases were identified, making a total of seven cases. All probable cases had at least one negative stool sample. There were no hospitalizations and no cases of hemolytic uremic syndrome. All cases were under 5 years of age. Two confirmed cases were siblings who attended the daycare. The combined attack rate in the daycare was 13% (7/56 children); the highest attack rate, 30% (3/7), occurred in the 2-year-old room where all children were diapered. There were no other cases among siblings, family members, or staff.

CONCLUSIONS: A fairly large but localized outbreak of STEC O111 occurred at a daycare. As most hospital and commercial labs are not capable of testing for non-O157 STEC, it is likely that many of these infections go undiagnosed and unreported. When evaluating patients with diarrheal illness, clinicians should consider non-O157 STECS as a possibility, and forward specimens to their state public health lab for additional testing when tests indicate the presence of shiga toxin but O157 cannot be identified.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Epidemiology; Outbreaks

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9020
Abstract Type	Quick
Abstract Title	Beyond the Numbers: Using Qualitative Tools to Supplement Outbreaknet Enhanced Performance Metrics

Abstract

BACKGROUND: Foodborne diseases (FBD) cause illness in approximately 1 in 6 Americans annually, resulting in approximately 128,000 hospitalizations and 3,000 deaths. Limited resources impact the ability of public health to identify, respond to, and control FBD outbreaks. CDC uses a tiered approach to improve FBD surveillance and outbreak response. The middle tier, OutbreakNet Enhanced (OBNE), began in 2015 and funds are used to build capacity to support improved enteric disease investigation processes; including interviewing all *Listeria* and Shiga toxin-producing *E. coli* (STEC) case-patients, all enteric case-patients with whole genome sequencing (WGS) and antimicrobial testing results, and as many *Salmonella* case-patients as possible.

METHODS: OBNE sites report 12 collaboratively developed performance metrics annually. Metrics focus on quantitative process evaluation and record timeliness and completeness of enteric disease surveillance and response activities. Aggregate summary statistics were calculated for the first year of program metrics (January 1, 2016 – December 31, 2016). Additionally, CDC program staff incorporate program management tools, designed to support qualitative evaluation of the program, into OBNE's structure. Examples of program management tools include site visits, quarterly individual site one-on-one calls, and monthly program-wide conference calls.

RESULTS: The 18 OBNE sites reported a total of 29,803 (85 – 7,010 per site) cases of *Salmonella*, STEC, and *Listeria* in 2016. Sites attempted to interview over 90% of cases and the average time between case identification and first interview attempt was 3.3 days. It took sites an average of 3.2 days to complete pulsed-field gel electrophoresis (PFGE) subtyping and an average of 13.9 days to upload WGS data to a central database. Qualitative data from 29 one-on-one calls and 7 site visits provided additional context about the metrics. These data showed interviewing all case-patients in a timely manner was more feasible in some sites, depending on case burden. To address this, many sites established a student interview team or hired additional staff to improve completeness and timeliness of interviews. Additionally, qualitative information showed that sites maintained timeliness of completing PFGE while in the process of training staff and building capacity for WGS.

CONCLUSIONS: OBNE's qualitative program management tools provide important context to quantitative metrics data. Qualitative information reveals the barriers and successful practices sites experience as they work to improve the timeliness and completeness of their enteric disease program activities. Moving forward, qualitative data can be used to understand changes in the metric data over time, based on investigation processes improvements.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Epi / Lab Capacity (ELC); Capacity / Capacity Building
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9596

Abstract Type Quick

Abstract Title Building Enteric Disease (Food- and Waterborne) Surveillance and Response Capacity in States

Abstract

BACKGROUND: During the past 4 years, CDC funding to build state foodborne illness and outbreak surveillance and response capacity from multiple sources has doubled to ~\$45 million a year. Despite these increases, there continue to be major gaps in states' ability to respond to enteric disease issues in part because of cutbacks in funding at the state level that have led to a loss of >50,000 state and local staff since 2008.

METHODS: This presentation summarizes the current CDC funding to states for food and waterborne illness surveillance and outbreak response, the corresponding growth in associated programs and activities, remaining challenges and proposed changes in program integration.

RESULTS: Due to increased funding for food safety from sources such as antimicrobial resistance (~\$13 M), Food Safety (~\$10 M) and Advanced Molecular Detection (~\$1 M), CDC has been able to supplement food safety funding to states via a number of programs. These include EIP FoodNet; ELC including NARMS, PulseNet, OutbreakNet, FoodCORE, Integrated Food Safety Centers of Excellence, CaliciNet, NoroSTAT; EHS-Net; Prevent Block; Prevention Public Health Fund; Public Health Preparedness and affiliated partner support (e.g. CSTE, APHL, ASTHO, NACCHO, NEHA, etc.). Total funding provided by CDC per state now averages ~\$820,000 (range \$78,000 - \$4.0 million) with 12 states receiving >\$1 million. Growth in existing programs like FoodCORE, CaliciNet and NoroSTAT, creation of new programs like the Integrated Food Safety Centers of Excellence and OutbreakNet Enhanced, and expansion of laboratory genomic (WGS) and antimicrobial resistance testing have helped improve reporting and outbreak identification. However, significant gaps remain and 17 states are without funding to cover Outbreak enhanced activities. Federal support for waterborne illness surveillance is minimal.

CONCLUSIONS: Despite improvements in state capacity and an increase in programs to provide assistance (e.g. CoEs, OutbreakNet Enhanced), gaps in funding levels and in program performance measures remain. In addition, as the level of funding to states for food safety has reached a critical mass, it has become increasingly important to consider ways to provide better integration and coordination as is done by larger more established programs like Immunization and STD. The upcoming 5-year ELC grant cycle provides a further opportunity to help accomplish this. CDC is developing a roadmap to better prevent, detect, investigate and control enteric diseases, but is requesting state and local input to make it a relevant endeavor.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Capacity / Capacity Building; Enteric Infectious Diseases; Epi / Lab Capacity (ELC)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9914

Abstract Type Quick

Abstract Title Community Incidence of Acute Gastrointestinal Illness Associated with Viruses in Groundwater Drinking Water Sources

Abstract

BACKGROUND: Waterborne viral illness outbreaks have been associated with groundwater sources. However, it is unknown whether these viral contaminants are responsible for a significant proportion of sporadic illnesses, or if they are responsible for outbreaks with no identified transmission route. Previous studies to examine the occurrence of viruses in drinking water in Minnesota have been limited. The Minnesota Department of Health conducted a study to evaluate the association between the presence of viruses in groundwater drinking water sources and acute gastrointestinal illness (AGI) in the communities served by these water sources.

METHODS: Six non-transient community water supplies were recruited to participate in a 1-year prospective double-cohort study during May 2015-April 2016: three that disinfect their water and three that do not. Weekly drinking water source samples from each community were collected prior to disinfection and tested for norovirus, adenovirus, enterovirus, rotavirus, Hepatitis A virus, pepper mild mottle virus, and human polyomavirus via PCR. Randomly selected residents from study communities were recruited to complete weekly health surveys for 1 year via phone, mail, or online. Due to limited enrollment initially, a second group of participants was recruited for the final 6 months. Data were aggregated at the household level and analyzed using a generalized estimating equations model.

RESULTS: Of 306 drinking water source samples collected, 33 (10.8%) tested positive for a virus. Nine (2.9%) tested positive for a virus that could cause AGI in people; all concentrations were ≤ 5 gene copies L^{-1} . 351 people from 181 households enrolled in the study, and 96% completed the study. After controlling for potential confounders (community type, household size, gender, age composition, home water treatment, and month of collection), during the weeks viruses were detected in the drinking water source, higher rates of AGI were reported; however, this was not statistically significant (adjusted incidence rate ratio [aIRR]=1.30; 95% confidence interval [CI]=0.64-2.65). People who had a water filter at home reported higher rates of illness (aIRR=1.48; 95% CI=1.06-2.06).

CONCLUSIONS: Finding low levels of viruses does not necessarily mean that people consuming water from these systems would become ill, but it does indicate that a potential pathway for drinking water contamination exists. Further study is needed to better understand how the contamination is occurring and what can be done to mitigate it. Additionally, home water filters were associated with illness; these units need to be installed and maintained according to manufacturers' recommendations.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Waterborne Disease; Enteric Infectious Diseases; Water

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9521

Abstract Type Quick

Abstract Title Cryptosporidiosis in New York City, 2000-2017

Abstract

BACKGROUND: Cryptosporidiosis is a gastrointestinal illness caused by the protozoan parasite *Cryptosporidium*, and is the leading cause of waterborne outbreaks in the United States. We examined cryptosporidiosis surveillance data to describe demographic and socioeconomic characteristics of patients, and trends in incidence and diagnostic testing in New York City (NYC) over a 17-year-period.

METHODS: All laboratory-confirmed and probable cases of cryptosporidiosis reported to the NYC Department of Health and Mental Hygiene (DOHMH) are investigated using a standardized questionnaire detailing clinical, demographic and risk factor information including travel and high-risk sexual activity. Using 2000–2016 data, we calculated summary statistics and age-adjusted rates by age group, sex, borough, race/ethnicity, census tract level neighborhood poverty and immune status. The number and proportion of cases diagnosed by multiplex culture-independent diagnostic testing (M-CIDT) and the proportion of these that were also positive by microscopy or antigen testing at the New York State Department of Health Wadsworth Center Laboratory (NYSDOH-WC) were calculated.

RESULTS: During 2000–2016 there were 2,127 confirmed and probable cases of cryptosporidiosis reported to DOHMH. During this period, the annual age-adjusted incidence of cryptosporidiosis declined steadily from 2000 (2.1 per 100,000) to 2014 (1.2 per 100,000), and increased starting in 2015 to 2.2 per 100,000 in 2016. Among immunocompetent individuals the age-adjusted incidence declined from 0.99 per 100,000 in 2000 to 0.60 per 100,000 in 2014, and then rose to 1.5 per 100,000 in 2016. Among persons living with HIV/AIDS (PLWHA), age-adjusted incidence declined throughout the study period, from 1.13 per 100,000 in 2000 to 0.59 per 100,000 in 2016. Males aged 20–59 consistently accounted for the majority (55%) of reported cases. A total of 21% of cases were diagnosed by M-CIDT in 2015 and 34% in 2016. Of all specimens originally diagnosed by M-CIDT and sent to NYSDOH-WC, 84% and 75% were positive by microscopy or antigen testing in 2015 and 2016, respectively.

CONCLUSIONS: Cryptosporidiosis incidence declined in both immunocompetent individuals and PLWHA in NYC until 2015, when we observed an increase in diagnoses among immunocompetent individuals likely because of increased case ascertainment by M-CIDT. Disproportionately high rates observed among males aged 20-59 likely reflect an increased burden in men who have sex with men (MSM). Understanding how M-CIDT utilization impacts cryptosporidiosis surveillance data will be critical as its use increases. Furthermore, public health efforts including safe-sex education should be focused on high-risk groups such as MSM.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Enteric Infectious Diseases; Surveillance; Local Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9477

Abstract Type Quick

Abstract Title Emergence of Multi-Drug Resistant Salmonella Serotype I 4,[5],12:i:- in the United States, 2006–2015

Abstract

BACKGROUND: In the United States, non-typhoidal *Salmonella* (NTS) causes an estimated 1.2 million infections annually. Approximately 50 serotypes are responsible for most human infections. *Salmonella enterica* serotype I 4,[5],12:i:- is a monophasic variant of Typhimurium (the second most common serotype) that has been increasing as a cause of human infections in the United States. We reviewed 10 years of national surveillance data to characterize the emergence of I 4,[5],12:i:- infections in the United States and to describe the epidemiology, resistance, and outbreaks due to this serotype.

METHODS: We compared data from 2006–2010 with 2011–2015 from three national surveillance systems: the Laboratory-based Enteric Diseases Surveillance System (LEDS) which includes all isolates reported by public health laboratories; the National Antibiotic Resistance Monitoring System (NARMS) which includes antimicrobial susceptibility testing performed at CDC on 1 in 20 isolates; and the National Outbreak Reporting System (NORS). We compared isolates with serotype I 4,[5],12:i:- to other NTS serotypes.

RESULTS: There were 5,309 cases of I 4,[5],12:i:- reported to LEDS during 2006–2010 and 10,425 cases during 2011–2015, representing a proportionate increase of total NTS from 2.7% to 4.4% ($P < 0.001$). This absolute increase in the number of I 4,[5],12:i:- cases was driven by an increase in multidrug resistant (MDR) isolates. I 4,[5],12:i:- isolates in NARMS with resistance patterns that included ampicillin, streptomycin, sulfisoxazole, and tetracycline (ASSuT) were the most frequent, and increased from 6.8% of I 4,[5],12:i:- isolates in 2006–2010 to 42.9% in 2011–2015 ($P < 0.001$), whereas the proportion of I 4,[5],12:i:- isolates without this pattern declined. Outbreaks in NORS caused by I 4,[5],12:i:- increased from 13 (2.2% of all NTS outbreaks with known serotype) in 2006–2010 to 42 (6.2%) in 2011–2015 ($P < 0.001$). Of the 55 outbreaks caused by I 4,[5],12:i:-, 8 (14.5%) were linked to pork or pig exposure compared with only 3.2% of outbreaks caused by other serotypes ($P < 0.001$).

CONCLUSIONS: During 2006–2015, serotype I 4,[5],12:i:- caused an increasing proportion of *Salmonella* infections and outbreaks in the United States. This was driven by the emergence of MDR isolates with the pattern ASSuT. The stronger association with pork and pig exposures compared with other *Salmonella* serotypes is consistent with the hypotheses that pigs are an important source of this serotype in the United States. Efforts to improve antimicrobial stewardship in the pork industry and to prevent transmission from pigs or pork products may avert morbidity from these *Salmonella* infections.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Emerging Infections; Enteric Infectious Diseases; Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9888
Abstract Type	Quick
Abstract Title	Enhancing Enteric Disease Investigation and Outbreak Response for Local Health Departments in New York State

Abstract

BACKGROUND: In March 2016, the New York State Department of Health conducted a needs assessment for local health departments (LHD) to determine training needs and capacity for enteric disease surveillance and outbreak response. Results of the needs assessment were used to create an agenda for two-day trainings targeted at LHD staff in spring 2017. The trainings were evaluated for effectiveness.

METHODS: The needs assessment was split into two sections, the first assessing outbreak response utilizing the ‘Selecting Focus Areas Worksheet’ from the Council to Improve Foodborne Outbreak Response (CIFOR) Toolkit. The second referred to specific training topics and type of training considered most useful for regional, district, and LHD staff. The needs assessment was entered in SurveyMonkey and a link sent via email to communicable disease and environmental health staff at local, regional, and district levels. Responses were analyzed and collated on a regional and state level.

RESULTS: There were 136 respondents, with the majority answering from LHD staff (79%). Respondents identified as being in Environmental Health (33.1%), Epidemiology (39.9%), Other (22.3%) or Laboratory (4.7%) fields. Statewide, activities related to CIFOR Focus Areas 1 (Relationships with relevant agencies and organizations), 2 (Necessary resources), and 3 (Communication) were identified as needing improvement. Topic areas respondents identified as a need for additional training included legal issues in surveillance (83.0%), debriefing (80.4%), writing outbreak reports/completing forms (80.4%), availability of overall resources (77.7%) and National Environmental Assessment Reporting System (76.8%). Training needs varied slightly across regions. Training methods identified by respondents as being the most effective were one-two day in-person lecture based (69%), one-two day hands-on workshop (62%), and one-day in-person tabletop exercise (50%).

CONCLUSIONS: Based on the results of the needs assessment, eight two-day trainings were conducted throughout the state with staff from 56 of the 57 LHDs. The training included Focus Areas 1 and 2 of the CIFOR Toolkit on day one and a variety of training topics identified as highest need on day two. The trainings were well received, with overall average ratings of 3.8 out of 5.0 for the CIFOR toolkit discussion and 4.2 out of 5.0 for the variety of training topics. An informal review of participants at the training showed an interest in a one-day tabletop exercise to practice the skills learned in the training. Four one-day in-person tabletop exercises are planned for February-March, 2018.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Capacity / Capacity Building; Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9725

Abstract Type Quick

Abstract Title Evaluating Mail-Based Campylobacter Surveillance in New York City, 2017

Abstract

BACKGROUND: In New York City (NYC), >1,600 campylobacteriosis cases are reported each year. The NYC Department of Health and Mental Hygiene (DOHMH) contacts all patients reported to work in high-risk transmission settings and a random sample of six cases each week by telephone. We piloted mail-based campylobacteriosis surveillance to enhance existing telephone-based surveillance.

METHODS: Between June 19 and December 18, 2017, we randomly selected 20 campylobacteriosis patients weekly for mail-based surveillance. Patients eligible for selection were NYC residents with infections reported in the past week. Patients were excluded from selection if they were associated with known outbreaks, co-infected with *Salmonella*, or already assigned for telephone interview. Selected patients received an introductory letter explaining the questionnaire, with information directing non-English speakers and those wishing to complete a phone interview to a DOHMH phone number; a questionnaire with clinical, demographic, and exposure questions based on patient age (adult, child, infant); a campylobacteriosis factsheet; and a pre-paid envelope for return to DOHMH. We assessed mail-based surveillance response rates, timeliness and completeness of returned questionnaires, and whether questionnaires aided in cluster investigations or triggered public health action. We used multivariable logistic regression to assess whether age, sex, county of residence, and neighborhood-based poverty were associated with mailed questionnaire response.

RESULTS: Questionnaires were mailed to 538 patients, 16 of whom were excluded from analyses because of reporting errors (one), undeliverable return to DOHMH (seven), or were interviewed for other investigations (eight). Of the remaining 522 patients, 120 (23%) completed questionnaires, 11 of whom called DOHMH. Median time from questionnaire send-out to receipt was 16 days (range: 3–50 days), and 96% of questionnaires had ≥50% of parent questions complete; 55% had ≥90% of parent questions complete. Information from returned questionnaires aided in investigations of nine previously unknown outbreaks or clusters, and one Hazard Analysis and Critical Control Point food preparation review was performed. Questionnaire response was associated with living in a census tract with 0% to <10% of the population living below the federal poverty level (FPL) (odds ratio [OR]: 2.01, 95% confidence interval [CI]: 1.02, 3.98) or 10% to <20% living below the FPL (OR: 2.15, 95% CI: 1.11, 4.17).

CONCLUSIONS: While response rates to mail-based questionnaires were low, patients who replied did so in a timely manner with high questionnaire completeness. The inability to know selected patients' primary language or reading level were limitations. DOHMH should work to improve response rates among New Yorkers in lower-income neighborhoods.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9426

Abstract Type Quick

Abstract Title Foodcore Centers Demonstrate Improvements in Isolate Testing during a Shift in Laboratory Techniques for Enteric Disease Surveillance

Abstract

BACKGROUND: In 2009, CDC started the Foodborne Diseases Centers for Outbreak Response Enhancement (FoodCORE) program to improve the completeness and timeliness of laboratory, epidemiology, and environmental health activities for foodborne disease surveillance and outbreak response. To demonstrate the impact of their resources, FoodCORE centers use performance metrics to evaluate the burden, timeliness, and completeness of foodborne disease outbreak surveillance and response activities. Laboratory subtyping of *Salmonella*, Shiga toxin-producing *Escherichia coli* (STEC), and *Listeria* (SSL) is one critical component to detecting and solving outbreaks. Currently, FoodCORE centers are moving towards using whole genome sequencing (WGS) because it is more precise and provides more detailed information than traditional subtyping methods such as pulsed-field gel electrophoresis (PFGE). However, PFGE is being maintained while the transition to WGS occurs.

METHODS: FoodCORE centers submit isolate/specimen-based metrics biannually to evaluate 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 capture timeliness and completeness of WGS, in addition to PFGE. The expanded metrics went into effect in Year 7 (Y7, 1/1/2017 – 12/31/2017). Current FoodCORE centers are Colorado, Connecticut, Minnesota, New York City, Ohio, Oregon, South Carolina, Tennessee, Utah, and Wisconsin.

RESULTS: From the beginning of Y6 through July 2017, centers reported a total number of 14,471 primary SSL isolates/isolate-yielding specimens and maintained the percentage of SSL isolates with complete PFGE information at 94.6%. WGS completeness varied by pathogen. During Y6, WGS was performed for 40.2% of *Salmonella*, 64.2% of STEC, and 97.7% of *Listeria* isolates. Among all SSL isolates, the proportion with WGS information increased from 45.2% in Y6 to 86.2% during 1/1/2017 – 7/31/2017. Additionally, from the beginning of Y6 through July 2017, the average time from completion of PFGE subtyping for SSL to upload to a national database remained constant at 2.4 days; the average time from sequencing to upload to a national database decreased from 12.0 days to 9.0 days. During this transition period, FoodCORE centers reported needing to train microbiologists, order new supplies, and upgrade systems for data analysis to perform PFGE and WGS simultaneously.

CONCLUSIONS: Despite numerous challenges during their transition from PFGE to WGS, FoodCORE centers continue to maintain timeliness and completeness of PFGE while demonstrating improvements in enteric disease outbreak surveillance and response activities using WGS, leading to faster, better, and more complete investigations to help stop the spread of enteric diseases.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Capacity / Capacity Building; Foodborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9816

Abstract Type Quick

Abstract Title Gastrointestinal Illness Outbreak at Multiple Outdoor Festivals — Pennsylvania, 2017

Abstract

BACKGROUND: On June 13, 2017, the Pennsylvania Department of Health was notified of acute gastrointestinal illness (AGI) among attendees of a festival held at Venue A. Further cases were identified from two additional Venue A festivals held May 31–June 18.

Another festival was scheduled to occur July 26–30. We investigated to assess transmission risk factors and prevent additional illnesses.

METHODS: We defined a case as vomiting or diarrhea in a person linked to a Venue A event after May 31, 2017. Social media pages for Venue A and affected events were used to solicit illness reports. Stool and vomitus specimens were collected and tested for enteric pathogens. We conducted an environmental assessment during July 18–19 at Venue A and tested well, creek, and ground water for fecal microbes. We provided recommendations before the July festival and conducted onsite active surveillance.

RESULTS: We received 179 self-reports of AGI associated with 3 festivals during June. Norovirus was detected in 7/8 clinical specimens from event attendees. Creek and well water samples also contained norovirus and other fecal microbes. A septic leach field was identified as the likely source of well contamination. Venue A installed a new well located farther from the leach field, increased portable toilet and handwashing station availability, and promoted proper hand hygiene during the July festival. Active surveillance during this festival identified 5 ill persons; one submitted a stool specimen, which tested negative for norovirus and other enteric pathogens.

CONCLUSIONS: An AGI outbreak affected 3 festivals at a venue where norovirus was detected in the primary drinking water source. Interventions to ensure access to clean water, proper hand hygiene, and adequate sanitation were implemented for the next large event. No outbreak occurred during this event, highlighting the potential of these interventions to prevent AGI.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Waterborne Disease; Enteric Infectious Diseases; Environmental Exposures

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9238

Abstract Type Quick

Abstract Title Impact of the Epidemiology and Laboratory Capacity for Infectious Disease Cooperative Agreement on Reporting of Historical Waterborne Disease Outbreaks

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) has conducted national surveillance for waterborne disease outbreaks since 1971 in partnership with the Council of State and Territorial Epidemiologists and the United States Environmental Protection Agency. Since 2013, this work has been supported in part by state funding through the Epidemiology and Laboratory Capacity for Infectious Disease (ELC) Cooperative Agreement. Since 2014, funded states have been required to review their data sources for previously unreported outbreaks and report them to the National Outbreak Reporting System (NORS). This requirement was based on the findings of an earlier project completed by three states. CDC examined data reported to NORS in 2015 to evaluate the impact of this requirement.

METHODS: ELC grantee applications for Activity Z (capacity for states to detect, investigate, and report waterborne disease outbreaks) from 2014 and 2015 were examined to assign a completion status to the ELC review activity (e.g., completed before 2015, completed in 2015, not yet completed). Previously unreported outbreak reports that were entered into NORS in 2015 were characterized by state, illness onset date, and type of water exposure.

RESULTS: In ELC grant years 2014 and 2015, 19 states received funding for waterborne disease capacity building. In 2015, ten states (53%) reviewed data sources for previously unreported outbreaks; nine states reported 57 previously unreported outbreaks to NORS with illness onset dates from 1971 through 2012. These additional reports represent a 12% increase in the number of outbreaks for these nine states during 1971-2012 (n=477). These outbreaks resulted in an estimated 2,086 cases of illness, 41 hospitalizations, and 2 deaths. Implicated water exposures were categorized as treated (n=18) or untreated (n=8) recreational water, drinking water (n=21), environmental or unknown exposures to water (n=8), or missing (n=2). Of the remaining nine ELC-funded states, 22% (n=2) completed the review before 2015, 44% (n=4) listed the review as not yet completed, and 33% (n=3) did not report information regarding the activity.

CONCLUSIONS: Funding through ELC supports capacity for states to detect, investigate, and report waterborne disease outbreaks. This review of previously unreported outbreaks showed that, with funded support, capacity can be built that enables reporting of waterborne disease outbreaks that were not previously reported, potentially due to a lack of capacity. These data provide additional information to inform our overall understanding of the epidemiology of waterborne disease outbreaks in the United States to guide prevention and control activities.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Epi / Lab Capacity (ELC); Outbreaks; Waterborne Disease

**Consider for
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Submission Type Breakout/Quick/Lightning/Poster

ID 9544

Abstract Type Quick

Abstract Title Improving Food History Questions for Reported Cases of Campylobacteriosis and Salmonellosis in Massachusetts

Abstract

BACKGROUND: Campylobacteriosis and salmonellosis represent the largest numbers of enteric disease cases in Massachusetts, with an average of 2628 confirmed and probable cases reported annually from 2012-2016 (1467 and 1201, respectively). Among those with a completed case report form (CRF) over one year of age with no reported international travel, 77% (range 75%-79% annually) had no suspect food item identified.

METHODS: The Massachusetts Department of Public Health (MDPH) uses one generic case report form for investigating reported cases of enteric disease. Case investigation is performed using the state's web-based disease surveillance and case management system, Massachusetts Virtual Epidemiologic Network (MAVEN). The CRF collects limited food history information through the questions "Suspect food or drink" and "Did the case consume any high-risk animal products during incubation period?". Campylobacteriosis and salmonellosis CRFs from five CDC Integrated Food Safety Centers of Excellence were reviewed. A list of 31 food exposures was added to MAVEN using a virtual question package (QP), and piloted among all campylobacteriosis and salmonellosis cases reported February-March 2017. Pre- and post-pilot surveys were administered to local boards of health (LBOHs) using SurveyMonkey. Survey and MAVEN data were analyzed using Microsoft Excel and SAS 9.3.

RESULTS: A total of 136 campylobacteriosis and 109 salmonellosis cases were included in the pilot. Among combined cases with a completed CRF over one year of age with no international travel, 56% identified one or more high-risk food exposures using the QP, as compared to 23% during the same time period in 2016. The median time interviewing a case with the additional QP was 20 minutes (range 5-60), compared to 21 (range 5-120) with the generic enteric CRF. Seventy-seven percent of LBOHs found the pilot QP did not impose a significant burden to their workload, and 73% indicated assistance from a centralized interview team at MDPH would ease the burden of additional food history questions.

CONCLUSIONS: Improved food history information collected upon initial interview to evaluate illness attribution would allow for public health intervention and reduce the need for re-interview if the case is later included in a laboratory-defined cluster. The burden of adding food history questions on LBOHs who conduct case interviews should be considered. The piloted QP improved the identification of suspect food items for campylobacteriosis and salmonellosis cases and did not represent a significant burden to LBOHs conducting case interviews. A centralized interview team would ensure the success of adding the QP to campylobacteriosis and salmonellosis CRFs.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Data Collection; Enteric Infectious Diseases; Foodborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9537

Abstract Type Quick

Abstract Title Norovirus Outbreaks in Schools and Child Care Centers, United States, 2009–2016

Abstract

BACKGROUND: Over 55 million children attend public and private schools and an additional 6 million children attend child care centers (CCC) annually in the United States. Children in these settings are at increased risk of norovirus infection due to frequent, direct contact, shared items and facilities, and common food exposures. We analyzed epidemiologic and laboratory data from norovirus outbreaks in schools and CCC to guide prevention and control strategies.

METHODS: We extracted data from the National Outbreak Reporting System (NORS) on outbreaks resulting from any transmission mode that occurred in schools or CCC from January 2009 through December 2016 with norovirus reported as the sole suspected or confirmed etiology. NORS reports were supplemented with genotype data from matched CaliciNet reports. Outbreak size and duration were analyzed by Mann-Whitney U-test and health outcome rates by Fischer’s exact test.

RESULTS: A total of 984 norovirus outbreaks in schools and 338 in CCC that occurred during 2009–2016 were reported to NORS by 43 states and jurisdictions, resulting in 66,333 illnesses. Of these, 310 (32%) outbreaks in schools and 124 (37%) outbreaks in CCC were laboratory confirmed. Genotype information was reported for 186 (19%) school outbreaks, among which GII.2 (45, 24%), GII.6 (24, 13%), and GI.3 (20, 11%) were most common. Comparatively, genotype information for 80 (24%) of the CCC outbreaks was available, of which GII.4 Sydney (17, 21%), GII.2 (11, 14%), and GII.6 (10, 13%) were most common. The mode of transmission for most (1179, 89%) outbreaks was person-to-person. The median outbreak duration in CCC outbreaks (13 days; range: 1–402) was significantly longer than in schools (8 days; range: 1–106, $p<0.01$). Conversely, the median number of cases in school outbreaks (36 cases; range: 2–2,500) was significantly higher than in CCC outbreaks (17 cases; range: 2–93, $p<0.01$). Although CCC and school outbreaks resulted in similar rates of emergency department visits (1.2 vs 1.1 per 100 case-patients, $p=0.65$), CCC outbreaks resulted in significantly higher rates of outpatient visits (6.0 vs 4.3 per 100 case-patients, $p<0.01$) and hospitalizations (5.8 vs 1.3 per 1,000 case-patients, $p<0.01$). One death was reported in a school outbreak and none in CCC.

CONCLUSIONS: Norovirus outbreaks in schools and CCC represent a substantial public health burden. Prevention and control measures, such as isolation of ill cases, appropriate handwashing, and environmental disinfection, could decrease the frequency and spread of norovirus in these settings.

Committee Infectious Disease

Topic Enteric Diseases

Keywords NORS (National Outbreak Reporting System); School Health; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10274

Abstract Type Quick

Abstract Title Ongoing Outbreak of *Salmonella* Saintpaul Infections Linked to Raw Milk in Utah, 2016-2017

Abstract

BACKGROUND: In March 2016, the Utah Department of Health (UDOH) identified a cluster of four cases of *Salmonella* Saintpaul with indistinguishable pulsed-field gel electrophoresis (PFGE) patterns. On average, eight cases of *Salmonella* Saintpaul are reported each year in Utah. Over the next year and a half, an additional 31 outbreak cases were identified. Most of the cases were geographically clustered around the Wasatch Front.

METHODS: We interviewed the case-patients and found that of the 32 for whom raw milk exposure was known, 21 (60%) reported drinking raw milk during the week before illness onset. Of these, 19 (90%) reported that the raw milk was purchased from Dairy A, which is located in the Wasatch Front. UDOH worked closely with the Utah Department of Agriculture and Food (UDAF) to ensure that Dairy A complied with Utah's raw milk laws. The dairy was inspected and their milk was tested on multiple occasions. PFGE testing identified the outbreak strain of *Salmonella* Saintpaul in raw milk collected from the dairy on several occasions.

RESULTS: Between March 2016 and December 2017, a total of 35 Utah residents were infected with *Salmonella* Saintpaul. The median age of case-patients was 29 years (range 1-87); 14% (5/35) were under 18 years of age; 66% (23/35) were male; and 17% (6/35) were hospitalized. No deaths were reported. During the outbreak period, Dairy A's milk was tested by UDAF, Utah Public Health Laboratory (UPHL), and private laboratories. Raw milk from the dairy was PFGE matched to the case-patients. Based on laboratory evidence, Dairy A's license was suspended on multiple occasions.

CONCLUSIONS: Epidemiologic and laboratory evidence implicated raw milk from Dairy A as the source of this outbreak. Raw milk is not safe for consumption. Control measures undertaken by the dairy to prevent contamination of raw milk were unsuccessful, resulting in repeated illnesses among raw milk drinkers for over 18 months. Raw milk outbreaks illustrate how collaboration between agencies is key in trying to reduce the public health threat.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Collaboration; Foodborne Disease; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9253

Abstract Type Quick

Abstract Title Rise in Polymicrobial Detections Linked to Use of Culture Independent Diagnostic Tests, Foodborne Diseases Active Surveillance Network (FoodNet) — 2011–2016

Abstract

BACKGROUND: FoodNet conducts active laboratory-based surveillance for nine enteric pathogens in 10 FoodNet sites. In 2012, FoodNet began collecting reports of positive culture-independent diagnostic tests (CIDTs). Use of CIDTs to diagnose enteric infections is increasing, including highly sensitive multiplex polymerase chain reaction-based syndrome panels that can simultaneously detect multiple pathogens from a single specimen. Detection of multiple pathogens in search of the cause of infection complicate case classification, cluster detection, and treatment decisions. We describe polymicrobial detections (PD) and examine changes in their frequency.

METHODS: We analyzed data from FoodNet sites to describe PDs among cases of *Campylobacter*, Shiga toxin-producing *Escherichia coli*, *Listeria*, *Salmonella*, *Shigella*, *Vibrio*, *Yersinia*, *Cryptosporidium*, and *Cyclospora* infection. We defined a PD as detection of >1 pathogen, or >1 species or serotype by culture (CX) or CIDT in specimens collected ≤30 days apart during 2011–2016. We define a case as a laboratory confirmed infection; thus, a person with PD is reported as more than one case.

RESULTS: During 2011–2016, we identified 1,203 persons with PD, resulting in 2,430 cases (2% of cases reported to FoodNet). PDs were identified in specimens collected on the same day (0 days) for 957 (80%) persons, within 1–7 days for 121 (10%), and 8–30 days for 125 (10%). Among patients with PDs, 1,060 (88%) had pathogens of two genera detected, 120 (10%) had pathogens of two species or sub-species, and 23 (2%) had ≥3 pathogens, species, or sub-species. *Campylobacter* was the pathogen most commonly detected in PDs, paired most often with *Salmonella* (26%), followed by *Shigella* (15%), Shiga toxin-producing *E. coli* (11%), and *Cryptosporidium* (11%). Among the 1,203 persons with PDs, 729 (61%) were detected by CIDTs, 331 (45 %) were tested using PCR-based tests [123 (17%) syndrome panels, 107 (15%) laboratory-developed PCRs, and 101 (14%) unknown], 305 (42%) antigen-based tests, and 93 (13%) involved multiple types of CIDTs. Average annual incidence rates of PDs increased 83% in 2014–2016 compared with 2011–2013 (0.53 vs. 0.29 per 100,000 persons). The percentage of patients whose PDs were detected only by CIDTs increased from 0% in 2011 to 24% in 2016, and the percentage of patients whose PDs included a CX-confirmed pathogen decreased from 100% to 76%.

CONCLUSIONS: The number of polymicrobial detections has increased dramatically since the introduction of CIDTs. Additional data and recommendations are needed to inform interpretation of surveillance results, make treatment decisions, and guide public health action.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Epidemiology; Foodborne Disease; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9241
Abstract Type	Quick
Abstract Title	Risk Factors for Non-O157 Stec Infection in the United States, 2012-2015 – a Foodborne Diseases Active Surveillance Network (FoodNet) Case-Control Study
Abstract	BACKGROUND: More than 265,000 Shiga toxin-producing <i>E. coli</i> (STEC) infections are estimated to occur in the United States each year, ranging in severity from mild diarrhea to hemolytic uremic syndrome. STEC are categorized by their O antigens into O157 and non-O157. Although risk factors for O157 have been studied, less is known about factors associated with non-O157 STEC. We present findings from a multistate case-control study of sporadic non-O157 STEC infections. METHODS: A case was defined as isolation of non-O157 STEC from an ill person residing within the FoodNet catchment area. Controls were matched to cases by county of residence and age. Matched conditional logistic regression identified significant factors in univariate analysis. For each exposure in multivariate analyses, up to 20 controls were matched to each case based on age, sex, state, and all exposures except the one currently being considered. Mantel-Haenzel odds ratios and 95% confidence intervals (CI) were calculated using the strata derived from this approach. RESULTS: We enrolled 943 cases and 2,439 controls. Median age of case-patients was 19 years; 59% were female, 91% White, and 17% Hispanic. One hundred fifty-four (16%) were hospitalized, 8 (1%) had HUS, and none died. One hundred thirty-nine (15%) reported international travel during the seven days before illness. Risk factor analysis included 804 case-patients with domestically-acquired infections and 2,100 controls. Factors and exposures associated with illness included contact with a person who had a diarrheal illness (OR: 3.5; 95% CI 2.2-5.8), camping (3.5; 1.8-6.6), Hispanic ethnicity (2.6; 1.8-3.8), travel outside state of residence (2.0; 1.3-2.9), taking antacids 4 weeks before illness (1.8; 1.3-2.6), and eating at a sit-down (1.7; 1.3-2.2) or a fast food restaurant (1.7; 1.3-2.4). Water and environmental factors included visiting a farm (30.4; 5.1-181.5), seeing a cow (20.0; 3.7-108), living on a farm (14.8; 3.9-56.1), drinking untreated water (6.1; 2.3-15.7), and swimming or playing in a lake, river, or stream (3.4; 1.9-6.1). Foods associated with illness included raw fish (3.6; 1.8-7.3), cilantro (2.0; 1.4-2.9), and lettuce (1.9; 1.4-2.5); certain foods eaten at restaurants (pink ground beef hamburger [6.2; 2.0-19.3], ground beef hamburger [3.4; 2.0-5.7] and beef [3.0; 1.9-4.4]); and certain foods prepared outside the home (raw spinach [6.1; 2.3-15.7], pork [3.4; 2.0-5.9], chicken [1.9; 1.4-2.5], and peppers [2.9; 1.6-5.4]). CONCLUSIONS: Domestically-acquired non-O157 illnesses were linked to water, environmental, and personal contact exposures as well as to many food vehicles. These findings can help to inform prevention measures.
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Risk Factors; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10244
Abstract Type	Quick
Abstract Title	Salmonellosis Outbreak Associated with Laboratory Exposure, Not Dry Dog Food—North Dakota, 2015-2016

Abstract

BACKGROUND: Dry pet food has been linked to previous outbreaks of human salmonellosis in the United States. In January 2016, the North Dakota Department of Health (NDDoH) was notified that dry dog food from the home of a salmonellosis case tested positive for *Salmonella* at a microbiology laboratory (Laboratory A). A subsequent investigation involved Laboratory A, FDA, CDC, and state public health officials.

METHODS: A case was defined as a laboratory-confirmed infection of *S. Enteritidis* with the outbreak strain (PFGE-*Xba*I-pattern JEGX01.0013) in a North Dakota resident with a diarrheal illness onset date on or after December 19, 2015. Cases were identified via passive surveillance and PulseNet. The initial epidemiologic investigation involved collecting standard information from cases, including illness history and possible exposures. After the cluster was identified by PulseNet, cases were re-interviewed to gather specific information on dry dog food and exposure to a microbiology laboratory. Specimens from dog food and the environment were submitted to the NDDoH Division of Laboratory Services (DLS) for testing. Animal specimens from household pets of cases were submitted to an FDA Veterinary Laboratory Investigation and Response Network (Vet-LIRN) facility for culture, serotyping, PFGE and WGS analysis. The principal investigator at Laboratory A was interviewed. An isolate of the commercially available *S. Enteritidis* strain used at Laboratory A was submitted for PFGE and WGS analysis.

RESULTS: A total of 3 culture-confirmed cases were identified with onset dates from December 19, 2015, to February 3, 2016. Sixty-six percent of cases were female. No hospitalizations and no deaths were reported. Dog food specimens tested positive for *Salmonella* using the Reveal® 2.0 immunoassay, but the NDDoH DLS was unable to culture *Salmonella*. Isolates cultured from fecal specimens of household pets matched the outbreak strain of *Salmonella*. Animal and human isolates from the outbreak matched the *S. Enteritidis* strain used in the microbiology laboratory, and WGS analysis revealed the isolates were closely related (i.e., within 0-3 SNPs). Upon re-interviewing cases, investigators discovered that all cases either worked at Laboratory A or lived in a household with a person who worked at Laboratory A.

CONCLUSIONS: This salmonellosis outbreak initially appeared to be linked to dry dog food, but further investigation revealed it was associated with direct or indirect exposure to a strain of commercially available *S. Enteritidis* used in a microbiology laboratory. This outbreak highlights the importance of biosafety practices in laboratory settings.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Epi / Lab Capacity (ELC); One Health
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10109

Abstract Type Quick

Abstract Title Salmonellosis Outbreak at a Chili and Chowder Cook-Off — Virginia, 2017

Abstract

BACKGROUND: After a chili and chowder cook-off featuring 11 local vendors and attended by ~2,500 persons, the Accomack County Health Department received reports of gastrointestinal illness among event attendees. Clinical stool specimens tested positive for *Salmonella* serotype Javiana. We investigated to determine the outbreak exposure source, identify practices that might have contributed, and provide recommendations to prevent future outbreaks at similar events.

METHODS: We performed a cohort study, recruiting event attendees through press releases and social media posts containing the link to an online survey about cook-off foods consumed and gastrointestinal illness. A case was defined as ≥ 3 episodes of diarrhea in < 24 hours, or unquantified diarrhea and another symptom (either abdominal pain, chills, dehydration, fever, nausea, or vomiting) in an attendee or someone who consumed festival food. In addition to unadjusted relative risks (RRs), Mantel-Haenszel adjusted RRs were calculated to address potential confounding by multiple exposures. Environmental health specialists interviewed food handlers and conducted inspections of restaurants where professional competitors had prepared food. Available food samples and stool samples from asymptomatic food handlers were tested for *Salmonella*.

RESULTS: Of 439 survey responses, 172 met the case definition. Of all exposures, Chowder A had the strongest association with illness (RR: 8.9; 95% CI: 5.7–13.7). When stratified by exposure to Chowder A, all other chili or chowder RRs were < 1.4 . Environmental health inspections and interviews did not identify a specific source of contamination. An uneaten sample of Chowder A tested positive for *Salmonella* serotype Javiana. Frozen clams and food handler samples tested negative.

CONCLUSIONS: Epidemiologic and laboratory analyses provide evidence Chowder A was the most likely outbreak source; however, the original source of *Salmonella* is unknown. Recommendations to prevent future outbreaks included requiring all food to be prepared on-site and ensuring safe temperatures are maintained during food preparation and service.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Foodborne Disease; Epidemiology; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9597

Abstract Type Quick

Abstract Title Shiga Toxin-Producing *Escherichia coli* O157:H7 Outbreak Following the Unintentional Use of Unpasteurized Cider at a Festival — Kansas, 2016

Abstract

BACKGROUND: On October 21, 2016, Kansas Department of Health and Environment (KDHE) was notified of six Shiga toxin-producing *Escherichia coli* (STEC) O157:H7 isolates with indistinguishable pulsed-field gel electrophoresis patterns, five of which were from specimens submitted by attendees of a cider festival. KDHE and Kansas Department of Agriculture (KDA) investigated to identify the outbreak source and prevent additional illness.

METHODS: A press release requested festival attendees self-report illness to KDHE. A case was defined as diarrhea (>2 watery stools per day) lasting >24 hours starting ≥ 1 day after festival attendance. A matched case-control study was conducted; case-patients and well persons who attended the festival together were matched into attendance groups for analysis. Case-patients and control subjects were interviewed about festival exposures. Odds ratios (ORs) and 95% confidence intervals (CIs) were calculated for associations between illness and festival exposures. Investigators visited the cider mill to meet with management and conduct an inspection of the mill. During this visit, the mill's food-handling processes were observed, food safety procedures were reviewed, environmental samples were collected, and recommendations were made to prevent future illness. A follow-up inspection was conducted prior to the 2017 festival.

RESULTS: Fifty-six persons reported illness meeting the case definition; 9 (16%) were hospitalized, 2 (4%) developed hemolytic uremic syndrome, and 7 (13%) had laboratory-confirmed STEC O157:H7 infection. Thirty-eight case-patients and 46 control subjects were included in the analysis. Eating cider doughnuts (OR: 10.3; CI: 1.1–94.8) and drinking cold cider (exact OR: 6.6; CI: 1.2–infinity) were associated with illness. The mill's written policy was to serve only pasteurized cider, and proper pasteurization techniques were documented. However, discussion during the on-site inspection revealed that in high-volume times during the festival, food handlers obtained cider to serve customers and possibly prepare doughnuts directly from a chilled cider storage tank that contained unpasteurized cider. Employees were unaware this was unpasteurized cider. Testing revealed no STEC O157 among environmental samples taken one month after the festival. No cases were found to be associated with the mill's nationally-distributed finished cider products, and no reports of illness were received following the 2017 cider festival.

CONCLUSIONS: The on-site investigation of the mill's processes was critical to identification of unpasteurized cider as the likely infection source despite the intention of the mill to serve only pasteurized cider. Investigators recommended labeling unpasteurized cider tanks and educating employees to prevent future illness and revisited the mill to ensure recommendations were followed.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Food Safety; Foodborne Disease; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9457

Abstract Type Quick

Abstract Title Successive Norovirus Outbreaks at an Event Center — Nebraska, October–November 2017

Abstract

BACKGROUND: Norovirus, an extremely contagious enteric virus, is transmitted through contaminated food or surfaces or person-to-person contact and can be challenging to eradicate from environments. While investigating a norovirus outbreak among wedding attendees, we received reports of similar illnesses after later events at the same event center (Facility A). We expanded our investigation to identify cases, investigate transmission, and provide control recommendations.

METHODS: We worked with Facility A management and event sponsors to disseminate Internet-based questionnaires to employees and event attendees to identify ill persons, capture symptom history, and assess potential exposures. Probable cases were defined as diarrhea (≥ 3 loose stools < 24 hours) or vomiting with nausea or abdominal cramps, in Facility A employees, or in attendees who reported onset 6–72 hours following Facility A-hosted events, during October 27–November 18, 2017; confirmed cases had norovirus RNA detected in stool by real-time reverse transcription-polymerase chain reaction. Using sponsor-estimated number of attendees, we calculated estimated attack rates (AR) per event. We also provided decontamination strategies and recommended excluding ill food handlers.

RESULTS: In total, 18/25 (72%) employees and 324/1,383 (23.4%) attendees from 9/10 events completed questionnaires. We identified 159 cases, including 3 confirmed as norovirus genogroup II. Estimated ARs for the first 6 events ranged from 7% to 35% per event (median: 18.5%). After these events, Facility A attempted decontamination as recommended by public health officials but failed to exclude ill food handlers. Illness transmission continued, with subsequent ARs of 4% (6/150 attendees) and 15% (53/360 attendees). After Facility A contracted professional cleaning services and agreed to exclude ill food handlers, the last event's estimated AR was 0.9% (3/350 attendees).

CONCLUSIONS: Partial adherence to public health recommendations likely contributed to continued norovirus transmission at Facility A. Mitigation efforts should focus on comprehensive prevention strategies including extensive environmental decontamination and strict exclusion of ill food handlers.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Outbreaks; Foodborne Disease; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10121

Abstract Type Quick

Abstract Title Unsolved Cluster of *Salmonella* Cubana – Kansas, 2016-2017

Abstract

BACKGROUND: On September 23, 2016, Kansas Department of Health and Environment identified two cases of *Salmonella* Cubana among residents of one county. An outbreak investigation was immediately initiated. In both cases, the ill persons had urinary tract infections (UTI) and reported no diarrhea. Limited information exists regarding the incubation period for UTIs caused by *Salmonella* ; however literature indicates it may be longer than for gastrointestinal salmonellosis.

METHODS: A case was defined as *Salmonella* Cubana in a Kansas resident between August 25, 2016 and July 6, 2017. Ill persons were interviewed using a standard hypothesis-generating questionnaire. Early interviews identified that ill persons lived in or traveled to the county and patronized several restaurants therein. An outbreak-specific questionnaire was developed which focused on county-specific exposures and locally-distributed items; the exposure period was expanded to two weeks to account for the predominance of UTIs. Interviews were reviewed for commonalities, and case-case analysis compared outbreak cases to sporadic salmonellosis cases. Kansas Department of Agriculture (KDA) visited restaurants patronized by ill persons, particularly those patronized by travelers to the county, to assess for ill employees and common food sources.

RESULTS: Thirteen cases were identified. Twelve ill persons resided in or visited the same county; one person was lost to follow-up but resided in a neighboring county. The median age of ill persons was 53 years; 85% were female. *Salmonella* was cultured from urine in ten (77%) cases, from stool in two cases, and from a wound in one case. Three (23%) ill persons reported diarrhea. Neither review of questionnaires nor case-case analysis identified a common locally-distributed product among ill persons. Fast food and barbeque-style restaurants were significant in case-case analysis, but no one restaurant was patronized by more than four ill persons. KDA did not identify any ill employees or common locally-distributed products among food establishments.

CONCLUSIONS: Despite interviewing ill persons with hypothesis-generating and outbreak-specific questionnaires and conducting case-case analysis, the source of this protracted salmonellosis outbreak was undetermined. Geographic clustering of cases indicated a local source, most likely associated with a restaurant, but no common locally-distributed product was identified among ill persons or food establishments they patronized, and no restaurant was patronized by more than four ill persons. The fourteen-day exposure period assessed in the outbreak-specific questionnaire may have been insufficient to identify the exposure of interest; the exposure period may need to be further expanded to identify the source of salmonellosis outbreaks in which UTIs predominate.

Committee Infectious Disease

Topic Enteric Diseases

Keywords Epidemiology; Outbreaks; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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State Public Health Agency

Submission Type	Roundtable
ID	9374
Abstract Type	Roundtable
Abstract Title	Cifor Update: Third Edition of the Cifor Guidelines for Foodborne Outbreak Response and Other New Cifor Products

Abstract

Key Objectives:

-Discuss the development and new content of the expanded Third Edition of the *CIFOR Guidelines* -Obtain feedback from CSTE conference attendees on other new CIFOR products.

Brief Summary:

The Council to Improve Foodborne Outbreak Response (CIFOR) is a multidisciplinary collaboration of eight diverse national associations and three federal agencies whose goal is to improve epidemiologic, laboratory and environmental health methods at the local, state, and federal levels to detect, investigate, control, and prevent foodborne disease. CSTE is co-chair of CIFOR. The Second Edition of the *CIFOR Guidelines* is 255 pages in length and covers fundamental concepts of public health surveillance and foodborne disease, planning and preparation, foodborne disease surveillance and outbreak detection, cluster and outbreak investigation, control measures, multijurisdictional outbreaks, performance indicators, and legal issues. CIFOR has begun production of the Third Edition of the *Guidelines* that will include major modifications and additions including culture independent diagnostic testing, whole genome sequencing, and case-case comparisons. The Roundtable will provide an opportunity for conference participants to discuss the many important Guidelines changes with CSTE members who are engaged in the update process. Several other new CIFOR products will be presented and discussed during the Roundtable.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10171
Abstract Type	Roundtable
Abstract Title	Democratizing Access to Whole Genome Sequence Data: Using Sequence-Based “Allele Codes” to Give Epidemiologists New Tools to Investigate Listeriosis Clusters
Abstract	Key Objectives: • Gain a conceptual understanding of how “allele codes” represent information on genetic relatedness of <i>Listeria monocytogenes</i> • Learn about different ways that “allele codes” can be used in a foodborne outbreak investigation • Understand what resources are available to access and query “allele codes” from PulseNet Brief Summary: Bacterial subtyping has been the cornerstone of detecting and investigating foodborne outbreaks linked to commercially distributed products. Over the last 4 years, whole genome sequencing (WGS) of <i>Listeria monocytogenes</i> (<i>Lm</i>) has ushered in a transformation in how these outbreaks are detected, defined, and solved. In January 2018, the traditional <i>Lm</i> subtyping method in PulseNet, pulsed-field gel electrophoresis (PFGE), will be phased out in favor of WGS-based methods. Although this transition will lead to more effective outbreak investigations, epidemiologists have historically relied on PFGE pattern names to identify bacteria that may share a common source and to have a common vocabulary to communicate with investigation partners about isolates that are part of outbreaks. To address this challenge, CDC has developed a WGS-based analogy to the PFGE pattern name, called an “allele code.” This code, consisting of five numbers and based on core genome multilocus sequence typing, allows for easy recognition and communication of isolate relatedness. Isolates that only have the first digit in common may be very different (e.g. > 70 allele differences) and unlikely to share a common source, while isolates with the first four digits in common are closely related genetically and likely to be part of an outbreak. By making these allele codes available to epidemiologists in local, state, and federal agencies through SEDRIC, a secure, web-based platform that already provides access to PulseNet data, queries can be easily performed to identify genetically related isolates without the need for computationally-intensive bioinformatics methods.
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Genomics; Foodborne Disease; Outbreaks
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9709
Abstract Type	Roundtable
Abstract Title	Enteric Disease Exclusion Guidelines for Food Handlers across State and Local Jurisdictions

Abstract

Key Objectives:

- Describe differences regarding exclusion and reinstatement criteria for food handlers diagnosed with enteric diseases across jurisdictions, including differences in public health practice.
- Identify strengths and limitations of differing exclusion and reinstatement criteria.
- Discuss strategies used for cross-jurisdictional exclusions.

Brief Summary:

Exclusion and reinstatement criteria for ill persons working in high risk situations are important public health measures that aid in controlling the spread of enteric disease in communities. However, although jurisdictions in the U.S. must follow the FDA Food Code exclusion and reinstatement guidelines for individuals diagnosed with salmonellosis, shigellosis, enterohemorrhagic or shiga toxin-producing E. coli, norovirus and hepatitis A virus, guidelines for other conditions differ across state and local jurisdictions. For example, some jurisdictions in Pennsylvania require 3 negative stool cultures before reinstatement for an individual who was diagnosed with giardia while others allow reinstatement when asymptomatic without any follow-up stool cultures. An epidemiologist representing a state health department (the Pennsylvania Department of Health) and an epidemiologist representing a local health department (the Allegheny County Health Department), will discuss differences in food handler exclusion and reinstatement criteria for enteric diseases within Pennsylvania. They will also share differences in practices used between the state and local health departments, such as routinely sending letters to employees or relying on a state public health laboratory to submit stools. The presenters will also discuss strategies adopted by the state and local health departments in handling cross-jurisdictional exclusions. Participants will have the opportunity to discuss how their jurisdictions determined exclusion guidelines for enteric diseases, examine the rationale behind specific guidelines, discuss the pros and cons of various criteria and consider consequences of differing guidelines. Participants will also have the chance to compare the perspectives of food safety inspection programs with that of epidemiology programs when developing food worker exclusion guidelines.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Surveillance; Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9424
Abstract Type	Roundtable
Abstract Title	Learning from Each Other: A Roundtable Discussion about Experiences Investigating, Controlling, and Preventing Shigellosis.

Abstract

Key Objectives:

- Discuss experiences, challenges, and successes of shigellosis-related work being done by state and local health departments, and the CDC.
- Identify opportunities to apply lessons learned from state and local health departments to optimize shigellosis prevention and control efforts.
- Discuss interest in, and proposed structure and format for, a community of practice focused on shigellosis prevention and control.

Brief Summary:

Each year an estimated 500,000 people become sick with shigellosis 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. Although shigellosis is typically self-limiting there is growing concern about drug resistant shigellosis. Resistant shigellosis infections could result in more severe illness, and potentially worse outcomes, especially in vulnerable populations. As a result it is critical that effective prevention and control efforts are 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, research, communications, and health promotion. Through these activities, groups engaging in shigellosis related work have identified strategies that are effective in their local context. As the scope and type of activities may vary depending on local needs and capacity, it is important for groups engaging in *Shigella* related work to utilize information from shared experiences to optimize prevention and control efforts. Coming together to share experiences can develop and strengthen relationships, and allow for the dissemination of practices or strategies employable more broadly to prevent and control shigellosis. 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 engaging in *Shigella* related work. Participants will discuss strategies and best practices that have been utilized by state and local health departments, and will identify how approaches could be adapted in their local context. Participants will also discuss level of interest in, and possible format and structure for, a community of practice focused on the prevention and control of shigellosis.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Prevention
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9684
Abstract Type	Roundtable
Abstract Title	The Who, What, When, and How of the 2017-2019 Foodnet Population Survey

Abstract

Key Objectives:

Our objectives are to 1) provide updates on the latest cycle of the Foodborne Diseases Active Surveillance Network (FoodNet) Population Survey, including preliminary data, timeline for completion, and plans for making the data publicly available; 2) discuss the needs of FoodNet and non-FoodNet states regarding the data collected and availability; and 3) identify resources that can be used to assist states with conducting similar surveys.

Brief Summary:

The FoodNet Population Survey is a population-based survey conducted in FoodNet sites to collect data needed for estimating the burden of foodborne illnesses and background rates of exposures for hypothesis generation regarding exposure vehicles and routes. The FoodNet sites include ~48 million persons in Connecticut, Georgia, Maryland, Minnesota, New Mexico, Oregon, Tennessee, and select counties in California, Colorado, and New York. Five cycles of the FoodNet Population Survey have been completed. The most recent cycle was conducted during 2006–2007. The sixth cycle began in 2017 and included updated methods and questions. The updated methods include expanded administration modes (landline, cell phone, web, and mail) and sample size (~36,000 total). The questions were updated to include questions related to new food exposures of concern and food handling behaviors, and to align with FoodNet Case Exposure Ascertainment data elements, the National Hypothesis Generating Questionnaire, and other initiatives. Data collection will be complete in 2019. Data from the most recent cycle and the new cycle will be made publicly available through the FoodNet Fast web tool. Data from the FoodNet Population Survey are used by a wide variety of agencies including state and local health departments, CDC and other federal agencies, as well as academic institutions. As future cycles are planned, we would like input from users regarding data collected, methods used, and availability of the data. Because data are only collected within the FoodNet catchment area, data may not be representative of all states. Some states have undertaken efforts to conduct similar surveys among their own populations to address this. We would like to help identify resources available to states considering conducting similar surveys.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Foodborne Disease; Population
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10050
Abstract Type	Roundtable
Abstract Title	Whole Genome Sequencing and Next Generation Sequencing for Epidemiologists: Trainings, Resources, and Technical Assistance from the Integrated Food Safety Centers of Excellence

Abstract

Key Objectives: After attending this roundtable session, participants will be able to: • Identify whole genome sequencing (WGS) trainings and resources developed by the Integrated Food Safety Centers of Excellence (CoE), including online modules, webinar series, live learning series, and technical assistance

- Discuss how state public health agencies have used WGS CoE resources and technical assistance to improve communication with laboratory partners, interpret WGS results, and integrate WGS results with epidemiological data during foodborne illness outbreak investigations

- Describe the purpose of the CoEs and how to contact CoE coordinators

Brief Summary: The Integrated Food Safety Centers of Excellence (CoE) aim to improve foodborne illness outbreak detection and response by providing training, technical assistance, and resources to public health professionals. As public health laboratories adopt whole genome sequencing (WGS) and next generation sequencing (NGS), epidemiologists are faced with integrating these data into their routine practice. To address this challenge, the CoE WGS Working Group, in partnership with CDC, developed trainings and resources, including asynchronous online modules, webinar series, synchronous live learning series using bi-directional video, and one-on-one technical assistance. These are delivered free to epidemiologists at state health departments who use WGS data for foodborne disease surveillance and outbreak investigation. The online molecular training series “Molecular Epidemiology and Sequencing Approaches in Public Health” includes four introductory online modules: Genetics and Evolution 101, Introduction to Next Generation Sequencing, Introduction to Sequence Analyses, and Tree Building 101. The webinar series was attended by 890 participants and includes four recorded webinars with presenters from the CDC and state health departments: WGS for Epidemiologists; WGS Data Analysis Methodology; hgSNP, wgMLST and the WGS alphabet soup; and Case Studies on use of WGS in Foodborne Disease Surveillance and Outbreak Investigations. The live learning series “Whole Genome Sequencing for Epidemiologists Live Learning Course” uses bi-directional video technology to provide epidemiologists with an active, case-based learning opportunity using WGS outbreak scenarios. The first series was delivered in one-hour segments, weekly for five weeks in fall 2017 to 18 epidemiologists; additional courses are planned for spring 2018 in the Minnesota and Tennessee CoE regions. All CoEs routinely offer one-on-one technical assistance to meet specific agency needs as they implement WGS, including consultation and tailored training. CoEs can assist with interpretation during active outbreak investigations, meet with epidemiologists and laboratorians to strategize WGS implementation, and facilitate exercises focused on identified needs.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Epidemiology; Outbreaks
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10190
Abstract Type	Roundtable
Abstract Title	Working with the Food Safety Centers of Excellence: Peer Support Experiences

Abstract

Key Objectives:

- Inform CSTE participants of one-on-one consultations that the Integrated Food Safety Centers of Excellence (CoEs) have provided to state and local health departments including the 26 health departments in the OutbreakNet Enhanced program.
- Learn ways CSTE participants have interacted with and benefited from relationships with the CoEs.
- Educate CSTE members on products developed and services offered by the Integrated Food Safety Centers of Excellence (CoEs) that are available at no cost.
- Identify current areas of need to enable CoEs to focus their future work on projects that address these gaps.

Brief Summary:

As required by the Food Safety Modernization Act, CDC designated CoEs to serve as resources for other public health professionals to respond to foodborne illness cases and outbreaks. The CoEs are located at state health departments in partnership with academic institutions and provide peer support by developing educational materials, delivering trainings, and providing consultation services. During this roundtable session, participants will have the opportunity to meet CoE representatives and discuss services that the CoEs have provided. Each CoE covers an assigned geographic region to help health departments navigate the array of CoE resources. The roundtable format for this session will encourage participants to interact with their regional CoE to help build relationships for future assistance and consultation. Participants will hear from the CoEs and other jurisdictions to learn about consultations and projects to better understand the variety of services that the CoEs can provide, including site visits and outbreak support.. During this roundtable session, participants will also discuss the products that the CoEs have developed. The CoEs have created over 100 products that are available online at no cost. These products include training courses, videos, and guidance documents. In this session, participants will learn about CoE products and have a chance to provide feedback on products that they've used. In addition to discussing existing products, there will be time for participants to suggest products that the CoEs could develop based on gaps they have identified in their jurisdictions.

Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Capacity / Capacity Building; Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	No
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Submission Type Breakout/Quick/Lightning/Poster

ID 9965

Abstract Type Breakout

Abstract Title A Framework for Composite Measures for HAI Prevention in the National Healthcare Safety Network (NHSN)

Abstract

BACKGROUND: The National Healthcare Safety Network (NHSN), developed and used by the Centers for Disease Control and Prevention (CDC) for surveillance of healthcare-associated infections (HAIs), provides benchmark measures, such as standardized infection ratio (SIRs), that CDC and its partners in healthcare and public health use for prevention purposes. NHSN provides benchmarks for each HAI measure separately, enabling healthcare facilities to target their prevention efforts. However, a composite HAI measure that conveys summary information across multiple HAIs could provide a more rounded assessment of HAI problems and prevention opportunities.

METHODS: We addressed several methodological issues in an exploratory effort to produce a sound HAI composite measure. First, the method needed reliability in adjusting single HAI SIRs, particularly for facilities with low HAI exposure, e.g., low device days, operative procedure volume. To solve this issue, we used the Adjusted Ranking Metric (ARM), a new measure based on a commonly-used methodology that reliability-adjusts the SIR using a Bayesian mixed effects model. Second, exposure to separate HAI types is not consistent within facilities and the weight for a particular HAI should be proportional to the potential for the HAI (measured by exposure). We addressed this need for weighting by pooling the numerator and denominator before applying weights and calculating the ratio. Pooling leads to a third issue: events may not be directly comparable across HAIs in terms of relative frequency or severity. We took this issue into account by applying a scale adjustment to the numerator and denominator prior to pooling. The composite is calculated for six HAIs based on 2015 data.

RESULTS: Case studies of several facilities show that the new composite measure provides a meaningful measure of overall facility performance that is less prone to the biases that afflict simple combinations of SIRs. The cost weights used for the illustrative example slightly change the measure as anticipated.

CONCLUSIONS: We introduce a framework for calculating a composite HAI measure that is flexible, customizable and transparent. The current implementation of the framework is intended to assist in prevention efforts and can be easily modified. Flexibility in weighting the HAIs provides an opportunity for different stakeholders to customize the composite measure to their own needs, and several “flavors” of this composite might be useful to the wider community.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9142

Abstract Type Breakout

Abstract Title A Novel Adenovirus Outbreak in an Optometry Clinic

Abstract

BACKGROUND: Epidemic keratoconjunctivitis (EKC) is a highly contagious, severe form of inflammatory viral conjunctivitis that can cause severe pain and blurry vision for up to four weeks. In June 2017, the Los Angeles County Department of Public Health (LACDPH) was notified of seven patients with EKC infections seen at an optometry clinic. LACDPH sought to characterize the outbreak and determine associated exposures and risk factors.

METHODS: LACDPH conducted an outbreak investigation that included a site visit, case finding, medical record review, and laboratory analysis. A healthcare-associated case was defined as a case in a person who had visited the optometry clinic from June 7 to July 3, 2017 and ≤ 14 days before onset of symptoms. A secondary case was defined as a close and/or family contact of a primary case. Available cell culture isolates or conjunctival swab specimens from case patients were cultured and submitted for molecular typing.

RESULTS: Fourteen patients met the case definition of a healthcare-associated case. Two cases met the secondary case definition; both reported a symptomatic household contact. All case patients had repeat visits to either the clinic, a hospital emergency department, or an urgent care center. Medical chart review indicated a number of common exposures amongst the healthcare-associated case patients: all were seen by the same optometrist in the same exam room. Other common exposures included multi-dose sodium fluorescein eye drops (14, 87.5%) and tonometry (12, 75%). The site visit revealed that the clinic's equipment disinfection policy was not consistent with Healthcare Infection Control Practices Advisory Committee guidelines. Specimens from 11 case patients, all with symptoms of conjunctivitis, were positive for adenovirus D53.

CONCLUSIONS: Based on our observations, we hypothesize that once the virus was present on surfaces in the exam room, lapses in infection prevention practices most likely led to further transmission. Prior studies found that adenovirus may persist on environmental surfaces for several weeks. To our knowledge, this is the first reported EKC outbreak caused by adenovirus D53 in the United States. Enhanced infection prevention practices, including staff education on eye drop administration and increased tonometer disinfection, were implemented. No additional cases occurred after these measures were implemented. Proper infection prevention is critical to avoid healthcare-associated infections, especially in regard to hand hygiene, multi-dose eye drop use, and equipment disinfection. It is probable that community standards of practice do not meet national infection control recommendations. Outreach is planned for the optometry community.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infection Control; Outbreaks; Healthcare Associated Infections (HAI)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9073

Abstract Type Breakout

Abstract Title An Outbreak of Hepatitis A Virus Among Adult Patients of a Mental Health Facility, Los Angeles County, California

Abstract

BACKGROUND: In 2017, two cases of hepatitis A virus (HAV) were identified among patients of a multi-unit mental health facility, indicating possible HAV transmission within the facility. Both cases resided in the same 44-patient locked unit of this facility housing both conservatorship patients and patients transferred from incarceration.

METHODS: The Los Angeles County (LAC) Department of Public Health (DPH) conducted a site investigation to assess the environmental conditions and HAV risk to the patients of this facility. In addition, LACDPH conducted active case surveillance and implement control measures to mitigate HAV risk to the patients.

RESULTS: Several environmental cleaning issues were identified at the facility and addressed with the facility staff. LAC DPH recommended administering HAV post exposure prophylaxis to all patients and staff on the affected 44-patient unit. Twenty-nine patients were vaccinated (70%), 11 had documented HAV immunity (27%) and one refused vaccination (2%). Twenty-seven of the 61 staff members in the outbreak unit also received vaccination (44%). A total of four acute HAV cases (genotyped 1B) were identified in the unit over the surveillance period (attack rate of 9%). All four cases met the CSTE HAV case definition. The index case had HAV exposure prior to admission to this facility. Secondary case exposures included close sexual contact to the index case (n=1), shared living quarters of the index case (n=1), and shared environment of the facility unit where cases had occurred (n=1).

CONCLUSIONS: The investigational results suggest that this health facility outbreak of HAV was due to both close case-contact and environmental contamination in this unit from acute cases. Our findings suggest that patients in congregate living situations lacking the ability to adhere to hygienic practices be screened for HAV upon admission and be vaccinated if found to be susceptible.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infection Control; Hepatitis; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9479

Abstract Type Breakout

Abstract Title Assessing the Ability of Hospitals to Detect *Candida Auris* : Results from an Online Laboratory Survey and the National Healthcare Safety Network Hospital Survey — Connecticut, 2017

Abstract

BACKGROUND: The fungus *Candida auris* can spread through contact with affected patients or contaminated surfaces. Exposed patients can develop potentially fatal invasive infections or become colonized, which poses long-term risks for transmission. The organism can persist in health care environments, survive commonly used disinfectants, and is often multidrug-resistant. *C. auris* detection is challenging because some automated biochemical-based identification methods misidentify *C. auris*. For example, API® 20C (bioMérieux, Marcy L'Etoile, France) can misidentify *C. auris* as *Candida sake* or *Rhodotorula glutinis* and Vitek® 2 (bioMérieux) can misidentify it as *Candida haemulonii* or *Candida duobushaemulonii*. We assessed the ability of hospital laboratories in Connecticut to accurately identify and perform antifungal susceptibility testing (AFST) for *C. auris* isolates.

METHODS: During August 2017, we conducted an online survey of the 23 laboratories that serve Connecticut acute care hospitals regarding their *Candida* identification methods and protocols. We also accessed data from the 2016 National Healthcare Safety Network (NHSN) Patient Safety Component Annual Hospital Survey regarding AFST practices completed by Connecticut's 29 acute care hospitals. Frequency distributions and cross-tabulations of data from both surveys were calculated.

RESULTS: Twenty-one of 23 hospital laboratories participated in the online survey. Seventeen laboratories perform fungal identification on-site; these laboratories serve 80% of Connecticut acute care hospitals. Sixteen of the 17 laboratories performing *Candida* speciation on-site do so reflexively for all sterile-site isolates. Reflexive testing for nonsterile-site isolates was less common. Five laboratories routinely use matrix-assisted laser desorption ionization–time of flight mass spectrometry for *Candida* speciation using a database that can accurately identify *C. auris*. Eleven laboratories routinely use instruments that can misidentify or fail to speciate *C. auris*, most commonly the Vitek® 2 (6 laboratories) and the API® 20C (3 laboratories). Five laboratories have a protocol for investigating suspect *C. auris* isolates; however, only 2 have automated alerts for suspect *C. auris* misidentifications. Two of 29 CT hospitals reported to NHSN that the laboratory that serves their hospital performs AFST on-site. Six hospitals have access to reflexive AFST for azoles and echinocandins for sterile-site isolates of *Candida* species other than *C. albicans*, *C. glabrata*, and *C. parapsilosis*.

CONCLUSIONS: The diversity in *Candida* identification, speciation, and AFST methods among Connecticut hospital laboratories highlights challenges in the timely and sensitive detection of *C. auris*. These findings suggest a potential role for the state health department in assisting hospitals with rapid identification of this challenging pathogen.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Antimicrobial Resistance; Epi / Lab Capacity (ELC); Healthcare Associated Infections (HAI)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10146

Abstract Type Breakout

Abstract Title Assessment of Infection Prevention and Control Programs in Texas' Healthcare Facilities

Abstract

BACKGROUND: Healthcare-Associated Infections (HAIs) contribute to increased mortality, longer hospitalization time, and higher medical expenses for both patients and healthcare facilities. With the goal of reducing HAIs across the nation, the Centers for Disease Control and Prevention (CDC) developed the Infection Control Assessment and Response (ICAR) tools. These tools were designed to assist state and local health departments assess infection prevention practices in multiple healthcare settings and to guide quality improvement activities.

METHODS: From March 2016 to August 2017, HAI Epidemiologists from the Texas Department of State Health Services (DSHS) visited 163 healthcare facilities across the state to assess their Infection Prevention and Control programs utilizing the ICAR tools. These were voluntary and non-regulatory visits aimed to identify strengths and gaps in the facilities' programs and provide them with resources to help mitigate those gaps.

RESULTS: Data from the visits were collected and analyzed using descriptive statistics and compared with national data. From the 163 facilities: 56% were long-term care facilities (92), 27% acute care facilities (44), 14% dialysis clinics (23) and 3% outpatient clinics (4). Overall, the top 3 gaps identified during the visits were: the lack of antibiotic stewardship policies and practices, inadequate training of the person responsible for the Infection Prevention and Control program, and insufficient processes for auditing, and providing feedback to staff on infection control best-practices (e.g., hand hygiene, infection safety).

CONCLUSIONS: By utilizing the ICAR tools to assess the Infection Prevention and Control Programs of healthcare facilities across Texas, DSHS was able to better understand the most common infection control challenges and strengths in the state, provide facilities with resources to help mitigate identified gaps while at the same time improve communication and collaboration between the facilities and the Department.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infection Control; Health Care; Prevention

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9770

Abstract Type Breakout

Abstract Title Cases of *Candida Auris* in the United States Associated with Receipt of Healthcare in Countries with Known *C. Auris* Transmission, 2013–2017

Abstract

BACKGROUND: *Candida auris* is an emerging multidrug-resistant yeast that causes severe infections, can be transmitted in healthcare settings, and is challenging to identify. Twenty countries have identified *C. auris* cases, including some with extensive transmission. Whole-genome sequencing (WGS) of *C. auris* isolates from around the world suggests isolates group into four distinct clades associated with South Asia, South America, South Africa, and East Asia; U.S. isolates have been closely related to isolates from these clades. We investigated U.S. *C. auris* cases to identify epidemiologic links to other countries.

METHODS: In June 2016, CDC issued a clinical alert for *C. auris* requesting that healthcare facilities report cases to local and state health departments and CDC. Health departments obtained case-patient medical history, including recent international hospitalizations. CDC performed WGS to investigate a possible relationship to international clades.

RESULTS: As of November 2017, 174 clinical cases had been identified in ten states. Six case-patients had a documented history of receiving healthcare abroad: India (n=2), Pakistan (n=1), South Africa (n=1), the United Arab Emirates (n=1), and Venezuela (n=1), all countries with known transmission. Three patients were directly transferred to U.S. healthcare facilities from healthcare facilities abroad. The interval between hospitalization abroad and collection of *C. auris* positive culture ranged from one day to 21 months. *C. auris* was cultured from urine (n=3), wound (n=2), and blood (n=1) specimens. All six case-patients were infected by at least one other multidrug-resistant organism. In each case, WGS revealed the isolate was closely related to isolates from the country of healthcare exposure.

CONCLUSIONS: *C. auris* can be introduced into the U.S. by patients who receive healthcare abroad; prompt identification of *C. auris* can help prevent local transmission. For patients who have received healthcare in a country with known *C. auris* transmission during the previous year, any *Candida* isolated from sterile and non-sterile body sites should be identified to the species level. Providers should consider preemptively placing patients who have recently received healthcare in countries with extensive *C. auris* transmission in appropriate transmission-based precautions and screening for *C. auris*. If *C. auris* is identified, providers should notify public health agencies and implement infection control measures.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Infection Control; Emerging Infections

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10246

Abstract Type Breakout

Abstract Title Developing an Agent-Based Model of a Regional Healthcare Network for Infectious Disease Modeling: The North Carolina Modeling Infectious Diseases (NC MInD) Network

Abstract

BACKGROUND: Healthcare-associated infections (HAIs) cause substantial morbidity and mortality and are costly to healthcare and public health systems. Depending on the pathogen, unrecognized colonized patients and community sources can affect the HAI burden. Patient movement between healthcare facilities (e.g., hospitals and long-term care facilities (LTCFs)) and the community make HAI prevention challenging. Prevention efforts could be enhanced using agent-based models (ABMs), computational models with explicit representation of people (“agents”) and their interactions with each other and their environment. We developed a representative synthetic population and novel ABM of a North Carolina (NC) regional healthcare network to describe the movement of patients and model their risk of *Clostridium difficile* infection (CDI), the most common HAI in the United States.

METHODS: We generated a spatially-explicit, de-identified, synthetic population database of the regional healthcare network served by UNC Health Care, including nine hospitals in nine NC counties with an estimated population of 2.35 million. The synthetic population was comprised of the persons whose healthcare-relevant life events were simulated. We created multi-dimensional probability look-up tables to inform agent attributes, including demographics (i.e., age, sex, race, household size, income) and likely location assignment (e.g., households, LTCFs, hospitals). We used probability cross-tabulations to form rules for agent movement into and through the network. Based on agent characteristics and locations, we designated CDI health states (e.g., high-risk susceptible, low-risk susceptible, asymptomatic carriage, CDI, recurrent CDI, deceased) for individual agents with a 1-day time step over 1-calendar year.

RESULTS: The database represented the sociodemographic and CDI health-state attributes and spatial representation of the regional healthcare network served by UNC Health Care at the census block-group level. The ABM simulated the movement of persons throughout the network and their risk of CDI. The representative population and ABM were created to be adaptable to other HAIs and expanded to a NC statewide platform.

CONCLUSIONS: We developed a synthetic population and an ABM of a NC regional healthcare network for CDI. Future activities will include parameterization of the ABM with patient health and NC National Healthcare Safety Network data, further calibration and validation, and sensitivity and uncertainty analyses. Following these activities, the ABM will be used to simulate and evaluate HAI prevention interventions in partnership with NC public health agencies. Results could be used to inform public health practice and policy for HAI prevention in NC.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infectious Diseases; Healthcare Associated Infections (HAI); Epidemiologic Methods

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9377

Abstract Type Breakout

Abstract Title Group A *Streptococcus* Outbreak Among Residents and Employees of Two Skilled Nursing Facilities – North Carolina, 2017

Abstract

BACKGROUND: In January 2017, the North Carolina Division of Public Health (NC DPH) was notified by a local health department (LHD) of group A *Streptococcus* (GAS) outbreaks in two skilled nursing facilities (SNFs) owned by the same company.

METHODS: We initiated active and retrospective surveillance for additional cases in both SNFs. We defined a case as new GAS infection or colonization identified by culture in a resident or symptomatic employee of either SNF with a specimen collection date on or after November 24, 2016. The LHD issued control measures to both SNFs and conducted several site visits to assess compliance. NC DPH conducted an additional site visit at both SNFs in April 2017 to assess infection prevention policies and practices.

RESULTS: In total, 24 cases (20 residents and four employees) were identified by culture from wound (12, 50%), throat (7, 29%), blood (4, 17%) and nasopharyngeal (1, 4%) specimens. Six of 20 (30%) residents and no employees died. Isolates from 14 residents and one employee (63% of cases) were submitted to CDC for serologic testing and genomic analysis. The isolates from 13 of the residents and one employee shared the same T agglutination complex 13. Genomic sequence analysis revealed that these T13 isolates represented the globally emergent clade 3 *emm89* strain and indicated close temporal relatedness of the 14 subtype *emm89.0* isolates. Identified infection prevention deficiencies were related to hand hygiene, environmental cleaning/disinfection, and general infection control and prevention at both facilities. NC DPH and the LHD issued control measures related to these observations. Two employees worked at both SNFs and performed wound care. One of these employees was symptomatic, tested positive, and treated twice for GAS in January 2017. This employee's isolate was clade 3 *emm89.0*.

CONCLUSIONS: Clinical history and laboratory results suggested the symptomatic employee may be a GAS carrier and individual control measures were provided. Our findings suggest that the outbreaks in both SNFs were related and the shared employee was the link between the SNFs but not necessarily the source of the outbreaks. Infection prevention deficiencies were identified at both SNFs, demonstrating the need for strict adherence to infection prevention practices, especially during direct patient care. Public health authorities should inquire as to shared employees between facilities during similar outbreaks and consider implementing individual control measures for employees who may be carriers of GAS and who perform direct patient care.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Outbreaks; Healthcare Associated Infections (HAI); Infection Control

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10008

Abstract Type Breakout

Abstract Title Healthcare Associated Infection Outbreak Investigation of Resistant *Pseudomonas Aeruginosa* in an Intensive Care Setting

Abstract

BACKGROUND: The Nebraska Department of Health Human Services (NDHHS) Healthcare Associated Infections (HAI) program was notified of 2 cases (PB and PC) of highly drug-resistant *Pseudomonas aeruginosa* with the same pattern (resistant to 4 antibiotic classes) in the same Intensive Care Unit (ICU) that resulted within 1 week.

METHODS: Nebraska's antibiotic susceptibility registry was reviewed for isolates with this pattern. NDHHS HAI and facility infection control personnel conducted an ICU assessment, environmental sampling, staff interviews, and patient chart review. Patient and environmental isolates were sent to the Centers for Disease Control and Prevention for Pulsed-Field Gel Electrophoresis (PFGE). Patient isolates were also analyzed by whole genome sequencing (WGS) at the Nebraska Public Health Laboratory.

RESULTS: Of the 60,000 isolates reported across Nebraska in 2017, 1 historic isolate had a matching pattern. This index isolate was from patient A (PA), whose 21-month stay overlapped with the 2 initially identified cases (PB and PC). Reports showed isolates from PA developing the resistance pattern over 2 months during treatment with several antimicrobials. PA was discharged at the time PB and PC were identified; no isolates from PA were available for further testing. Recommendations were made to utilize contact precautions for affected patients and a flag was placed in PA's chart for re-admissions. Another case (PD) was identified 4 weeks after PC in the same ICU. All 4 cases were complex patients with many shared personnel and equipment. PB and PC had closely-related PFGE patterns with one band difference, whereas PD's isolate was unrelated, with more than seven band differences. WGS following a SNP analysis showed isolates from PB and PC matched but were divergent from PD, although all 3 shared common resistance genes. The PFGE patterns of PD, PC, and PB were unrelated to those of 5 environmental isolates.

CONCLUSIONS: An outbreak of resistant *Pseudomonas aeruginosa* occurred in an ICU with 4 isolates demonstrating similar resistance patterns, but 1 of the 3 isolates differing by PFGE and WGS. PFGE and WGS provided important insight into this outbreak, suggesting the mechanisms of resistance observed here, not just the organism, might be transferrable. Further, this investigation highlighted the utility of a public health antibiotic susceptibility data registry in an outbreak setting for identifying a likely initial source and making infection control recommendations to manage potential person-to-person spread for an outbreak of an organism traditionally associated with water exposure. Additional studies are needed to assess WGS for outbreak investigations.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Antimicrobial Resistance; Healthcare Associated Infections (HAI); Informatics

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10232

Abstract Type Breakout

Abstract Title Improving Minnesota National Healthcare Safety Network Data Quality through Facility Feedback Reports

Abstract

BACKGROUND: The Minnesota Department of Health (MDH) accesses National Healthcare Safety Network (NHSN) data through a Data Use Agreement with CDC. Hospitals participating in the Centers for Medicare and Medicaid Services (CMS) Inpatient Quality Reporting Program are required to report to NHSN. The quality of NHSN data is critical to ensure data accuracy for quality reporting and reimbursement, public reporting, and HAI prevention efforts. Data quality reports (DQR) addressing eight potential data quality issues are available to users within the NHSN application. In December 2016, MDH began distributing data quality feedback reports to Minnesota acute care hospitals using the NHSN DQR. In November 2017, MDH expanded the reports to include 15 additional data quality issues.

METHODS: Acute care hospital NHSN data for 2017Q2 were reviewed for 23 potential data quality issues addressing completeness, inconsistencies, and implausible values using SAS 9.4. Feedback reports were distributed two weeks before the November 2017 CMS deadline. To assess the impact of the expanded data quality reviews, we summarized the number and types of identified data quality issues and the associated standardized infection ratios (SIR), comparing 2017Q2 data before and after the CMS deadline.

RESULTS: Among 50 total hospitals, 266 potential errors from 24 hospitals were identified for 2017Q2 data before the CMS deadline. Only five (2%) of the errors from five hospitals appeared in the NHSN DQR. A majority (75%) of the total errors were due to missing data. Of the remaining 66 errors, the most common data quality issues included: too many patient days (16) or device days (14), procedures excluded from surgical site infection SIR calculations (15), and consistently reporting zero device and patient days (10); 38 (58%) of these were corrected by the CMS deadline. In three instances, these corrections resulted in changes to the SIR ranging from 2.6 to 3.9%. Errors resulting in SIR changes did not appear in the NHSN DQR.

CONCLUSIONS: We identified commonly occurring data quality issues not included in the NHSN DQR with the potential to influence the SIR. These feedback reports provide facilities with the opportunity to correct data quality issues before data are finalized for CMS reporting. Collaboration between CDC, state health departments, and other stakeholders could generate a more complete list of data quality issues and standardize methodology to improve NHSN data quality and consistency among all reporting facilities.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10292

Abstract Type Breakout

Abstract Title Legionella Prevention and Control Practices Among Acute Care Hospitals, Maryland, 2017

Abstract

BACKGROUND: On June 2, 2017, the Centers for Medicare and Medicaid Services (CMS), under 42 CFR §482.42 for hospitals (and under 42 CFR §485.635(a)(3)(vi) for critical access hospitals and 42 CFR §483.80 for skilled nursing facilities and nursing facilities), announced standards that Medicare certified healthcare facilities ensure “water management policies and procedures to reduce the risk of growth and spread of *Legionella* and other opportunistic pathogens in building water systems” as part of their infection prevention and control programs. Maryland Department of Health (MDH) has an active response to healthcare associated *Legionella* infections.

METHODS: In late June, 2017, MDH performed a statewide survey of Maryland’s 47 acute care hospitals, regarding the hospitals’ *Legionella* management systems. A survey was distributed to each facility’s infection prevention program. The survey addressed both infection prevention and control of *Legionella* as well as facility systems, such as water management programs.

RESULTS: Overall, 29 acute care hospital infection control programs responded to the survey. Twenty-one (72.4%) hospitals reportedly had water management plans already in place to address *Legionella* in their building water systems, while six (20.7%) were in the process of creating such a plan. Seventeen (58.6%) facilities reported that part or all of their potable water systems had secondary disinfection systems in place. Twenty-four (82.8%) respondents reported performing routine environmental sampling for *Legionella*, though practices varied greatly in terms of the number of sites sampled (range: 2-65) and the frequency of testing (range: biweekly to annual).

CONCLUSIONS: In Maryland, many hospitals have already acted to address the risk posed by *Legionella* and other waterborne pathogens by developing water management plans and taking steps such as treating their potable water and conducting environmental sampling for *Legionella*. While these results are encouraging, there is still room for improvement, given the CMS requirement for facilities to implement policies and procedures to address these risks. MDH and other state health departments can assist healthcare facilities by providing education on *Legionella* epidemiology and risk factors, distributing Centers for Disease Control and Prevention and the American Society of Heating Refrigerating and Air-Conditioning Engineers (ASHRAE) guidance for water management, and serve as a forum for sharing best practices regarding *Legionella* prevention.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Infectious Diseases; Waterborne Disease

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9254
Abstract Type	Breakout
Abstract Title	Mycobacterium Chimaera Infections Among Cardiac Surgery Patients Associated with Heater-Cooler Units — Hospital a, Los Angeles County, 2013–2016
Abstract	BACKGROUND: <i>Mycobacterium chimaera</i> (Mc) is a slow-growing nontuberculous mycobacterium in the <i>Mycobacterium avium</i> complex (MAC). Mc infections have been linked with a specific brand of contaminated heater-cooler units (HCUs) used during cardiac surgery. In December 2016, Hospital A in Los Angeles County reported two MAC case-patients. We investigated to detect additional cases, assess surgical practices, and determine risk factors. METHODS: We defined cases as laboratory-confirmed Mc after cardiac surgery at Hospital A during May 2013–December 2016. We abstracted patients’ medical records and tested specimens from one HCU. We conducted a case-control study with 4 control subjects/case-patient matched by age <2 years and year of surgery. We assessed differences between case-patients and control subjects by Fisher exact, <i>t</i>-test, and Wilcoxon tests; <i>a priori</i> risk factors and those associated with Mc infection ($P < .05$) in bivariate analyses were included in a multivariable conditional logistic regression model. RESULTS: We identified 17 cases; 10 (59%) had disseminated infection and 6 (35%) died. Three HCUs manufactured in 2012 were used during case surgeries; 5 of 6 samples (83%) from 1 of these HCUs had MAC isolated (speciation pending). Mean interval from surgery to infection was 25.7 months. Preoperative procedures for the day’s first surgeries occurred in the operating room (OR). In the multivariable model, valve insertion (adjusted odds ratio [aOR]: 6.1; 95% confidence interval [CI]: 1.4–26.2) and first surgery of the day (aOR: 3.3; 95% CI: 0.9–12.8) were associated with infection. CONCLUSIONS: Mc in aerosols from contaminated HCUs likely contributed to infection. Conducting preoperative procedures in OR for the day’s first surgery might lead to longer exposure. We recommended removing implicated HCUs, conducting preoperative procedures outside OR, positioning HCUs to mitigate possible surgical field contamination, and strictly adhering to additional CDC and Food and Drug Administration guidance and updated manufacturer HCU cleaning guidelines.
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10042

Abstract Type Breakout

Abstract Title Outbreak of Scalded Skin Syndrome in a NICU, Cook County, IL 2017

Abstract

BACKGROUND: On August 14th, 2017 Hospital A reported the presence of two cases of Staphylococcal Scalded Skin Syndrome (SSSS) in their neonatal intensive care unit (NICU) to the Cook County Department of Public Health (CCDPH). Outbreak cases continued until September 23rd, 2017. SSSS is caused by exfoliative toxins A and B resulting in rash, lesions, and desquamation. Outbreaks of SSSS are rare, especially among preterm infants, and most commonly affect children under five years old.

METHODS: CCDPH -- in coordination with Hospital A's infection prevention staff, the Illinois Department of Public Health, and the CDC -- implemented control measures designed to prevent further spread of infection. These included weekly surveillance screening, emphasis on hand washing, increasing contact precautions, and cohorting of positive patients. Approximately 100 patients within the NICU were tested to determine if they were positive through culturing and PCR, positive samples were sent to the CDC for PFGE testing. One hundred thirteen NICU staff were also tested for the outbreak strain. Additional data was collected through chart review of patients' medical records to collect additional information on potential exposures. A case was defined as being in the NICU between August 3rd and December 14th, 2017, having a laboratory confirmed positive with the outbreak strain.

RESULTS: Specimen were collected from approximately 100 patients between 08/14/2017 and 12/14/2017. PFGE results from these patients determined that twelve were positive with the outbreak strain of *S. aureus*, of which six were symptomatic. Of the 113 staff tested, five were found to be positive with either an identical or closely related strain, all staff were asymptomatic. PGFE results showed ten strains of *S. aureus* to be in circulation, three of which formed clusters. One mother was found to be positive with the outbreak strain. The NICU was placed on contact precautions and positive patients were cohorted with the same staff and to the same area of the NICU, proper hand hygiene was emphasized.

CONCLUSIONS: Appropriate use of infection control measures including: decolonizing NICU staff and patients, use of contact precautions, and increased hand hygiene helped bring an end to the outbreak. Weekly active surveillance was ended on 12/14/2017 with no new cases identified after 09/23/2017. Future outbreaks may be prevented through the use of contact precautions as the default for vulnerable patient groups, training physicians and nurses on the signs of SSSS may increase early detection of cases.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infection Control; Infant Health; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10294

Abstract Type Breakout

Abstract Title Self-Reported Public Health Department Healthcare-Associated Infection Outbreak Response Capacity and Improvements – United States, 2015-2017

Abstract

BACKGROUND: As part of the Infection Control Assessment and Response (ICAR) activities of the Epidemiology and Laboratory Capacity (ELC) Ebola Supplement, state and local health department (HD) healthcare-associated infection (HAI) programs were asked to assess outbreak reporting and response in healthcare facilities. During the project period of May 2015 – July 2017 HAI programs initially completed an Interim Self-assessment Tool to identify opportunities to improve capacity in HAI response activities. At the end of the project period we aimed to assess how HDs utilized the supplement to make improvements related to response activities in their jurisdiction.

METHODS: In July 2017, ELC-supported HDs completed a Final Progress Report to describe current capacity and improvements in response activities during the project period in four areas: 1. Tracking (i.e. documenting response activities in a database) 2. Detection and Reporting; 3. Investigation; and 4. Coordination, Communication, and Outreach. HAIs were defined as infections acquired in healthcare settings or while receiving medical care. Response activities were defined as efforts on the part of public health authorities to assist with investigation of specific HAI risks, including outbreaks, clusters of infection, sentinel cases including antimicrobial resistance (AR) threats, and serious infection control breaches.

RESULTS: HAI programs from 49 state and 6 local HDs reported a total of 6665 response activities in calendar year 2016. During the project period, HDs from 53 (96%) jurisdictions reported hiring new staff, 47 (85%) provided training for existing staff, and 43 (78%) developed new investigation tools to expand expertise and capacity to conduct HAI response activities. HDs from 10 (18%) jurisdictions reported developing capacity and 34 (62%) reported enhancing capacity to enter cluster and outbreak investigation information into a response tracking database. Three (5%) HDs reported developing reporting requirements for potential HAI outbreaks and 9 (16%) strengthened reporting requirements for potential HAI outbreaks. Reporting requirements for sentinel cases or AR threats were reported to have been developed by 3 (5%) HDs and strengthened by 18 (33%) HDs. Also, 38 (69%) HDs reported efforts to strengthen communication between their state and local HDs.

CONCLUSIONS: HDs indicated a high level of HAI response activity. Additional expertise and resources obtained during the ICAR funding period enhanced HD capacity to support investigations of potential HAI outbreaks as well as sentinel cases and AR threats. Many HDs developed or improved capacity to track response activities in a database and some strengthened HAI outbreak reporting requirements to better facilitate HAI outbreak reporting.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Emerging Infections; Healthcare Associated Infections (HAI); Outbreaks

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9098
Abstract Type	Breakout
Abstract Title	Shedding Light on Infection Prevention Breaches in Non-Traditional Settings: Investigations of a Dental Clinic, an Unpermitted Tattoo Artist, and a Plasma Donation Center – North Carolina
Abstract	BACKGROUND: Infection prevention (IP) breaches can cause pathogen transmission from individuals or the environment. The North Carolina Division of Public Health (DPH) led three IP breach investigations in non-traditional settings during December 2016-December 2017. Although settings differed (dental clinic, unpermitted tattoo artist, plasma donation center), the methods of investigation, intervention, control, and health communication were similar in all of these settings. METHODS: DPH investigated IP breaches with partners using the approach described for healthcare settings by P. Patel and colleagues (AJIC, 2008). Potentially exposed individuals were identified using available exposure information. Interviews with staff and potentially exposed individuals were conducted to describe each breach including the instruments, practices, and procedures involved. When possible, DPH conducted site visits to observe practices and procedures. DPH queried the NC Electronic Disease Surveillance System for reports of bloodborne diseases among potentially exposed individuals; and the NC Immunization Registry for hepatitis B virus (HBV) vaccination status of exposed individuals. Potential source individuals were screened for bloodborne pathogens (BBP) when possible. DPH assessed the exposure risk and determined the need for notification and testing. RESULTS: IP breaches included improper reprocessing of devices (dental clinic, tattoo artist) and IP deficiencies related to aseptic technique, hand hygiene, and environmental cleaning/disinfection (dental clinic, tattoo artist, plasma donation center). The dental clinic breach involved 25 exposed persons over one day; individuals were notified and referred for testing. The unpermitted tattoo artist exposed 18 individuals over three months; individuals were interviewed and referred for testing. DPH identified IP breaches at a plasma donation center while investigating a cluster of three acute HBV infections in donors over two months. DPH reviewed routine BBP screening records for other donors but did not recommend donor notification. All breaches posed a low risk of BBP transmission – no infections associated with the breaches were identified. CONCLUSIONS: IP breach investigations can be complex and may involve multiple pathogens. While DPH uses a standard investigation approach originally described for healthcare settings, this approach can be applied to all settings. Regardless of evidence of acute disease, IP breaches pose a risk for disease transmission and should be investigated. Investigation findings should be disseminated appropriately and used to inform prevention efforts in similar settings.
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infectious Diseases; Healthcare Associated Infections (HAI); Infection Control
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9956

Abstract Type Breakout

Abstract Title State Health Department Validations of Central Line-Associated Bloodstream Infection Events Reported Via the National Healthcare Safety Network

Abstract

BACKGROUND: Validation of healthcare associated infection (HAI) surveillance data that healthcare facilities report to the National Healthcare Safety Network (NHSN) is an important way to measure and improve adherence to NHSN's HAI definitions and criteria. Numerous State Health Departments (SHDs) have validated central line associated blood stream infection (CLABSI) data that hospitals in their jurisdiction have submitted to NHSN. Results from these studies and lessons, which previously have not been summarized in a single report, can provide important insights into the accuracy of CLABSI reporting to NHSN and remediable shortcomings in adherence to the CLABSI definition and criteria.

METHODS: State CLABSI validation results were obtained from peer-reviewed publications, presentations at scientific meetings, reports on SHD websites and via personal communications with the SHD HAI Coordinator. Data accuracy measures assessed included pooled mean sensitivity, specificity, positive predictive value (PPV) and negative predictive value (NPV). Total CLABSI "error rate" was computed as the proportion of mismatches among total records reviewed. When available, reasons for CLABSI misclassification reported by SHDs were reviewed.

RESULTS: At least 23 SHDs that have completed CLABSI validation projects indicated sensitivity (pooled mean: 82.9%, range: 32.4% –100%) specificity (pooled mean: 98.5% range: 93.1% –100%), positive predictive value (pooled mean: 94.1%, range: 87% – 100%), and negative predictive value (pooled mean: 95.9%, range: 92.4% – 99%) of CLABSI reporting. The pooled error rates of CLABSI reporting was 4.4% (range: 0% – 22.3%). Reasons for CLABSI mismatches were classified into six categories: incorrect secondary BSI attribution; misapplication of NHSN CLABSI definition; missed case finding; applying clinical over surveillance definitions, misapplication of LCBI-2 definition; and misapplication of general NHSN definitions.

CONCLUSIONS: While CLABSI under-reporting remains a concern, CLABSI validations conducted by SHDs provide an important impetus for improved reporting. SHDs are uniquely positioned to engage facilities in collaborative validation reviews that allow transparency, education and relationship building.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Surveillance; Evaluation; Healthcare Associated Infections (HAI)

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9080
Abstract Type	Breakout
Abstract Title	Validation of National Healthcare Safety Network (NHSN) Catheter Associated Urinary Tract Infection (CAUTI) Event Data in Tennessee

Abstract

BACKGROUND: Acute care hospitals (ACH) have been required to report Catheter-Associated Urinary Tract Infections (CAUTI) to the Tennessee Department of Health (TDH) through the National Healthcare Safety Network (NHSN) since January 2012. TDH conducted a validation of NHSN CAUTI data to assess data quality and identify common reporting errors or misconceptions among Tennessee facilities.

METHODS: NHSN's External Validation Toolkit was used to guide TDH's validation work. The tools (methods, letters, forms, survey, etc.) were converted into electronic versions using Research Electronic Data Capture (REDCap). Sixteen facilities were selected for validation during the evaluation time period (1/1/2016–6/30/2016). TDH targeted facilities with the highest number of predicted infections, stratified by SIR to identify potential over- and under-reporters of CAUTI events for Intensive Care Unit (ICU) and ward locations separately. Among the 16 facilities, 6 were selected for ICU only, 6 for wards only, and 4 facilities for both ICU and ward validation. Up to 20 reported CAUTI events and 40 eligible urine cultures were selected at random per location type. Cultures were eligible for selection even if collected during the present on admission (POA) timeframe (calendar days 1 and 2). Patient medical records, including documentation of indwelling urinary catheters, symptoms, location within the facility, and laboratory records, were reviewed to determine if CAUTI criteria were met.

RESULTS: Of the 4,460 urine cultures submitted to TDH by the 16 selected facilities, 78% represented urine cultures collected during the POA timeframe with no other eligible specimens for the patient during the admission. Using the medical record selection strategy from the NHSN toolkit, TDH reviewed 784 eligible cultures; 407 of these were single cultures for a patient, collected during the POA timeframe. TDH identified 125 reportable CAUTI events; 23% were reported with errors and 11% were not reported at all. The most common error was incorrect event date (79%). TDH also identified six reported events that did not meet CAUTI criteria. In post-validation interviews with infection preventionists, TDH identified gaps in understanding of the infection window period, as well as defining event date.

CONCLUSIONS: In order to address reporting errors, TDH developed CAUTI specific case studies to provide additional education and practice. CAUTI validation provided insight into surveillance practices and opportunities for education. TDH recommends modification of the medical record selection strategy from the NHSN toolkit to eliminate admissions that only have one urine culture within the POA timeframe, as these specimens cannot meet CAUTI criteria.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Data Collection; Healthcare Associated Infections (HAI); Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9626
Abstract Type	Lightning
Abstract Title	Cluster of Carbapenem-Resistant <i>Pseudomonas Aeruginosa</i> Infections Related to Care at an Outpatient Urology Clinic – Arkansas, 2016

Abstract

BACKGROUND: Multidrug-resistant *Pseudomonas aeruginosa* infections are listed as a serious threat in the Centers for Disease Control and Prevention’s publication, “Antibiotic Resistance Threats in the United States, 2013”. As such, clusters of these infections are prioritized for investigation and control. In November 2016, staff at an Arkansas acute-care hospital recognized a recent increase of positive cultures with imipenem-resistant *P. aeruginosa* from a recently acquired outpatient urology clinic. The Arkansas Department of Health (ADH) conducted an outbreak investigation to identify a potential source and provide recommendations to prevent further transmission.

METHODS: On December 13, 2016, staff from ADH completed an onsite visit at the clinic. Staff toured the facility to see how the patient rooms were organized as well as how medical instrumentation and supplies were stored and reprocessed, particularly cystoscopes. Medical charts were reviewed to help determine exposures, and line lists of all positive cultures submitted by the clinic to the hospital’s microbiology lab in the past year were collected to determine historical patterns.

RESULTS: Eight patients were identified with imipenem-resistant *P. aeruginosa* urinary tract infections with a common susceptibility pattern, and of those eight, two developed bloodstream infections and were hospitalized. In addition, two additional patients with *P. aeruginosa* urinary tract infections with a very similar susceptibility pattern were also included in the analysis. Two isolates were sent to the state Public Health Laboratory for pulsed-field gel electrophoresis (PFGE) testing which showed that they had indistinguishable patterns. The cluster was determined to have begun in July 2016 when the average number of urinary tract infections with imipenem-resistant *P. aeruginosa* rose to 2-3 infections a month from 0 infections a month. The major risk factor for the increase in these infections appeared to be having had cystoscopy (9 of 10 cases). Reprocessing of cystoscopes was improperly performed within the clinic, utilizing non-standard procedures and home-made equipment. Recommendations were provided based off findings from the visit and data analysis. Infection rates dropped to baseline once standard reprocessing recommendations were implemented.

CONCLUSIONS: This outbreak investigation revealed a potential source of transmission of imipenem-resistant *P. aeruginosa* infections within an Arkansas outpatient urology clinic due to improper reprocessing of cystoscopes. No additional imipenem-resistant *P. aeruginosa* infections have been reported. This investigation highlights the importance of proper device reprocessing in outpatient clinics.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infection Control; Outbreaks; Antimicrobial Resistance
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9367

Abstract Type Lightning

Abstract Title Health Care-Associated Infection and Emerging Pathogen Surveillance — Idaho, 2016–2017

Abstract

BACKGROUND: On any given day, approximately 1/25 U.S. acute care hospital inpatients has ≥ 1 nosocomial infection (2014 estimate). Certain hospitals are federally mandated and others voluntarily report select health care-associated infections (HAIs) to the National Healthcare Safety Network (NHSN). While HAIs and most associated pathogens are not specifically reportable in Idaho, certain hospitals voluntarily share NHSN data with the Idaho Division of Public Health (IDPH). We evaluated the utility of NHSN data for HAI and emerging pathogens surveillance by IDPH.

METHODS: HAIs occurring in Idaho during January 2016–June 2017 and reported to NHSN by November 17, 2017 were included. We described NHSN participation by hospital type; Centers for Medicare and Medicaid Services-designated critical access hospitals (CAHs), which are rural, versus non-CAHs. Using descriptive statistics, we evaluated report timeliness, pathogen and antimicrobial-resistant pathogen field completeness, and proportion of possible *Candida auris* infections, by HAI type.

RESULTS: 22.2% (6/27) of CAHs and 52.6% (10/19) of non-CAHs share NHSN reports with IDPH, representing 24.3% (132/544) of CAH beds and 90.3% (2471/2736) of non-CAH beds. Two-thirds (4/6) of CAHs and 100% (10/10) of non-CAHs reported on surgical site infections (SSIs), catheter-associated urinary tract infections (CAUTIs), and central line-associated bloodstream infections (CLABSIs). HAI reporting times ranged from median 36–105 days by infection type. Pathogens were identified for 100% of CAUTI (92/92) and CLABSI (61/61), and 77.5% (100/129) of SSIs, consistent with internal NHSN data controls. Antimicrobial-resistant pathogens were identified in 4.3% (4/92), 6.6% (4/61), and 9.0% (9/100) of CAUTI, CLABSI, and SSI, respectively. Unspiciated *Candida* was identified in 2.0% (2/100) of SSI.

CONCLUSIONS: Increased CAH participation would improve rural facility HAI surveillance representation. Reporting is timely, and data are complete, which supports using NHSN data for HAI and certain emerging pathogen surveillance. IDPH could update their statewide surveillance plan to reflect these findings.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Emerging Infections; Healthcare Associated Infections (HAI); Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9726

Abstract Type Lightning

Abstract Title MRSA Outbreak Among Patients at an Ambulatory Surgery Center

Abstract

BACKGROUND: Methicillin-resistant *Staphylococcus aureus* (MRSA) is a multidrug-resistant organism that can cause infections in a number of somatic sites. Ambulatory surgery centers (ASCs) are healthcare settings that can provide one or more services such as same-day surgical care, diagnostic services, and preventative procedures. Unsafe injection practices increase the risk of transmitting MRSA and other pathogens. On October 12, 2017, the Louisiana Department of Health (LDH) was notified of four patients who got MRSA infections after receiving steroid injections from the same ASC. LDH epidemiologists completed an investigation to review cases, confirm laboratory evidence, identify infection control breaches, and offer recommendations to prevent further transmission.

METHODS: Cases were identified by two acute care hospitals from October 7-10, 2017 and reported by a pathologist that reviewed results on patients at both facilities. The ASC was noted to be an orthopedic center whose services include general orthopedics, joint replacement, and other procedures. LDH epidemiologists conducted chart reviews for each case. Three patients had wound infections wherein cultures were obtained from the knee for Patient 1, hip for Patient 2, and shoulder for Patient 3. The fourth patient's infection was cultured from urine. The Louisiana Public Health Laboratory performed pulse field gel electrophoresis (PFGE) on remaining isolates to review genetic fingerprinting.

RESULTS: PFGE revealed the same band pattern for all isolates. Epidemiologists performed an on-site visit to the ASC to speak with facility leadership, tour the clinic, and perform a modified infection control assessment. All patients were seen by different physicians and clinic staff are shared between doctors. The facility has two medication casting rooms that are shared between providers, and three of the four patients were injected with medications that were drawn by technicians who utilized the same room. Each physician had different procedures for medications handling, and no technicians were noted to be sick. Training for technicians is on-the-job and no certification is required for performing job duties. The clinic discarded vials used for patients; therefore, medications testing was unavailable for the investigation.

CONCLUSIONS: The causal pathway was unable to be determined due to poor record keeping and discarded medications. Recommendations by LDH included the following: 1) auditing injection practices with spontaneous direct observations; 2) standardizing infection control education to be offered upon hire and at least annually; 3) updating medications logs to include persons who drew medications; and 4) maintaining infection control policies that should be reviewed at least annually.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infectious Diseases; Antimicrobial Resistance; Infection Control

Consider for Different Presentation? Yes

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State Public Health Agency

Submission Type Breakout/Quick/Lightning/Poster

ID 9867

Abstract Type Lightning

Abstract Title National Healthcare Infection Control Assessment and Response on-Site Facility Assessment Findings and Lessons Learned

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) Infection Control Assessment and Response (ICAR) Program provided funding from 2015 to 2018 for health departments to expand their outreach to healthcare facilities. Part of the outreach involved on-site assessments of infection prevention (IP) policies and practices in facilities across the continuum of care. ICAR assessments aimed to identify gaps in policies and practices, inform training and resource development, and strengthen partnerships between facilities and public health departments.

METHODS: Funded health departments prioritized and recruited acute care, long-term care, outpatient, and/or hemodialysis facilities to receive on-site ICAR assessments based on local determinations. Assessments were conducted using standardized, setting-specific tools assessing infection prevention policies and practices in eleven domains. Health departments submitted de-identified, aggregate data on identified gaps to CDC on a quarterly basis. CDC compiled the aggregate data into a national gap summary.

RESULTS: Between October 2015 and July 2017, 50 health departments completed 3,365 ICAR facility assessments in 970 acute care facilities, 1,463 long-term care facilities, 426 outpatient facilities, and 506 hemodialysis facilities. Identified infection control gaps common across settings include competency-based training, routine audits of adherence to recommended practices, and feedback from audits to personnel. In the acute care setting, for example, more than half of assessed facilities (63%, n=611) did not have a competency-based training program for insertion of urinary catheters. The majority of acute care facilities (72%, n=697) did not routinely audit adherence to recommended practices for insertion of urinary catheters and 665 (69%) facilities did not provide feedback from audits to personnel. ICAR assessments identified additional setting-specific challenges such as lack of IP expertise in long-term care and outpatient facilities, including outpatient hemodialysis facilities.

CONCLUSIONS: On-site ICAR assessments have identified multiple opportunities to improve infection prevention practices and to augment available training and resources. ICAR visits have enabled health departments to create and/or strengthen relationships with providers beyond the acute care setting and with state/local partners such as Quality Improvement Organizations. They have also helped health departments build assessment capacities that are critical to other core functions such as outbreak investigation.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infection Control; Healthcare Associated Infections (HAI)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9738

Abstract Type Lightning

Abstract Title Respiratory Syncytial Virus Outbreak in a Neonatal Intensive Care Unit

Abstract

BACKGROUND: Respiratory syncytial virus (RSV) is a common virus that causes cold-like symptoms, lower respiratory tract infections, and is the major cause of bronchiolitis and pneumonia in children younger than one year of age. On December 15, 2017 the Louisiana Department of Health (LDH) was notified of seven neonatal intensive care unit (NICU) patients with RSV at the same facility. LDH epidemiologists conducted an investigation to identify additional cases, potential breaches in infection control, and to recommend infection control measures to prevent further transmission.

METHODS: LDH epidemiologists collaborated with Centers for Disease Control and Prevention (CDC) colleagues in the Division of Viral Diseases (DVD) and the Division of Healthcare Quality Promotion (DHQP) to develop a medical chart abstraction form. On December 18th, LDH epidemiologists conducted a site visit to complete chart abstractions for each case, assess facility protocols, tour NICU locations, and review infection control practices. Hospital RSV laboratory results were not distinguished between RSV A and B. Swabs for each of the infants were sent to CDC for additional testing and whole genomic sequencing.

RESULTS: The facility has 6 NICU locations, and each baby on each location has private rooms regardless of infectious status. One RSV-infected infant was located on Unit A, another on Unit B, and five on Unit C. Neonates had symptoms that onset between December 5th and December 15th. The baby on Unit A was admitted with RSV, and two infants (Unit A and one on unit C) were visited by ill family members. Six babies were pre-term with gestational ages at birth that ranged from 25 to 36.9 weeks. The hospital conferred the following documents for review: palivizumab administration guidelines, visitation policies, infection control manual, maps of all NICU locations, and action items taken by the hospital. Staff showed epidemiologists personal protective equipment (PPE) availability, staff cohorting efforts, and daily and terminal cleaning procedures. Results of CDC testing showed that all specimens were detected with RSV-B and low cycle threshold (Ct) values indicating high viral load.

CONCLUSIONS: Additional RSV transmission was not identified. LDH offered recommendations to the facility that fell within several infection control domains: 1) timely reporting and public health coordination; 2) restricting visitation by children younger than 12 years of age; 3) increasing hand hygiene stations; 4) transmission-based precautions; 4) PPE use for staff and visitors; and 5) precautions for consult visits.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Respiratory Diseases; Healthcare Associated Infections (HAI); Infection Control

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9443
Abstract Type	Lightning
Abstract Title	Statewide Validation of the CDC's Core Elements of Hospital Antimicrobial Stewardship Programs

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) outlined seven Core Elements of Antimicrobial Stewardship that acute care hospitals should implement. The Tennessee Department Health (TDH) sought to gain better understanding of Antibiotic Stewardship Programs (ASP) in Acute Care Hospitals in Tennessee. Prior to this study, TDH used the National Healthcare Safety Network's (NHSN) Annual Facility Survey to gauge stewardship progress. Facilities self-reported stewardship progress based on core element achievement. Infection preventionists (IPs) usually complete this survey but may not always be the most informed about stewardship programs or may not have conferred with ASP facility champions. In June 2017, TDH distributed a longer, more in-depth assessment targeting ASP champions in the Acute Care Hospital setting and expanded upon the NHSN Annual Survey.

METHODS: TDH expanded the 12 NHSN stewardship questions into 76 detailed questions based on interventions listed in the National Quality Forum's Playbook on Antibiotic Stewardship in Acute Care. TDH identified key stewardship contacts at each facility and distributed the survey electronically via Research Electronic Data Capture (REDCap). Follow up phone calls were made to non-responders.

RESULTS: 93 facilities (83%) completed the validation survey in its entirety. Based on this survey, all facilities achieved five or more Core Elements, while 98% had 5 or more core elements in the NHSN survey. TDH found that 87.1% of facilities met all seven elements, but only 64.5% had achieved all seven Core Elements per NHSN. Individual Core Element agreement between NHSN and TDH ranged from 80.6% to 100.0%. The most common agreed upon element was Action (100.0%), while Reporting had the least agreement (80.6%). For 83.6% of the discordant results, TDH concluded that facilities were meeting the element, but NHSN had not. In only 9 instances (1.4%) did facilities report to NHSN that a core element was met, when TDH concluded they had not.

CONCLUSIONS: Although there was generally good agreement between the self-reporting to NHSN and TDH, gaps between the surveys were still identified. Targeting stewardship champions and offering more robust options likely explains the conflicting results. Additionally, this validation survey was conducted mid-July 2017, while NHSN assessed 2016 activities. TDH gained a more granular understanding of ASPs in Tennessee, including how facilities met Core Elements. This information will be used to tailor TDH's outreach and support of antimicrobial stewardship.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Epidemiology
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10302

Abstract Type Lightning

Abstract Title Survival of Patients Infected with Candida Auris in New York State

Abstract

BACKGROUND: The New York State Department of Health (NYSDOH) has been actively working with hospitals, nursing homes, and laboratories to identify and investigate patients infected with *Candida auris* since the second half of 2016. Information on mortality associated with this newly emerging pathogen is needed to support clinical and public health practice.

METHODS: A clinical case was defined by culture positive for *Candida auris* from any specimen collected to diagnose or treat disease. Cases identified through September 2017 were followed until death or December 2017. The primary outcome was death within 90 days of first positive specimen. Risk factors included patient age, gender, specimen source, and resistance to two or more classes of antifungals. Survival was evaluated using Kaplan-Meier curves and Cox regression.

RESULTS: Of the 98 cases, 53 died within the first 90 days, and 9 were lost to follow-up. The probability of surviving past 30, 60, and 90 days was 66%, 54%, and 44%, respectively. The 55 patients with blood infections and 15 patients with urine infections were 3.0 and 2.5 times more likely to die than patients with other infections. Age, gender, and resistance did not significantly predict mortality.

CONCLUSIONS: Blood and urine *Candida auris* infections were associated with high death rates, however, many of the patients may have had other serious illnesses that also increased their risk of death. NYSDOH continues to aggressively work with facilities to reduce the spread of *Candida auris*.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Emerging Infections; Surveillance; Healthcare Associated Infections (HAI)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9242

Abstract Type Poster

Abstract Title Carbapenem-Resistant Enterobacteriaceae (CRE) Outbreak in the U.S. Virgin Islands, March 2017

Abstract

BACKGROUND: Carbapenem-resistant *Enterobacteriaceae* (CRE) continue to be a major public health concern due to treatment difficulty, resulting in high mortality rates. CRE is not a notifiable condition in the U.S. Virgin Islands (USVI). The following describes an outbreak of CRE cases reported by a single facility in March 2017.

METHODS: A confirmed CRE case is defined as a patient whose isolate yields an *Enterobacteriaceae* *an confirmere* resistant to any carbapenem (imipenem, meropenem, doripenem or ertapenem) or documentation that the isolate possess a carbapenamase. We investigated reports of 8 laboratory confirmed CRE between March 4 and March 31, 2017. Community-acquired (CA) were defined if CRE was present on admission or before the fourth hospital day. Hospital-acquired (HA) cases were defined as present on or after the fourth hospital day. We conducted retrospective chart review to collect patient demographic, risk-factor data, lab tests results and patient outcome.

RESULTS: Of the 8 cases reported, 75% (n=7) were male. Median age was 64 years (range: 33–89); 6 (75%) patients were 55 years of age or older. Half (4, 50%) of all cases were identified as HA. Among HA cases, median length of stay was 56 days ($\bar{x}$ =89), compared to 6 days ($\bar{x}$ =8) in the CA group. All (4, 100%) patients in the HA group had at least two invasive devices placed during hospitalization, compared to 75% (n=4) in the CA group. Presence of diabetes was two times higher in the HA group (50%) than in the CA group (25%). All HA cases had at least one wound, underwent a surgical procedure and stayed in the intensive care unit (ICU). This is compared to 1 (25%) wound, no surgery, and 1 (25%) ICU stay in the CA group. Overall, the most common CRE isolated were *Enterobacter* spp (n=3, 37.5%), followed by *Klebsiella* spp (n=2, 25%); 2 cases were identified as carbapenamase-producing CRE (CP-CRE).

CONCLUSIONS: Most cases had at least one known risk factor for CRE including ≥ 1 invasive devices, surgical procedures, diabetes, and ICU stay. There was a 2-fold increase of multi-drug resistant HA infections in March compared to February, and a 6.5-fold increase compared to January. During this same period, facility-reported hand hygiene compliance rate declined by 10%. Ongoing efforts should focus on evidence-based practices in infection control to help prevent further outbreaks.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Antimicrobial Resistance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9158

Abstract Type Poster

Abstract Title Changing Epidemiology of *Clostridium Difficile* Reporting

Abstract

BACKGROUND: Lab reports indicating *Clostridium difficile* (*C.difficile*) are submitted to the Nebraska Department of Health and Human Services (NDHHS) through the National Electronic Disease Surveillance System (NEDSS). Reports have increased from 31/100,000 in 2010 (N=565) to 115/100,000 (N=2,177) in 2016. Culture independent diagnostic testing (CIDT) accounted for 15% (N=84) of reports in 2010 and 70% (N=1,523) in 2016. NDHHS investigated a subset of positive CDI reports from the NEDSS to better understand the epidemiology and improve surveillance.

METHODS: A case investigation form was developed incorporating demographics and patient history. In July 2017, the first 100 positive lab results reported electronically were extracted from NEDSS. Researchers defined a case of *C. difficile* infection (CDI) as a positive *C. difficile* toxin assay (PCR, EIA) stool specimen from a patient (>1yo) with reported diarrhea. Researchers dichotomized CDC's Emerging Infections Program's definitions and assigned each case inpatient status (HCFO, CO-HFCA) or outpatient status (CA). Frequencies of demographic and clinical variables were performed. Fisher-exact analysis compared risk factors between inpatient and outpatient groups. Analysis was completed using SAS, EpiInfo, and Microsoft Excel.

RESULTS: Out of 100 reports, 84 met the case definition. Among inpatients (60.71%, N=51), ages ranged from 11 to 93 years (median = 62), and 45.10% (N=23) were male. Forty-four cases (88%) reported antibiotic exposure, and eight (25%) reported proton pump inhibitor (PPI) use. Testing included EIA only (5.88%, N=3), PCR only (64.71%, N=33), and reflex confirmatory test (29.41%, N=15). Among outpatients (39.28%, N = 33), ages ranged from 1–98 years (median = 60), and 30.3% (N=10) were male. Twenty-three cases (27.38%) reported antibiotic exposure and nine (39.13%) reported PPI use. Testing included PCR alone (52%, N=62), EIA alone (10.71%, N=9), and reflex confirmatory test (23%, N=6). Chi-square analysis comparing antibiotic and PPI use between inpatients and outpatients found an OR of 3.19 (1.03–9.87), and 0.52 (0.16–1.65) respectively.

CONCLUSIONS: Due in large part to CIDT, CDI reports in Nebraska have nearly tripled over the last six years. Using our case definition, 16% of reports were found not to be clinically compatible with illness. Older age, female predominance, antibiotic exposure, PPI use, and PCR-testing majority are consistent with other CDI investigations. More than half the cases were inpatients and had an increased odds of antibiotic exposure. This investigation identified opportunities for stewardship and alternative CDI surveillance systems including the Syndromic Surveillance database and hospital discharge data sets.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9163

Abstract Type Poster

Abstract Title Development of an Inter-Facility Transfer Form for Infection Control- Nebraska, 2017

Abstract

BACKGROUND: It is estimated that, with concerted efforts and proven strategies, up to a 70% reduction in healthcare-associated infections (HAIs) is possible, saving tens of thousands of lives annually. Despite increasing use of electronic records, healthcare facilities frequently fail to communicate infection control needs to other facilities upon patient transfer. The Nebraska Department of Health and Human Services (NDHHS) developed a communication tool to emphasize the need for personal protective equipment (PPE) and specific infection control measures at the time of inter-facility transfer.

METHODS: Three versions of transfer forms (from the Centers for Disease Control and Prevention, Utah Department of Health, and Chicago Department of Public Health) were reviewed by the Nebraska HAI Advisory Council. Based on this review, an inter-facility transfer form was developed and distributed for review of clarity and quality to the Nebraska HAI Advisory Council and to select health care providers, including public health nurses, physicians, and infection prevention specialists from a variety of patient care settings.

RESULTS: All stakeholders emphasized the importance of 1) simplicity and ease of use by a wide range of discharge staff; 2) readily understood, intuitive images; 3) minimal time necessary to complete at discharge; 4) ease of incorporation into the patient chart; and 5) preservation of confidentiality so that no disease-specific information would appear on the front of the form and expressed the lack existing resources to communicate this information. After four months of collaboration to incorporate these priorities, NDHHS developed a novel inter-facility form based on simplicity and imagery. The front of the form features checkboxes next to images of PPE to indicate necessary protection for the provider, as well as a place for previous-provider contact information. The back of the form lists potential communicable diseases to guide a receiving facility in terms of appropriate isolation protocols. The form is posted on the NDHHS website as a free tool for hospitals, emergency services personnel, long-term care facilities, and local health departments.

CONCLUSIONS: The provision of information about the presence of organisms requiring particular precautions upon arrival of a patient at a new facility is critical to aid in the prevention of HAIs and the transmission of resistant organisms. NDHHS engaged key partner organizations to gather valuable input in the development of a simplified tool for effective communication during patient transfers. An inter-facility transfer form is an easy and freely accessible method to communicate this information at the point of transfer.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infection Control; Communication

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9494
Abstract Type	Poster
Abstract Title	Epidemiology of New Delhi Metallo- β -Lactamase-Producing Carbapenem-Resistant Enterobacteriaceae in Chicago, Illinois, 2013-2017

Abstract

BACKGROUND: Since November 2013, carbapenem-resistant *Enterobacteriaceae* (CRE) are reportable to the Illinois Extensively Drug Resistant Organism (XDRO) Registry. Resistance mechanism is captured in the registry for isolates tested using molecular methods. New Delhi metallo-beta-lactamase-producing CRE (NDM-CRE) are emerging in the United States. Understanding the local epidemiology of NDM-CRE is needed to improve regional response to this urgent threat.

METHODS: Patients with NDM-CRE in Illinois were identified by clinical laboratories using molecular methods, point prevalence surveys conducted by the Chicago Department of Public Health (CDPH) in response to clusters, or as part of an ongoing project to understand carbapenemase-producing CRE prevalence in high-risk healthcare settings in the Chicago region. Chicago patients with NDM-CRE reported to the XDRO registry are investigated by CDPH to identify risk factors present within 6 months of culture collection and implement infection control measures to prevent further transmission. Descriptive statistics were performed on reports from epidemiologic investigations conducted from November 2013 to December 2017.

RESULTS: Since November 2013, 36% (959/2672) of CRE-positive specimens collected from Chicago patients and reported to the XDRO Registry were tested using molecular methods; NDM-CRE were isolated from 43 (5%) patients. Patient median age was 66 years (range, 21-92 years); 26 (61%) were female. The annual number of NDM-CRE first reported increased from 2 in 2014 to a peak of 21 in 2017. Twenty-two (51%) NDM-CRE were identified from clinical cultures (16 urine, 3 blood, 2 sputum, 1 tissue) and 21 (49%) from screening cultures. Among 39 patients with risk factor history obtained, 9 (23%) were recently hospitalized outside the U.S., including only 1 patient in 2017. Among 30 patients without travel, 23 (77%) had recent stays at a high-acuity long-term care facility (HA-LTCF) or long-term acute care hospital (LTACH). Five (13%) patients had no recent overnight stays at an Illinois healthcare facility; all 5 patients had a history of foreign travel. Three (8%) patients had undergone endoscopy, 16 (41%) had other invasive procedures, 17 (44%) were mechanically ventilated, 20 (51%) had a tracheostomy, and 20 (51%) had a gastrostomy tube.

CONCLUSIONS: All investigated patients with NDM-CRE had a history of foreign travel or overnight healthcare stay, suggesting community transmission in the Chicago region is not common. Stays in a HA-LTCF or LTACH were present among more than 75% of individuals with NDM-CRE and no foreign travel, underscoring the need for infection control training and surveillance of carbapenemase-producing CRE in these settings.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Emerging Infections; Healthcare Associated Infections (HAI); Local Epidemiology
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9828

Abstract Type Poster

Abstract Title Evolution of Elc Healthcare-Associated Infections/Antimicrobial Resistance (HAI/AR) Programs, 2009-2018

Abstract

BACKGROUND: Since 2009, health departments have received funding and other support from CDC's Division of Healthcare Quality Promotion (DHQP) as part of the Epidemiology and Laboratory Capacity Cooperative Agreement (ELC). The original objective of this support was building and sustaining State programs to prevent healthcare-associated infections, in line with overall ELC goals.

METHODS: We reviewed internal CDC/DHQP programmatic documents and other records to summarize goals, sources and amounts of funding, scopes of work, staffing support and related characteristics in order to describe the overall evolution of HAI/AR Programs from 2009 to the present.

RESULTS: In 2009, 51 programs (49 states plus DC and Puerto Rico) were funded using a \$40 million investment from the American Recovery and Reinvestment Act. This initial funding provided support for an HAI Coordinator staff position and required the formation of a multidisciplinary advisory groups; these efforts were enhanced by a separate requirement for each state to develop an HAI Plan to maintain eligibility for Preventive Health and Health Services Block Grant funds. Through the Affordable Care Act of 2010, funding was maintained at roughly baseline levels, with expansion of program goals related to non-acute care settings. During the current 5-year ELC cycle, which began in 2014, the goals and scope of the HAI/AR Programs have grown to include antibiotic stewardship as well as prevention and containment of novel pathogens and emerging AR threats. The 2015 Ebola Supplement (\$85 million) included Ebola and other preparedness elements, HAI Plan revisions, outbreak reporting and response capacity assessments, and on-site infection control assessments in >3000 healthcare facilities. Regular ELC HAI/AR Program funding reached new levels beginning in 2016 with funds appropriated to CDC as part of the National Action Plan for Combating Antibiotic-Resistant Bacteria; over \$110 million was disbursed over project years 3 and 4. Currently, there are 57 HAI/AR programs with over 500 staff positions that are at least partially funded through the ELC mechanism. Funding now offers support for the HAI Coordinator as well as AR Expert and AR Laboratory Expert positions.

CONCLUSIONS: ELC-funded HAI/AR programs have grown substantially over the ten years of their existence, as reflected in major increases in funding, staffing, and scope. This growth has increased local capacities to eliminate HAI and prevent the spread of AR threats. Increased attention to performance measurement and evaluation is needed to better demonstrate the value of these programs going forward.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Epi / Lab Capacity (ELC); Infection Control; Antimicrobial Resistance

Consider for Different Presentation? No

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9917
Abstract Type	Poster
Abstract Title	Impact of Infection Control Assessment and Response (ICAR) Team on Infection Control Programs in Acute Care Hospitals in Nebraska

Abstract

BACKGROUND: Limited data is available to assess the effectiveness of the Infection Control Assessment and Response (ICAR) program on improving infection prevention (IP) practices in healthcare facilities. We studied the effectiveness of the Nebraska ICAR team intervention model (peer-to-peer feedback and coaching using evidence-based guidance) on mitigating IP gaps in acute care hospitals (ACH).

METHODS: Nebraska ICAR program, also known as Nebraska Infection Control Assessment and Promotion Program (ICAP), working in conjunction with the Nebraska Department of Health and Human Services Healthcare-Associated Infections Program, conducted on-site assessments of infection control programs in ACH between 11/2015 and 9/2016. Following the assessments, subject matter experts provided individualized and prioritized evidenced-based recommendations for improvement to each facility based on their identified IP gaps. Follow-up phone assessments were conducted between 03/2017 and 11/2017 with the ACH infection preventionists one year post visit to evaluate improvement as well as factors promoting or inhibiting the implementation of recommendations.

RESULTS: Overall, 45 ACH were assessed. The top 5 IP categories requiring improvement were risk assessments (22 of 45 ACH, 49%), medical supply & linen storage (44%), high-level disinfection (42%), surveillance (40%) and audit & feedback practices (36%). Follow-up assessments were completed for 268 recommendations in 32 ACH (including 30 critical access hospitals). Recommendations ranged from 3 to 21 per ACH (median=9). Most (80.2%) recommendations had been implemented (61.2% completely and 19.0% partially) by the ACH. ICAP visit and the provided resources were identified as the main reason for many of the successful implementations. For example, 71% of the 14 ACH that needed to improve high-level disinfection processes and documentation indicated that the ICAP visit facilitated the implementation. The most commonly cited barriers to implementation included lack of staffing and administrative support. For example, 66.7% (12 of 18) hospitals conducted an IP risk assessment after ICAP recommendations but lack of personnel to implement the recommendation was indicated as the barrier by three (50%) of the remaining six hospitals. When recommendations were completely implemented (n= 164), implementation methods most frequently involved additional staff training (n=41), review of policies and procedures (n=32), implementing audit (n=23) and feedback (n=18) programs and improved training with competency assessment (n=11).

CONCLUSIONS: The Nebraska ICAR model for IP gap mitigation, prioritized to the unique needs of the surveyed facilities, resulted in implementation of most recommendations and overall improvement of infection control programs in our state.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infection Control; Prevention; Evaluation
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10359

Abstract Type Poster

Abstract Title Improving Coordination of Response for Category B Infectious Breaches

Abstract

BACKGROUND: The state Healthcare Associated Infections Program (HAIP) and state regulators have different goals in responding to infectious lapses identified in healthcare facilities. Siloed responses have occasionally led to inconsistency, tension, and adverse media coverage. We identified a need for improving communication and standardizing departmental responses to healthcare associated infectious risks to ensure regulatory compliance, address potential patient harm, and provide assistance for achieving best practices for infection prevention.

METHODS: The HAIP and state regulators developed a new process, flow chart and templates for communicating about and responding to infectious lapses. The HAIP communicates to regulators any infectious lapse that occurs in a state or CMS-licensed facility. Regulators communicate to the HAIP any infectious lapse that may pose an infection risk to patients. Email and letter templates are used to standardize communications between programs and between the HAIP and healthcare facilities.

RESULTS: The new process for communication regarding and responding to infectious breaches was piloted in 2017. We will share the flowchart and templates. The process has improved communication between programs and standardized the public health response to these lapses.

CONCLUSIONS: Infectious lapses identified by state regulators, reported to the HAIP by facilities or local health, and identified during Infection Control Assessment and Response on-site assessments are handled in a standardized manner.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infection Control; Collaboration; Communication

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9653

Abstract Type Poster

Abstract Title Methicillin-Resistant *Staphylococcus Aureus* Trends Using Hospital Discharge Data in Washington State, 2010-2016

Abstract

BACKGROUND: Methicillin-resistant staphylococcus aureus (MRSA) is a prevalent multidrug resistant organism that impacts the care and outcomes of hospitalized patients. Since 2010, hospitals in Washington State have been required to report MRSA in hospitalized patients using the Department of Health's (DOH) Comprehensive Hospital Abstract Reporting System (CHARS). Furthermore, hospitals must test patients in the adult or pediatric intensive care unit for MRSA within twenty-four hours of admission. We conducted a seven-year review of statewide MRSA infection and colonization trends in hospitalized patients.

METHODS: Hospital discharge data from 106 unique hospitals in Washington State were accessed for the years 2010 to 2016 through CHARS. ICD-9 and 10 discharge diagnosis codes were classified as MRSA non-infection or infection. Non-infection codes included carrier or suspected carrier of MRSA and personal history of MRSA. Those that indicated infection were MRSA sepsis, pneumonia, unspecified, or classified elsewhere. Discharges were not limited to one diagnosis, but a discharge of multiple infections were counted as one MRSA discharge. Incidence rates were calculated based on person-years at risk. Deduplication was performed based on last name, first name, date of birth and year of discharge to limit one discharge per individual per year.

RESULTS: A MRSA diagnosis was identified in 90,267 (2.0%) hospital discharges from 2010 to 2016. For 2010, the incidence of MRSA infection and non-infection discharge diagnoses was 8.4 and 8.9 per 1,000 discharges, respectively. By 2016, MRSA infections decreased to 7.2 per 1,000 discharges, while non-infections increased to 15.4 per 1,000 discharges. The age group with the highest MRSA infection incidence was 40-54 years, averaging 13.1 (range: 12.6 to 13.8) per 1,000 discharges throughout the study period. For patients ≥ 70 years, infection incidence dropped from 10.3 per 1,000 discharges in 2010 to 6.3 per 1,000 discharges in 2016. Males had four more infections per 1,000 discharges than females throughout the study period. The majority (53.7%) of patients with a MRSA infection were discharged home, but 20.4% went to skilled nursing facilities and 15.6% went to other healthcare facilities.

CONCLUSIONS: The use of statewide hospital discharge data is a viable option for analyzing hospitalizations impacted or caused by MRSA. With the proportional breakdown of infection versus colonization discharges shifting towards the latter, it's paramount to understand the infection control implications of MRSA colonization. Additionally, with the preponderance of infections identified in males and in those aged 40-54, education can be better targeted to those most at risk.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Hospital Data; Healthcare Associated Infections (HAI)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9296

Abstract Type Poster

Abstract Title Vermont's ICAR Experience

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) developed the Infection Control Assessment and Response (ICAR) toolkit to guide health departments during non-punitive, on-site assessments of infection control capacity in hospitals, long-term care facilities (LTCFs), dialysis centers, and outpatient clinics in a comprehensive and systematic way. The tool itself comprises a series of yes or no questions, direct observation auditing tools, and evidence-based guidance and resources to improve identified gaps. The utility of ICARs was assessed for making improvements in infection control across the state.

METHODS: Facilities were recruited by the Healthcare-Associated Infection (HAI) Coordinator, and ICAR visits were conducted on a voluntary basis beginning in 2015. The Vermont Department of Health (VDH) has conducted a total of 30 ICARs in 12 hospitals (8 critical access and 4 acute care), 16 LTCFs (2 psychiatric facilities, 1 residential care facility, and 13 nursing homes), 1 dialysis center, and 1 outpatient clinic. The results were analyzed by facility type, and the gaps were addressed in three phases: 1) on-site immediate education and feedback, 2) resource distribution and planning, and 3) presenting results and implementing education opportunities and trainings. Additional ICAR reassessments also were conducted upon facility request to track progress, or in response to Infection Preventionist (IP) turnover.

RESULTS: The most frequent gaps identified were in the areas of competency-based training programs, routine audits, and providing feedback to personnel. The domains with the most gaps were hand hygiene, personal protective equipment (PPE), injection safety, environmental cleaning, and antibiotic stewardship for both hospitals and LTCFs. In addition, urinary catheter care and central venous catheter care were identified as gaps in hospitals. ICAR reassessments suggested programmatic improvements; however, tasks such as training, auditing, and feedback for which the IP is solely responsible had varying results based on the IP's experience level.

CONCLUSIONS: ICAR visits have been useful tools to enhance relationships between VDH and various facilities across the state. Results from ICAR analyses have helped influence VDH programmatic decisions and will lead to targeted educational initiatives across the state. Continued initial and ICAR reassessments are recommended and considered a valuable contribution by the VDH HAI program.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Health Care; Infection Control

**Consider for
Different
Presentation?** Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9352
Abstract Type	Quick
Abstract Title	<i>Elizabethkingia Anophelis</i> Outbreak Among Ventilator-Dependent Patients at a Subacute Long-Term-Care Facility — Los Angeles, 2017

Abstract

BACKGROUND: Health care-associated *Elizabethkingia* outbreaks are uncommon. In July 2017, a subacute long-term-care facility (Facility A) notified the Los Angeles County Department of Public Health of 10 *Elizabethkingia* cases (baseline: 5.5 cases/year). We investigated possible infection sources and recommended control measures.

METHODS: A case was defined as *Elizabethkingia* isolated from any Facility A patient during January–October 2017 from cultures conducted by the facility. We reviewed medical records, interviewed staff, observed health care practices, sampled sinks, showers, and ventilators, and conducted whole-genome sequencing (WGS) on 8 available patient isolates.

RESULTS: We identified 18 *Elizabethkingia anophelis* cases from respiratory culture reports, including 4 infected and 14 colonized ventilator-dependent patients. Mean age was 70 years (range: 52–89 years). Median time from admission to positive culture was 140 days (range: 13–2,822 days). Other bacterial pathogens were concurrently isolated with *E. anophelis* from respiratory cultures in 14 patients. We observed ventilator parts reused between patients without cleaning and sterilization per manufacturer's instructions, ventilator storage in wet shower rooms, inadequate ventilator cleaning, and insufficient hand hygiene during tracheostomy care. *E. anophelis* was not isolated from sinks, showers, or ventilators. Water samples from 66% of 41 patient room, shower, and nursing station outlets had heterotrophic plate counts >500 CFU/mL, of which 52% were >3,000 CFU/mL. Chlorine residuals were low (range: 0–0.16 ppm). Seven of 8 patient isolates were closely related by WGS.

CONCLUSIONS: Multiple infection control lapses likely contributed to this *E. anophelis* outbreak. We recommended correcting respiratory care, ventilator equipment reprocessing, and hand hygiene practices, cohorting patients, and implementing water management actions. WGS strongly suggested a common source. High bacterial burden in water possibly limited *E. anophelis* recovery. Facilities should consider reviewing care practices for ventilator-dependent patients to prevent exposure to and transmission of *E. anophelis* and other respiratory pathogens.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9607
Abstract Type	Quick
Abstract Title	<i>A Stenotrophomonas Maltophilia</i> Outbreak Investigation at a Community Hospital — Assessment of Appropriate Antibiotic Use

Abstract

BACKGROUND: Excessively broad spectrum antibiotic use can be a risk factor for *Stenotrophomonas maltophilia* infection. The Tennessee Department of Health investigated the role of broad-spectrum antibiotic use in a community hospital *S. maltophilia* outbreak. Initial infection control and laboratory practices assessments at the hospital revealed no major infection control breaches or evidence of pseudo-outbreak.

METHODS: The stewardship outbreak response team consisted of three pharmacists, one epidemiologist and one physician. The team used a modified version of the Australian National Antibiotic Prescribing Survey (NAPS) for data collection during a one day visit to the facility. The tool was modified to retrospectively collect demographics, antibiotic use within 30 days prior to *S. maltophilia* isolation, clinical indications for antibiotic use, and other risk factors in the 60 days prior to organism isolation. The primary outcome was total days of therapy (DOT) of antibiotics and the proportion of antibiotic courses deemed inappropriate based on the NAPS tool, available clinical guidelines and clinical expertise. Statistical analyses were done using SAS 9.4.

RESULTS: Between April and September 2017, 21 patients with clinical cultures with *S. maltophilia* were identified. Six *S. maltophilia* isolates (29%) were pure isolates. The most common sources were lower respiratory (57%) and wounds (29%). Ten (48%) isolates were obtained after day ten of hospitalization. There were 476 total DOT, with patients receiving an average of 4.2 antibiotics (range 0–12) and 22.7 DOT (0–106). The most frequently prescribed antibiotics were vancomycin (67%), meropenem (57%), and ertapenem (24%). Courses of vancomycin and ertapenem were classified as inappropriate in 21% and 17% of patients, respectively, compared to 73% of meropenem courses. The most common reasons for inappropriate prescribing were an excessively broad spectrum and incorrect dosing. All-cause mortality was 19%.

CONCLUSIONS: Focusing on stewardship practices during an outbreak investigation provided a unique opportunity to evaluate appropriateness of antimicrobial use in one community hospital. We observed high use of carbapenems and anti-MRSA therapies which are both known risk factors for *S. maltophilia* infection. Many of these cases were deemed excessively broad. While the cause of the outbreak remains unknown at this time and may be multi-factorial, excessively broad antimicrobial prescribing was a likely contributing factor.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Outbreaks; Healthcare Associated Infections (HAI); Infection Control
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9734
Abstract Type	Quick
Abstract Title	An Outbreak of Methicillin-Resistant <i>Staphylococcus Aureus</i> Infections in an Outpatient Orthopedic Clinic

Abstract

BACKGROUND: On 8/16/2017, the Healthcare-Associated Infection (HAI) Prevention Program at the Kentucky Department for Public Health (KDPH) was notified of an epidemiologically linked cluster of methicillin-resistant *Staphylococcus aureus* (MRSA) infections in patients who had received joint injections at an orthopedic clinic. Five patients were hospitalized after complaints of increased pain in a knee joint after receiving an injection of the joint at the clinic. All received an injection of bupivacaine, lidocaine, and methylprednisolone acetate on 8/10/2017. The clinic was advised to notify the US Food & Drug Administration (FDA) about these patients and to sequester all vials in lots associated with identified patients. On 8/16/2017, the FDA was notified of the cluster.

METHODS: Staff from the FDA, the Kentucky Board of Pharmacy, and the HAI Prevention Program visited the clinic. Clinic staff were interviewed regarding standard office practices and were observed while drawing up medication for the joint injections. A confirmed case was defined as any patient who: 1) received a joint injection on 8/10/17, and 2) had MRSA cultured from an incision and drainage (I&D) procedure after pain, redness, or swelling occurred following the injection.

RESULTS: Five confirmed cases of MRSA infection post-injection were identified. All were admitted to a hospital after complaints of increased or abnormal pain, difficulty with weight bearing, and swelling. All underwent I&D of the joint with cultures taken; all were positive for MRSA. Pulsed-field gel electrophoresis (PFGE) was conducted by the Division of Laboratory Services, the state public health laboratory, on seven MRSA isolates from five unique patients. Three isolates were obtained from one patient. PFGE fingerprint patterns for all seven isolates were indistinguishable and highly likely to have originated from a common source.

CONCLUSIONS: It is most likely that medications and/or syringes were contaminated during immediate use compounding of medications, prior to injection into sterile body sites. There had been no national recall of any of the medications used in these injections. The probable mechanism of contamination was unsafe medication preparation practices in the clinic. Recommendations included 1) discontinue of all immediate use compounding of medications, and 2) establish a contract with a compounding pharmacy or with affiliated hospital pharmacy to compound, under sterile conditions, medications used for injection into sterile body sites.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Outbreaks; Infection Control; Disease Prevention
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9638
Abstract Type	Quick
Abstract Title	Candida Auris Point-Prevalence Surveys and Environmental Sampling in Facilities without Currently Admitted C. Auris Patients — New York, 2017
Abstract	BACKGROUND: <i>Candida auris</i> is a multidrug-resistant yeast that can spread in healthcare settings by colonizing patients and persisting in the environment for at least 28 days. New York State has identified the majority of <i>C. auris</i> patients since it was first reported nationally in 2016. Most patients are linked to a regional network of healthcare facilities, identified through point-prevalence surveys conducted at facilities with multiple <i>C. auris</i> patients. To understand if <i>C. auris</i> is widespread in facilities with fewer <i>C. auris</i> links, we screened patients and obtained environmental samples at such facilities. METHODS: Facility inclusion criteria included caring for ≤ 2 known <i>C. auris</i> patients, all discharged ≥ 2 months previously. Nares and composite axilla and groin swabs were obtained from facility residents who were on a unit where a <i>C. auris</i> patient was previously admitted. Environmental samples were collected from high-touch facility surfaces and rooms previously occupied by <i>C. auris</i> patients. The Wadsworth Center Mycology Laboratory cultured and performed polymerase chain reaction (PCR) on samples. RESULTS: We screened 203 patients at 6 facilities; 1 (0.5%) patient was found to be colonized with <i>C. auris</i>. This patient was admitted to facilities with known <i>C. auris</i> patients before the current facility admission. Four facilities had environmental detection, with 23 (9.5%) of 241 samples positive for <i>C. auris</i> by PCR, including a sample from the unit of the newly found patient; 2 (0.8%) samples from bedside furniture at 2 facilities were culture-positive. CONCLUSIONS: The low colonization percentage suggests <i>C. auris</i> is not widespread in facilities linked to few <i>C. auris</i> patients. <i>C. auris</i> in facility environments was unexpected. Findings might indicate the existence of previously unidentified colonized persons, longer environmental persistence of <i>C. auris</i>, or lapses in facility cleaning, and highlight the importance of infection control and environmental disinfection to control <i>C. auris</i> spread.
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Antimicrobial Resistance; Infection Control; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9987

Abstract Type Quick

Abstract Title Healthcare Associated Infection Outbreak Investigation of an Elevation of Surgical Site Infections at a Critical Access Hospital

Abstract

BACKGROUND: Reported incidence of surgical site infections (SSIs) in the United States commonly ranges from approximately 0.5–20%. An infection preventionist at a critical access hospital (CAH) notified the Nebraska Department of Health Human Services (NDHHS) Healthcare-Associated Infection (HAI) program of a surgeon with a six-month SSI rate of 29% (N=7) and requested assistance.

METHODS: NDHHS HAI program and local health department personnel conducted an onsite investigation, including surgical suite tour, staff interviews, and patient chart reviews. SSI rates were calculated, and seven reported SSI charts were abstracted using the Centers for Disease Control and Prevention's HAI Outbreak Investigation Form. An additional nine patient charts with similar characteristics were abstracted and used as the control group. These cases had the same procedures performed at the same facility, by the same surgeon, and during the same period of time but did not develop infections.

RESULTS: In 2016, of the 452 procedures at this CAH, 17 developed SSIs (rate = 3.8%). SSIs occurred following the most invasive procedures being performed on the sickest patients at this CAH. Of the 17 SSIs, 15 (88.2%) were orthopedic and performed by three surgeons. Surgeon A performed 24 procedures with seven SSIs (rate = 29.2%). Surgeon B performed 171 procedures with five SSIs (rate = 2.9%) and Surgeon C performed 13 procedures with three SSIs (rate = 23.1%). The seven SSIs associated with Surgeon A used different operating room (OR) personnel, rooms, antibiotics, and durations. There were zero deaths. The seven SSIs and nine controls were evaluated using a stepwise regression model set at the 0.15 significance level. Using the variables for bone graft, hardware, OR location, and number of people in the OR, the only significant variable was the number of people in the OR. There was an average of 10 people in the OR among cases and seven among controls. Logistic regression yielded an odds ratio of 1.8 (95% CI: 0.99–3.26). Recommendations were made to limit door openings and OR traffic.

CONCLUSIONS: SSIs occurred primarily after orthopedic procedures, and two of three surgeons were found to have elevated rates. Chart review of the seven SSIs of concern revealed no systematic patterns of specific personnel, procedures, or management. Analysis showed the number of people in the OR was potentially associated with SSIs. After following NDHHS recommendations, there were no additional orthopedic SSIs at this CAH in the subsequent six months.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Infectious Diseases; Healthcare Associated Infections (HAI); Epidemiology

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9169
Abstract Type	Quick
Abstract Title	Hepatitis C Cluster in an Alternative Medicine Practice — New York State, 2015–2017

Abstract

BACKGROUND: In June– July 2017, Westchester County (New York) Department of Health (WCDOH) reported 2 cases of hepatitis C virus (HCV) genotype 1b infection in residents who had received an intravenous (IV) infusion at alternative medicine practice A. The New York State Department of Health (NYSDOH) and WCDOH investigated to detect the infection source, identify additional cases, and prevent further infections. **METHODS:** A case was an HCV-positive result in a person who had received an IV infusion, injection, or phlebotomy at alternative medicine practice A during November 2015–August 2017. Public health personnel visited the practice to interview staff, observe infection control practices, and review patient records. We matched patient records with reportable disease registries. NS5b Sanger sequencing and HVR1 next generation sequencing was conducted for phylogenetic analysis of HCV. Public notification was conducted through media, mass mailings, and a telephone hotline. **RESULTS:** Reportable disease registries revealed 6 additional persons with HCV meeting the case definition, for a total of eight cases. Specimens from 5 patients underwent phylogenetic analysis; all were genetically linked within a single transmission cluster. Specimens from the remaining 3 patients were not analyzed given HCV clearance. An infusion timeline implicated >1 transmission event. Site visits found an unlicensed person preparing and infusing therapies where manipulations of blood occurred. The medical practice was closed, and the physician's license was suspended. NYSDOH mailed alerts to 584 practice patients; WCDOH tested 109 practice A patients; the NYSDOH hotline received 80 calls. Additional persons were tested by private providers. No additional cases have been identified. **CONCLUSIONS:** Inadequate infection control and unsafe injection practices likely contributed to HCV transmission at this practice. Surveillance and reporting of HCV is crucial for identifying healthcare associated HCV clusters. This investigation highlighted the value of phylogenetic analysis in epidemiologic investigations.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Hepatitis; Healthcare Associated Infections (HAI); Surveillance
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10240

Abstract Type Quick

Abstract Title Hospital-Associated Cluster of Mucormycosis—Chicago, Illinois, 2017

Abstract

BACKGROUND: On October 18, 2017, Hospital A notified the Chicago Department of Public Health of 8 patients with mucormycosis in 2017, a two-fold increase from prior years. Mucormycosis, a rare and often fatal invasive mold infection affecting immunocompromised patients, is typically acquired by inhalation of spores ubiquitous in the environment. Outbreaks have been linked to inpatient hospital exposure. We aimed to characterize cases, identify a source, and prevent further infections.

METHODS: Cases were Hospital A inpatients or outpatients with clinically compatible mucormycosis confirmed by histology or culture during 2017. We abstracted medical charts, evaluated inpatient and outpatient visit and procedure locations during the 3 months before diagnosis, reviewed hospital repair and construction records, and performed environmental assessments.

RESULTS: Of 8 Hospital A mucormycosis patients, 6 had diagnoses clustered during August 1–October 31, 2017. Of these 6 patients, 3 (50%) had stem cell transplant, 2 (33%) kidney transplant, and 1 (17%) hematological malignancy. Five (83%) patients developed pulmonary and 1 (17%) cutaneous mucormycosis; 4 (67%) died. The 6 patients collectively visited 6 Hospital A buildings 236 times. No common locations were shared by all patients, except a major inpatient and outpatient diagnostic imaging center. Inpatient days range was 25–67 days (median 48.5); 2 patients spent >60% of time as outpatients. Among >1,000 repair and construction orders potentially generating soil and dust exposures during 2017, no single exposure affected all patients. Environmental assessments did not reveal widespread mucormycete exposure, but identified visible mold on linen storage area walls and potted plants in Hospital A common areas.

CONCLUSIONS: No definitive mucormycosis source has been implicated in this cluster, although active surveillance is ongoing. We recommended consideration of antifungal prophylaxis effective against mucormycetes and high-efficiency respirator use among patients at high-risk, linen storage area mold remediation, and limiting soil and dust exposure.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9503

Abstract Type Quick

Abstract Title Methicillin-Resistant *Staphylococcus Aureus* (MRSA) in Neonatal Intensive Care Units (NICUs), Virginia

Abstract

BACKGROUND: Acute care hospitals are required to report laboratory-identified MRSA bacteremia to the Virginia Department of Health (VDH) through the National Healthcare Safety Network (NHSN). Prior to October 2016, laboratories were required to report invasive MRSA cases, but that requirement was removed from state reporting regulations. Other state regulations require facilities to report two or more epidemiologically related *Staphylococcus aureus* infections in obstetrical or nursery units. In November 2017, delayed reporting of two fatal cases of invasive MRSA infections in a Central Region NICU initiated a VDH investigation, an analysis of NHSN data to determine if other NICU outbreaks had gone unreported, and a summation of available data to determine if the burden is higher in Central Region NICUs compared to the rest of the state.

METHODS: The Central Region Epidemiologist conducted site visits to assess infection control policies and observe NICU practices. Screening was done for all patients within the NICU. Staffing logs were collected to construct bed tracing. MRSA isolates were submitted to the state public health laboratory for confirmatory testing and pulsed-field gel electrophoresis (PFGE) analysis. VDH reviewed NHSN NICU data from the past 2.5 years and analyzed MRSA NICU outbreak data.

RESULTS: Bed tracing revealed that the two MRSA bacteremia infants were adjacent to one another, and <10 total staff were shared. Screening identified four additional patients with MRSA colonization. PFGE patterns from five of six patients were indistinguishable. Upon reviewing NHSN data, in one quarter, four invasive MRSA infections in a NICU in the Southwest Region were unreported. These cases were not epidemiologically linked as they overlapped in time but not in space or staff. Since 2006, 12 MRSA outbreaks have been reported in Virginia NICUs; of those, eight were in the Central Region. The 12 outbreaks resulted in approximately 100 infected or colonized cases and six deaths.

CONCLUSIONS: Recommendations for the Central Region outbreak included continuing weekly enhanced surveillance screening, screening staff members who provided care for both bacteremia patients, and increasing environmental cleaning and bioburden sampling. State reporting regulations were reviewed with each hospital's infection preventionist and administration for the Central and Southwest regions. Generating awareness of the burden in the Central Region and the morbidity/mortality associated with these infections should lead to increased focus and updated facility policies. NHSN data are delayed, but VDH can use the data to identify baseline rates, determine geographical differences, and retrospectively detect outbreaks.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Outbreaks; Surveillance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10048
Abstract Type	Quick
Abstract Title	Methicillin-Resistant <i>Staphylococcus Aureus</i> Infections in Patients Receiving Injections at an Outpatient Pain Clinic—Pennsylvania, 2017

Abstract

BACKGROUND: Unsafe injection practices and a failure to adhere to standard precautions have been implicated in the transmission of bacterial infections, including methicillin-resistant *Staphylococcus aureus* (MRSA). In November 2017, we were notified of 4 cases of MRSA infections since September in persons who had received injections by a single provider at a pain clinic. We investigated to identify risk factors and prevent further cases.

METHODS: During November 30–December 1, we completed a site visit to perform case confirmation and finding through medical record review and observe infection control practices. We performed active surveillance by asking area hospitals to review medical records for patients of the provider during September 18–October 6. A confirmed case was a patient with a specimen positive for MRSA who had received an injection at the clinic on or after September 1, 2017; a probable case was one who had symptoms consistent with MRSA infection that resolved upon receipt of therapy appropriate for MRSA.

RESULTS: We identified 8 confirmed and 1 probable case. Eight of the case-patients had procedures on September 25 and one on September 27. Case-patients had severe sequelae including bacteremia, epidural abscess, osteomyelitis, and retroperitoneal abscess. All received injections containing iohexol radiographic contrast dye, lidocaine, triamcinolone, 0.9% sodium chloride, and bupivacaine. Staff reported routinely preparing 20ml aliquots of iohexol contrast dye each day from a 50ml single-dose vial; on the third day 10ml was obtained from the open vial and an additional 10ml from a new vial, using the same needle. The practice was reportedly thought to be cost saving. We observed additional infection control breaches; among 16 indicated opportunities, hand hygiene was performed once (8% success rate). We provided recommendations accordingly. All patients seen in the clinic by the provider during September 21–September 27 received notice of the outbreak by phone and mail, and their primary care provider was notified.

CONCLUSIONS: A large outbreak of invasive MRSA infections likely occurred due to local contamination of one vial of contrast dye, possibly through poor hand hygiene practices. We hypothesize that the contaminated vial incubated over a weekend, causing infections in patients injected on a Monday. Improper use of single-dose vials over multiple days and unsafe injection practices likely led to the contamination of a second vial. The outbreak highlights the critical importance of strict adherence to safe injection practices and the potential consequences of improper use of single-dose vials.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Infection Control; Antimicrobial Resistance
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10345

Abstract Type Quick

Abstract Title Multifaceted Approach to Improve Healthcare Personnel Influenza Vaccination Rates in Hawaii

Abstract

BACKGROUND: In accordance with Healthy People 2020 the national goal is to have 90% of health care personnel (HCP) vaccinated against influenza. HCP vaccination against influenza has been associated with fewer deaths among elderly hospitalized patients. HCP vaccination data are publicly reportable in Hawaii and was published for the first time in the 2013 Hawaii Healthcare Associated Infection (HAI) report. For the 2013-14 influenza season the overall vaccination rate for Hawaii was 67%, placing Hawaii third worst in the nation according to CDC. Hawaii Department of Health (HDOH) has implemented several initiatives to improve HCP vaccination rates. The improvement in HCP vaccination rates were assessed over the four-year period.

METHODS: Before the 2014-15 influenza season HDOH engaged in educational efforts to ensure facilities were entering data correctly and have high-performing facilities share best practices. This was done via emails, webinars, and in-person meetings. Additionally, with the 2015-16 influenza season HDOH began to offer facilities mini-grants to develop a plan to improve their vaccination rates. Facilities submitted plans with a variety of activities, for example: additional flu clinics, badges/stickers for vaccinated HCP, vaccination incentives, etc. Data are collected from CDC's National Healthcare Safety Network, a web-based system for tracking HAIs, for the following groups: employees, licensed independent practitioners (LIPs) and volunteers.

RESULTS: The overall vaccination rate of all HCP in reporting facilities has increased from 66% during the 2013-14 influenza season to 83% in the 2016-17 season. Increases in influenza vaccination rates over time were observed across all groups of HCP. Volunteers showed the greatest increase in influenza vaccination rates, from 51% to 86%, and had the highest rate among HCP groups. LIPs had an increase of 17% but had the lowest rate among HCP at 76% during the 2016-17 season. Twelve of 15 facilities reported an increase in influenza vaccination rates over the four-year period.

CONCLUSIONS: Facilities in Hawaii have made progress in improving their influenza vaccination rates, with a 16% increase from the 2013-14 season to the 2016-17 season. Overall, publicly publishing influenza vaccination data, educating facilities, and offering mini-grants increased reported vaccination rates in HCP in reporting facilities in Hawaii. However, facilities in Hawaii still have much work to be done to achieve the 90% national goal.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Immunization; Influenza / Pandemic Influenza

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9167

Abstract Type Quick

Abstract Title The Hidden Carbapenem-Resistant Enterobacteriaceae (CRE) Burden in Two Los Angeles County Skilled Nursing Facilities with Ventilator Care (VSNFs): A Challenge for CRE Control

Abstract

BACKGROUND: The Los Angeles County Department of Public Health (LAC DPH) issued a Health Officer Order in January 2017 mandating reporting of all CRE cases in acute care and skilled nursing facilities (SNFs). In September and November of 2017, we investigated two unrelated CRE outbreaks in two VSNFs. We describe the CRE prevalence in the high-acuity residents of the subacute units in these two facilities.

METHODS: CRE cases were defined as residents with specimens from any source that tested positive for a carbapenemase or identified by standard MIC testing. Site visits were made to assess infection control practices. Point prevalence surveys (PPS) were conducted to detect gram-negative bacteria carrying carbapenemases; one at the beginning of the outbreak investigation and subsequent follow-up rounds 2-4 weeks later to assess if transmission was ongoing. Rectal swab specimens were tested at the west region Antimicrobial Resistance Lab Network (ARLN) Laboratory using Cepheid GeneXpert real-time PCR. Organism identification was conducted at the LAC DPH Public Health Laboratory using Nanosphere and MALDI-TOF.

RESULTS: Facility A: 3 cases of carbapenem-resistant *Klebsiella pneumoniae* (CRKP) infections were initially reported within a 2-month timeframe. PPS screening identified an additional 7 residents colonized with a carbapenemase resulting in an overall prevalence of 27% (10/37). Of those, *blaKPC* (KPC) was identified in 9 residents and *blaVIM* in 1. **Facility B:** 23 cases of CRKP were reported between January-September 2017, of which 6 were current residents. Surveillance testing found KPC in an additional 17 residents resulting in a prevalence of 59% (23/39). Due to the high rate of colonized residents identified by the PPS, we recommended more aggressive infection control measures including closing the subacute unit to new admissions, chlorhexidine bathing, and contact precautions for the entire unit. Multiple organisms were isolated from the KPC-positive specimens (*Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter baumannii*, and *Pseudomonas sp.*).

CONCLUSIONS: We identified a high prevalence of CRE in the subacute units of 2 VSNFs. Our investigation indicates that the CRE colonization status of many VSNF residents is unknown, which complicates prevention of CRE transmission. The presence of multiple organisms and carbapenemases in the facilities suggest that various introductions of CRE into the VSNFs contributed to the high prevalence. Mandating CRE as a reportable condition has unmasked what may be a widespread problem in these facilities. Screening new residents on admission may help facilities better assess a baseline rate of CRE to guide their infection control efforts.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Outbreaks; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10044

Abstract Type Quick

Abstract Title Utilizing the Infection Control Assessment and Response (ICAR) Program at the Arkansas Department of Health

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) distributed funding in 2015 to state health departments to evaluate infection control capacity within their jurisdiction and to mitigate common gaps. The Infection Control Assessment and Response (ICAR) program is structured around CDC-developed Infection Control Assessment tools used by health departments in evaluating the infection prevention (IP) activities of infection control programs in various healthcare settings. Health department staff assess major domains of infection prevention while on-site and provide in-depth feedback to IP staff and facility leadership at both the conclusion of the visit and in writing. As of December 2017, the Arkansas Department of Health (ADH) has completed 30 visits at acute care hospitals, 8 at critical access hospitals, and 18 at long-term care facilities. The ICAR tools have provided a robust method of highlighting strengths and deficiencies in IP programs. To determine the impact of these visits regarding improvements in infection control, we surveyed facilities who completed an ICAR visit.

METHODS: Survey data were collected and managed using REDCap electronic data capture tools hosted at the ADH. The survey was distributed via REDCap to infection preventionists present at an ICAR visit as of November 2017. The survey contained 4 multipart questions in which the quality of the ICAR visit and tool were assessed using a 5-point Likert scale and qualitative input.

RESULTS: The survey was completed by 18 out of 50 facilities (36%), of which 12 (67%) were acute care hospitals, 2 (11%) were critical access hospitals, and 4 (22%) were long-term care facilities. Feedback was overwhelmingly positive: all 18 respondents agreed (17%) or strongly agreed (83%) that the health department adequately covered infection control topics and provided useful feedback. The domains of infection prevention with the greatest reported changes were hand hygiene (61%), catheter-associated urinary tract infection prevention (71%), central-line associated bloodstream infection prevention (71%), *Clostridium difficile* infection prevention (71%), and antibiotic stewardship (83%). Seven respondents (39%) reported increases in full-time IP staffing as a result of the ICAR visit. Infection preventionists cited the passion and expertise of health department staff, the high quality of the post-visit feedback, as well as the non-regulatory nature of the visit as strong positives of the program.

CONCLUSIONS: The ICAR program has motivated much-needed changes in infection prevention and has been invaluable in fostering a strong relationship between the health department and the infection control community of the Arkansas healthcare system.

Committee Infectious Disease

Topic Healthcare-Associated Infections

Keywords Healthcare Associated Infections (HAI); Evaluation; Infection Control

Consider for Different Presentation? Yes

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State Public Health Agency

Submission Type	Roundtable
ID	10297
Abstract Type	Roundtable
Abstract Title	Alignment of Federal, State, and Local Efforts for Sustainable Prevention of Healthcare-Associated Infections (HAIs)

Abstract

Key Objectives:

- Discuss the benefits of aligning federal/state/local government and non-government partner efforts to reduce HAIs
- Review examples of how alignment of partner efforts has enhanced HAI prevention
- Discuss challenges to creating and maintaining partnerships and how to overcome them
- Explore opportunities to further leverage partnerships to sustain HAI prevention

Brief Summary:

HAIs and antimicrobial resistance (AR) are important public health priorities and major investments have been made to address these issues. Examples of Centers for Disease Control and Prevention (CDC) investments to address HAI/AR include the Epidemiology and Laboratory Capacity (ELC) cooperative agreement program to support HAI/AR programs at state, local, and territorial health departments, and the "States Targeting Reductions in Infections via Engagement" (STRIVE) contract awarded to the Health Research & Educational Trust (HRET) to implement infection prevention efforts in hospitals by leveraging relationships and collaboration among state prevention partners. Other federal agencies also invest in HAI/AR prevention, an example of which is the Centers for Medicare & Medicaid Services' Partnership for Patients and the Hospital Improvement Innovation Networks (HIINs). This session will review lessons that have been learned through the ELC cooperative agreement and the STRIVE contract about how to engage partners and build relationships to support and enhance HAI prevention efforts. Effective working relationships between partners can help streamline and reduce duplication of infection prevention efforts, reduce initiative fatigue for healthcare facilities, and promote long-term, sustainable improvements. In addition to inter-governmental partnerships, participants will explore the value of partnerships with non-government organizations, such as state hospital associations and healthcare systems. This includes partners who support specialty healthcare settings, such as long-term acute care hospital (LTACH) systems. Some of the specific methods by which partnerships can aid in prevention will be discussed, and will include co-sponsorship of infection prevention meetings, site visits, webinars, and initiatives to make collaboration efforts clear to the hospital, as well as engagement of hospital leadership. Opportunities to further leverage partnerships to sustain HAI prevention efforts will be discussed and will include the use of the Targeted Assessment for Prevention (TAP) Strategy to identify specific hospital gaps and to link healthcare facilities to appropriate local or national prevention collaboratives based on their specific needs, promotion of the utility of on-site hospital visits (e.g., ICAR assessments), facilitation of networking among hospitals, and improving HAI data access and data sharing among partners.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Collaboration; Prevention; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10147
Abstract Type	Roundtable
Abstract Title	Council for Outbreak Response: Healthcare-Associated Infections and Antibiotic Resistance (CORHA): Supporting Efforts for Outbreak Detection and Response
Abstract	Key Objectives: Participants will learn about CORHA’s work over the last year, including options for engaging with the Council and accessing resources developed to assist in detection, reporting, investigation, and control of infectious disease outbreaks in healthcare settings. 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) has funded the Association of State and Territorial Health Officials (ASTHO) and the Council of State and Territorial Epidemiologists (CSTE) to create and co-lead the Council for Outbreak Response: HAI/AR (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), and Centers for Medicare and Medicaid Services (CMS). CORHA functions as a multidisciplinary collective 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. In 2017, CORHA added FDA and CMS as partner organizations, launched a website, developed a variety of outbreak detection and response products, and began addressing new topics relevant to policy and laboratory aspects of outbreak response. CORHA products developed to date include: outbreak definitions and thresholds tailored to specific types of infections and a data dictionary and activity tracking system to assist health departments and large healthcare systems with managing information related to investigations of possible HAI-AR outbreaks. In 2018, CORHA is expanding workgroup activities to address policy considerations and laboratory issues, while continuing to develop products through the established the Detection and Reporting and the Investigation and Control workgroups. During this roundtable session, CORHA members will share newly developed products and discuss new activities related to laboratory and policy priorities with session participants.
Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infectious Diseases; Antimicrobial Resistance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10168
Abstract Type	Roundtable
Abstract Title	Creating Effective and Sustainable Infection Control and Antibiotic Stewardship Trainings

Abstract

Key Objectives:

- Creating content for infection control and antibiotic stewardship trainings
- Methods for identifying gaps in infection control competencies
- Engaging stakeholders for collaboration and promotion
- Evaluating effectiveness of infection control and antibiotic stewardship trainings

Brief Summary:

Activities of state Healthcare-Associated Infections and Antibiotic Resistance (HAI/AR) programs include infection control and antibiotic stewardship trainings for providers across the healthcare spectrum. These activities were largely increased through supplemental Epidemiology and Laboratory Capacity Grant (ELC) funding as well as reinforced in core ELC support for HAI/AR. Approaches to infection control trainings are variable between states and depend upon resources, funding level, and infection control expertise available for providing these opportunities. Outcomes of such trainings can benefit public health collaboration, enhance provider relations, and improve reporting compliance for conditions and outbreak detection. This session aims to review approaches to conducting infection control trainings, engaging stakeholders for shared goals, and accessing acute and non-acute care providers. Participants will share best practices for conducting infection control and antibiotic stewardship trainings, exchange ideas for shaping audience-specific messages, and provide innovative approaches to completing grant goals.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Infection Control; Antimicrobial Resistance; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10158
Abstract Type	Roundtable
Abstract Title	Implementation of a Legionella and Water Management Workshop for Washington State Healthcare Facilities

Abstract

Key Objectives:

- *Legionella* and waterborne pathogens are a source of healthcare-associated infections.
- The Centers for Medicare and Medicaid Services (CMS) mandated that facilities implement water management programs for control of *Legionella* and other waterborne pathogens.
- Many facilities needed assistance developing and implementing water management programs. To fill this need, we developed a one-day *Legionella* workshop.
- At this roundtable, we will discuss the planning and execution of this workshop as well as lessons learned, so that other jurisdictions may more readily develop their own educational materials.
- Topics will include: • Organization and content of a *Legionella* and water management workshop • Stakeholder engagement and partnership
- Key objectives for attendees
- Lecture content and tabletop organization
- Evaluations from attendees
- Lessons learned
- Assessing success of workshop—how could we measure our effectiveness?

Brief Summary:

Legionella is a pathogenic group of gram-negative bacteria causing legionellosis, including Legionnaires' disease, a serious form of pneumonia. *Legionella* found in healthcare facility water systems may cause illness in at-risk patients. CMS guidelines changed in June 2017, requiring healthcare facilities to develop policies and procedures that reduce water pathogen growth and spread. Washington State Department of Health (DOH) has received concerns from healthcare facilities wanting to better understand waterborne pathogens and the necessary components of a water management plan. DOH partnered with the Puget Sound chapter of the Association for Professionals in Infection Control and Epidemiology (APIC) and Pall Medical to organize a one-day workshop to address these concerns. This workshop, entitled "Watching Water: A *Legionella* and Water Management Exercise for Healthcare Facilities," took place October 30, 2017 in Tukwila, Washington and featured a morning of lectures and panels followed by a hands-on tabletop exercise in the afternoon. Speakers discussed *Legionella*, waterborne pathogens, and water management from the laboratory, facilities/engineering, and infection preventionist perspectives. Panels assembled experts in public health and healthcare facility regulators to answer audience questions. The tabletop exercise was based on the Centers for Disease Control and Prevention water management toolkit and was divided into three sections: 1) Case Investigation, 2) Environmental Assessment, and 3) Water Management Program. The workshop was a success, with approximately 130 attendees from approximately 45 healthcare groups. Attendees scored the workshop a 4.8 on a 1-5 scale (5 being optimal) for overall effectiveness. This workshop will be given again at a critical access hospital conference in Spokane, WA (March 2018). All tabletop materials will be shared with roundtable attendees on request.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Epidemiology; Infection Control; Healthcare Associated Infections (HAI)
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9259
Abstract Type	Roundtable
Abstract Title	Publishing Healthcare-Associated Infection Data from Small Healthcare Facilities

Abstract

Key Objectives:

- Discuss difficulties with publishing HAI data from small facilities, and encourage idea sharing among states
- Consider updates to the DAPS toolkit regarding data display for small facilities

Brief Summary:

Organizations including health departments, federal agencies, and consumer groups disseminate healthcare-associated infection (HAI) surveillance data from the National Healthcare Safety Network (NHSN). The standardized infection ratio (SIR) is a summary measure used to track HAIs, in which the number of observed infections is divided by the number of predicted infections to produce an observed to predicted ratio. The number of predicted infections is calculated using a national baseline of HAI incidence, adjusted for significant predictors (e.g., bed size). To account for the diminished precision in a facility's SIR when its exposure volume (e.g., device days, operative procedure volume) is relatively low, NHSN does not calculate a SIR for a facility when the number of predicted infections is less than 1.0. Small healthcare facilities tend to have lower exposure volume than larger facilities. As a result, small facilities are more likely to have less than 1.0 predicted infection and do not have an SIR. This scenario presents several challenges, including constraining quality assessments predicated on a comparison of the facility's HAI experience with a national benchmark and omission of the facility's data from a state's published report. Hawaii's 15 acute care facilities face these challenges, as most are small facilities with less than 150 beds. It is challenging to explain why these facilities do not have an SIR, or why their SIR is not statistically significant. Additional analyses and display techniques are needed to track HAI prevention in these facilities. The Data Analysis and Presentation Standardization (DAPS) toolkit, which defines best practices to analyze and present HAI data, provides several examples for displaying data from small facilities. Many states have adapted recommendations from the toolkit or developed their own methodologies for quality assessment and data presentation. For example, Hawaii's HAI report recognizes facilities with zero infections, regardless of whether an SIR is calculated. The purpose of this roundtable is to discuss challenges organizations have with assessing quality and publishing HAI data, emphasizing data from smaller facilities. We will present examples from the DAPS toolkit and encourage states to share how they have addressed this challenge. The information gathered will be used to inform future enhancements to the DAPS toolkit.

Committee	Infectious Disease
Topic	Healthcare-Associated Infections
Keywords	Healthcare Associated Infections (HAI); Data Sharing
Consider for Different Presentation?	No
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Submission Type Breakout/Quick/Lightning/Poster

ID 9865

Abstract Type Breakout

Abstract Title Characteristics of Hepatitis B and Hepatitis C Mono- and Co-Infections, Philadelphia, 2013 - 2017

Abstract

BACKGROUND: Hepatitis B virus (HBV) and hepatitis C virus (HCV) are the causative agents for two common chronic blood-borne infections in the United States. HBV infections are preventable with vaccination, but have no cure. HCV infections are curable, but cannot be prevented through vaccination. Both HBV and HCV infections damage the liver, and co-infection causes synergistic liver disease. In the US, newly reported HBV infections are most common among individuals born in countries where HBV is endemic and HCV is most common among those born 1945-1965 and illicit drug using populations. Little is known about co-infected individuals. This analysis evaluates the demographic and risk factor profiles of individuals with mono-HBV, mono-HCV, and co-HBV/HCV infections in Philadelphia.

METHODS: The Philadelphia Department of Public Health collects positive and negative laboratory data via routine reporting and enhanced investigations. Individuals with a past or present HBV infection and no HCV infection history were categorized as having mono-HBV infections ("mono-HBVs"). Those with past or present HCV infection and no HBV infection history were mono-HCV infections ("mono-HCVs"). Co-HBV/HCV infections ("co-infections") are identified by the presence of a biomarker for past or present infection with both viruses. During 2013-2017, enhanced surveillance investigations were performed on a sample of newly reported infections. Differences among investigated individuals with mono-HBV, mono-HCV, and co-HBV/HCV infections were measured using chi-square analyses.

RESULTS: In 2013-2017, 244 mono-HBVs, 736 mono-HCVs, and 375 co-infections were identified and investigated. Co-infections were more commonly male and older versus mono-HBVs and mono-HCVs. Mono-HBV were more likely to be foreign-born (56%; n=111; p<0.0001) compared to co-infected (23.4%; n=66) or mono-HCV (17.2%; n=105). Forty percent (n=73) of co-infections indicated homelessness versus 16.4% (n=19; p<0.0001) with mono-HBV and 30.7% (n=84; p=0.049) with mono-HCV infections. Additionally, 59.4% (n=187) of co-infections had a history of injection drug use versus 9.7% (n=16; p<0.0001) of mono-HBVs and 52.7% (n=668; p<0.0001) of mono-HCVs.

CONCLUSIONS: Certain measured differences between co-HBV/HCV, mono-HCV, and mono-HBV infections are likely driven by the trends within each mono-infected populations. This analysis illustrates, however, possible factors driving HBV/HCV co-infection including injection drug use and specific populations at risk for multiple infections including homeless populations. These associations should be explored further to determine opportunities for targeted outreach including harm reduction education and HBV vaccination. Collection of negative laboratory reports should continue to further assess drivers of co-infection, areas for intervention, and testing performed for multiple infections.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Substance Use

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10112

Abstract Type Breakout

Abstract Title Epidemiology of Hepatitis A in Miami-Dade County, Florida, 2012–2017

Abstract

BACKGROUND: Hepatitis A virus (HAV) infection is a vaccine-preventable disease that is usually transmitted person-to-person through the fecal-oral route or through consumption of contaminated food or water. In 2017, the Florida Department of Health in Miami-Dade County (DOH-Miami-Dade), Epidemiology, Disease Control, and Immunization Services (EDC-IS) noted a four-fold increase in HAV cases.

METHODS: EDC-IS interviewed cases, identified potential contacts, administered post-exposure prophylaxis (PEP), and conducted site visits for workplace investigations. Variables of interest included: age, sex, race/ethnicity, symptomology, origin of infection, vaccination history, and sexual and travel histories. HAV cases between January 1, 2012 and December 31, 2017 were abstracted from Merlin, the Florida Department of Health surveillance system, and analyzed using SAS v9.4.

RESULTS: A total of 312 HAV cases were identified between January 1, 2012 and December 31, 2017 with 125 (40.0%) cases identified in 2017. The majority of cases were between the ages of 18 and 44 (81, 64.8%), male (96, 76.8%) and Hispanic (68, 54.4%); however, an increase was noted among the non-Hispanic population in 2017 (28 cases in 2017 versus an annual average of 4 cases between 2012 and 2016). Seventy-two (57.6%) cases were likely infected in Florida, a notable change from historical trends of infections while abroad. In 2017, peaks in reported cases occurred in the months of March, (19, 15.2%), June (18, 14.4%), and August (15, 12.0%); incidence by month was stable in previous years with the exception of a similar peak identified in July 2015. Nine (7.2%) reported contact with a person with confirmed or suspected hepatitis A infection in the 2-6 weeks prior to onset of symptoms. Of the 96 males, 72 (75.0%) provided sexual histories of which 30 (41.7%) reported having sex with men. Injection drug use (IDU) was reported among 4 (3.2%) cases. Three (2.4%) had received at least one dose of the HAV vaccine prior to infection. Seventy-two (57.6%) HAV cases identified additional contacts. Among the 72, close contacts of 65 (90.3%) cases received recommendation for PEP based on epidemiologic risk of exposure.

CONCLUSIONS: Between January and September 2017, the EDC-IS Hepatitis Program nurses conducted 68 vaccination clinics at local homeless shelters, drug rehabilitation clinics, correctional facilities, and workplaces of cases with sensitive employment, administering nearly 400 doses of PEP, in addition to providing PEP recommendations to close contacts. This report further emphasizes the need to continue current vaccination efforts for vulnerable populations in Miami-Dade County.

Committee Infectious Disease

Topic Hepatitis

Keywords Epidemiology; Hepatitis; Surveillance

Consider for Different Presentation? Yes

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Local Public Health Agency

Submission Type Breakout/Quick/Lightning/Poster

ID 10161

Abstract Type Breakout

Abstract Title Hepatitis A Cluster in a Small Popular Area in Miami-Dade County

Abstract

BACKGROUND: Hepatitis A virus (HAV) is a highly contagious liver infection transmitted by the fecal-oral route, person-to-person contact or consumption of contaminated food or water. The number of reported confirmed hepatitis A cases in Miami-Dade County has gradually increased from 28 in 2014 to 47 in 2016 to 125 in 2017. Among the 2017 cases, a small cluster was detected in a popular tourism area in a particular one-square mile where confirmed HAV cases increased from 1 in 2015 to 15 in 2017.

METHODS: HAV case data between January 2012 and December 2017 were obtained from Merlin, the Florida Department of Health Epidemiology Surveillance System. SAS 9.4 and ArcGIS were employed to calculate descriptive statistics and spatial clustering.

RESULTS: ArcGIS revealed a total of 15 confirmed HAV cases in a one-square mile popular area during 2017. Five of 15 cases occurred in May 2017. All cases were male aged 27 to 54 with mean of 38 years. Eight of 15 (53.3%) were non-Hispanic white in contrast to the area outside of this one-square mile where only 18.2% of HAV cases were Non-Hispanic white. All cases reported at least 2 or more HAV-related symptoms. Only 5 of the 15 cases reported out-of-state travel history. Eleven provided responses regarding sexual partners; among these, 5 identified as men-who-have-sex-with-men (MSM). Of the 15 cases, 14 reported no sensitive occupation. No cases had received the HAV vaccination prior to HAV infection.

CONCLUSIONS: Since March 2017, several areas in the United States have identified HAV outbreaks. HAV clusters have been identified in Miami-Dade County in 2016 and 2017, in particular in the aforementioned area of interest. In 2017, there were a total of 125 HAV cases identified among Miami-Dade County residents; greater than the average 37 cases seen within the county in the previous five years.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Geographic Information Systems (GIS)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10081

Abstract Type Breakout

Abstract Title Hepatitis C Seroprevalence and Screening Practices Among Pregnant Women from Countries Where Hepatitis C Is Endemic, Philadelphia

Abstract

BACKGROUND: Many people with hepatitis C virus (HCV) infection are unaware of their infection and may not have a known HCV risk. The estimated US seroprevalence of HCV from 2010 is 1.5%; however, this rate is higher in other countries. There is no US recommendation for HCV screening among people originating from these countries as there is for hepatitis B virus. If the HCV seroprevalence is similarly elevated among women of child-bearing age, the associated risk of perinatal HCV transmission would be under recognized. There is a 5.6% rate of perinatal HCV transmission, but prenatal HCV testing is risk-based and not performed on all women. This study aims to determine HCV seroprevalence and identify prenatal HCV screening practices in Philadelphia among women from countries where HCV is endemic.

METHODS: Electronic birth records were used to identify women who gave birth in Philadelphia January 1, 2016–March 31, 2017 and originated from a country with a $\geq 5\%$ seroprevalence of HCV (Endemic Countries). National seroprevalence rates were determined from a literature review. HCV testing history for these women was assessed by searching Philadelphia Department of Public Health HCV surveillance data and positive and negative HCV testing information from facilities that report comprehensive laboratory results. The absence of a reported laboratory result at these facilities was categorized as not HCV screened.

RESULTS: During the study period, 2.0% (n=618) of all births in Philadelphia were to women originating from Endemic Countries. Of the 442 (71.5%) women who either delivered at a reporting facility or for whom HCV laboratory data was available, 79.0% (n=349) were HCV screened and the resulting seroprevalence was 3.2% (n=11). The remaining 21.0% (n=93) were not HCV screened. The highest seroprevalence was found among Egyptian women, correlating with the literature-based rate (15.8% [n=3] and 17.5%, respectively). The lowest HCV prevalence was among Uzbek women and was lower than the literature (1.4% [n=1] and 11.3%, respectively). Of the births to currently HCV-infected (RNA-positive) Philadelphia women (n=2), both infants are receiving HCV follow-up testing.

CONCLUSIONS: The study's HCV seroprevalence of 3.2%, elevated from the US rate, suggests originating from Endemic Countries should be considered as an indication for prenatal HCV screening. Since several prenatal providers perform universal HCV screening, more infections may have been identified than if providers used current national screening recommendations alone. More research is needed to confirm the generalizability of one-time HCV screening amongst not only pregnant women but all individuals from Endemic Countries.

Committee Infectious Disease

Topic Hepatitis

Keywords Maternal and Child Health; Screening; Hepatitis

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9386

Abstract Type Breakout

Abstract Title Identifying High-Risk Populations and Settings for Targeted Hepatitis C Virus (HCV) Testing – North Carolina, 2016

Abstract

BACKGROUND: Prevalence of chronic HCV in NC is unknown, but reported cases of acute HCV increased 276% during 2012-2016. In 2016, free HCV testing for high-risk persons was available from local health departments (LHDs), jails, and community organizations using HIV prevention funding. Data from all HCV tests conducted at the State Laboratory of Public Health (SLPH) during 2016 were analyzed to characterize the HCV epidemic in NC and identify populations for targeted screening.

METHODS: Data was restricted to HCV tests for NC residents with a sample collection date during January 1-December 31, 2016. A positive HCV test result was a reactive HCV antibody test; or non-reactive HCV antibody test with HCV RNA detected. Prevalence (P) of HCV positivity was calculated overall and by demographics and behavioral risk factors; prevalence ratios (PR) and 95% confidence intervals (CI) were estimated using log binomial models.

RESULTS: SLPH conducted 16,818 HCV tests for NC residents during 2016; 1,445 (8.6%) were positive. Prevalence of HCV was greater among males than females (PR: 1.3; 95% CI: 1.2, 1.5) and among Native Americans (PR: 6.7; 95% CI: 4.3, 10.6) and white persons (PR: 6.0; 95% CI: 4.4, 8.2) compared with Hispanics (P: 2.3%). Prevalence among persons who reported two or more risk factors (i.e., baby boomer [BB] born during 1945-1965, injection drug use [IDU], HIV positive) was significantly greater than those who reported no risk factors (PR: 8.3; 95% CI: 7.0, 9.7). Prevalence among BB (P: 14.5%) was nearly twice that of non-BB (PR: 1.9; 95% CI: 1.7, 2.1). Prevalence among persons who reported current IDU (P: 33.5%) was almost six times that of those who did not report current IDU (PR: 5.9; 95% CI: 5.3, 6.5). IDU was associated with greater HCV prevalence among BB (P: 31.7%; PR: 2.3; 95% CI: 1.7, 3.0) and non-BB (P: 33.7%; PR: 7.8; 95% CI: 7.0, 8.7). HCV prevalence was greater among persons tested at drug treatment centers (P: 19.9%; PR: 5.7; 95% CI: 4.7, 6.8) and jails (P: 14.3%; PR: 4.1; 95% CI: 3.3, 5.0) compared to those tested in LHD STD clinics (P: 3.5%).

CONCLUSIONS: The majority of HCV positive tests with reported risk factors were for non-BB who reported IDU (41.7%) and BB who did not report IDU (16.9%). Testing of persons with at least one risk factor (i.e., BB, IDU) and at high-risk testing sites (i.e., drug treatment centers, jails) should be prioritized if funding for HCV testing is limited.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9913

Abstract Type Breakout

Abstract Title Modeling the Age-Related Burden of HCV in 5 US States: Results from 2016-2050

Abstract

BACKGROUND:

The introduction of direct acting antivirals (DAAs) for hepatitis C (HCV) has been met by calls for improved management strategies from health organizations and patient groups. Reliable estimates of the size and scope of the disease burden are needed to support these strategies. In this analysis we demonstrate the utility of disease burden models to estimate trends in five US states: California (CA), Colorado (CO), Louisiana (LA), New York (NY) and Washington (WA).

METHODS:

Excel-based disease progression models seeded with published and/or expert-verified unpublished epidemiological data were used to estimate 2016-2050 trends in chronic infections. To model the expected depletion in the pool of warehoused patients (consistent with no expansion of screening and diagnosis), a trend to reduce treatment numbers annually after 2016 was applied to simulate a 50% reduction in the number of treated patients by 2020. Treatment and diagnosis rates were modeled to remain constant after 2020.

RESULTS:

In 2016, there were ~1,186,000 chronic cases in all five states, ranging from 47,000 cases in CO to 509,000 cases in CA. CA and NY accounted for 80% of cases across the states considered. By 2030, there will be 880,500 cases overall, with CA seeing the largest (53%) and LA the smallest (24%) reduction. Chronically infected individuals aged >50 years outnumbered those aged <50 in all states in 2016, with CA, LA and WA seeing over 100% more cases in the >50 age group than in the <50 group. A reversal, however, occurs such that there will be more chronic cases in the <50 age group in CO by 2027, CA by 2034, LA by 2035, WA by 2043 and NY and by 2044. By 2050, there will be 3-4 times more chronically infected individuals aged <50 than aged >50 in CA and CO and roughly equal numbers in LA, NY and WA.

CONCLUSIONS:

Models can be used to forecast disease burden and provide guidance to policy makers. In the US, available data have been used to estimate current and future disease burden. In light of the age-related and costly-to-manage end stage outcomes of chronic HCV infection, the high disease burden in the >50 age group as of 2016, coupled with the increasing burden in <50 age groups indicates the need for carefully designed strategies to maximize resources.

Committee Infectious Disease

Topic Hepatitis

Keywords Surveillance; Hepatitis; Policy / Policy Development

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9446

Abstract Type Breakout

Abstract Title Operational Challenges to Responding to Local Outbreaks of Hepatitis A in Multiple US Cities

Abstract

BACKGROUND: Communities across the United States are responding to or preparing for significant outbreaks of Hepatitis A. These outbreaks have primarily impacted transient populations and have proven difficult to contain using traditional public health interventions, leading some communities to declare a public health emergency.

METHODS: To understand the impact of these outbreaks on local communities and to identify the operational challenges to preventing, preparing, and responding to them, we are surveying public health officials in affected communities. Semi-structured interviews are being conducted with dozens of responders either actively working to control outbreaks or preparing for potential outbreaks in their communities.

RESULTS: Based on these discussions, we are identifying challenges inhibiting the effectiveness of these responses. Data collection and analysis is on-going; we will be able to present results from this study.

CONCLUSIONS: We are identifying lessons for improving outbreak preparedness and response to Hepatitis A, as well as future public health emergencies that involve hard-to-reach patients or infrastructure-poor environments.

Committee Infectious Disease

Topic Hepatitis

Keywords Outbreaks; Hepatitis; Emergency Preparedness & Response

Consider for Different Presentation? Yes

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Academic Institution

Submission Type	Breakout/Quick/Lightning/Poster
ID	9636
Abstract Type	Breakout
Abstract Title	Using Hepatitis C Surveillance Data to Identify Harm Reduction Needs and Drug Use Behaviors, Philadelphia

Abstract

BACKGROUND: Across the United States, increasing rates of hepatitis C virus (HCV) infections are being driven by the opioid epidemic. Specifically, unsafe injection and other drug using behaviors drive HCV transmission and intertwine these epidemics. While HCV is a reportable condition in Philadelphia, non-fatal overdoses and illicit drug use are not reportable, hindering efforts to estimate their incidence and prevalence or develop best practices for prevention and intervention. Data-driven harm reduction is needed to reduce the rates and burden of HCV transmission and drug use. This analysis uses data on drug use behaviors that was collected through HCV surveillance to identify harm reduction gaps within Philadelphia.

METHODS: Philadelphia Department of Public Health (PDPH) staff investigate a sample of all newly reported acute and chronic HCV infections. Both patients and providers are contacted to collect demographic, clinical, and risk factor information. If the individual indicates a history of illicit drug use, PDPH collects drug-use-related information including method of illicit drug use, drugs used, age at first drug use, overdose history, and paraphernalia-sharing behaviors. For the purposes of this study, differences between individuals with a drug use history and those without were explored using chi-square analyses, along with trends in drug use-related behaviors.

RESULTS: Of the 2,578 people with newly reported HCV infections investigated in 2013-2017, 69.9% (n=1802) disclosed current or historic illicit drug use; of whom 81.0% (n=1460) were persons who had ever injected drugs (PWID). A quarter of PWID (n=461) had injected drugs within 6 months of their interview (PWID6M). PWID were more likely than non-drug users and non-injecting drug users to be younger and non-Hispanic white. Of PWID6M, 96.0% (n=332) injected heroin. Fifty-four percent (n=67) of PWID had ever overdosed, 70.0% (n=44) of whom had overdosed more than once. Of PWID6M, 71.3% (n=246) knew the location of the needle exchange program in Philadelphia and 85.9% (n=342) had ever been in a drug treatment program.

CONCLUSIONS: This analysis of enhanced HCV surveillance data shows a Philadelphia-specific snapshot of drug use behaviors among HCV-positive individuals. While those interviewed may not be representative of the entire drug-using population in Philadelphia, the data may be descriptive of those practicing the highest risk behaviors. This data can be used to help estimate the incidence of overdoses, guide naloxone distribution efforts, and identify drug treatment service needs. The analyses leverage robust HCV surveillance data and will serve as a tool for prevention and harm reduction services in Philadelphia.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Epidemiology; Hepatitis; Substance Use
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9854

Abstract Type Lightning

Abstract Title An Examination of Chronic and Acute Hepatitis B Cases in Young Adults (ages 18-30) Using Data from Florida's Hepatitis in Young Adult Project (YAP), 2012-2015

Abstract

BACKGROUND: The incidence of hepatitis B and C have steadily increased in Florida since 2006, presenting significant public health concerns. Florida identified an increase in hepatitis cases among young adults age 18-30 years. Subsequently, the Florida Department of Health (FDOH) began the hepatitis in Young Adult Project (YAP) to collect detailed risk factor information for newly identified cases and improve timeliness and accuracy of reporting in 10 Florida counties with the highest incidence of hepatitis in young adults. This study examined data collected for chronic and acute hepatitis B cases under YAP in Florida between 2012-2015.

METHODS: A descriptive analysis was conducted on Florida reported confirmed and probable chronic (n=1956) and acute (n=56) young adult (18-30 years old) hepatitis B cases between 2012-2015. Inclusion criteria included chronic (n=523) and acute (n=53) hepatitis B cases in young adults who answered at least 9 out of 11 extended data questions and were Florida residents at the time the case was reported. Florida's communicable disease reporting database, Merlin, was employed to obtain case-related information. A geographic information system, ArcGIS, was utilized to review case distribution and identify patterns. Microsoft Excel was used to manage and analyze risk factor question data, such as drug use, number of sexual partners, incarceration history, medical history, tattoos, and STD status.

RESULTS: During 2012-2015, YAP identified 2,012 cases of newly reported acute and chronic hepatitis B from participating counties. Large, urbanized counties, such as Broward, Miami-Dade, Hillsborough, Orange, Palm Beach and Pinellas reported two-thirds of all young adult hepatitis B cases, with Broward and Miami-Dade reporting the highest incidence of acute (36%) and chronic (51%) cases. Most reported cases of acute (57%) and chronic (47%) hepatitis B were between 27-30 years old. Among 1,956 chronic hepatitis B cases analyzed, the largest proportion were black females (81%). Acute hepatitis B cases were primarily white males (61%). Injection (41%) and non-injection (43%) drug use within six months of symptom onset was the leading risk factor reported by white male acute cases.

CONCLUSIONS: The largest proportion of young adult acute and chronic hepatitis B cases were between 27-30 years old. Black females and white males comprised most chronic and acute cases, respectively. Injection and non-injection drug use were repeated self-reported risk factor exposures among acute cases. YAP data highlight the continued need for targeted interventions and education on hepatitis B prevention in young adult high-risk groups.

Committee Infectious Disease

Topic Hepatitis

Keywords Epidemiology; Prevention; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10280

Abstract Type Lightning

Abstract Title Early Results of Acute Hepatitis C Case Finding, Saint Louis County, MO, 2016 to 2017

Abstract

BACKGROUND: Between 2011 and 2015, the Saint Louis County Department of Public Health (DPH) reported no cases of acute hepatitis C virus (HCV) infection, but noted parallel increases in the rate of newly reported chronic HCV infections and the rate of heroin overdose deaths among Saint Louis County residents. Furthermore, the group most at risk for dying of a heroin overdose in Saint Louis County (25 to 44 year old males living in the county's South or Inner North regions) accounted for a larger proportion of newly reported HCV cases in 2015 (11%) than in 2011 (3%). To learn more about HCV transmission in Saint Louis County, DPH began to investigate a subset of HCV case reports in late 2016.

METHODS: Lacking dedicated funding for HCV case investigations, DPH re-assigned a nurse investigator from its perinatal hepatitis B prevention program to investigate HCV case reports. DPH investigated reports of HCV infection in persons aged 30 years or younger, or reports which included clinical or laboratory evidence of acute infection (e.g., jaundice, elevated liver enzymes). DPH sought additional information from reporting providers and contacted cases to discuss exposures and risk factors, educate them about HCV, and refer them to the services they need.

RESULTS: Between July 2016 and December 2017, DPH investigated 249 reports of HCV infection, of which 24 (9.6%) were ultimately classified as confirmed acute HCV cases, 140 (56.9%) were classified as chronic cases, and 85 did not meet case definitions or were provisionally classified as suspect cases at the time of this writing. Of the 24 acute cases, the median age was 30 years (IQR 27 to 45). Seventeen (71%) cases were male. Eleven (46%) were white, 6 (25%) were black, and 7 (29%) were of unknown race. Eleven (46%) lived in the county's Inner North region, 6 (25%) in the Outer North region, 4 (17%) in the South region, and 3 (13%) in the West region. Eighteen (75%) reported current or previous injection drug use.

CONCLUSIONS: As anticipated, DPH found evidence of injection drug use among people with acute HCV in Saint Louis County. DPH is using these data to inform HCV prevention strategies, promote harm-reduction policies, and make treatment more available to HCV-infected persons who inject drugs. These results illustrate that a local public health agency can leverage existing resources to investigate HCV transmission in the absence of dedicated HCV surveillance funding.

Committee Infectious Disease

Topic Hepatitis

Keywords Surveillance; Hepatitis; Substance Use

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9892

Abstract Type Lightning

Abstract Title Hepatitis C Virus Testing and Diagnostic Delays in Rural Northern California

Abstract

BACKGROUND: Butte County Public Health Department (BCPHD) receives approximately 330 newly reported chronic Hepatitis C virus (HCV) cases annually. Between July 1, 2014 and June 30, 2015, only 49% of patients with HCV antibody (Ab) positive tests had no confirmatory Nucleic Amplification test (NAT) results reported. Lack of confirmatory testing can result in delayed diagnosis, missed opportunities for HCV clinical management and interruption of transmission. In September 2016, BCPHD analyzed HCV surveillance data and identified that significant proportion of facilities and providers with the lowest rates of HCV confirmatory testing utilized local hospital laboratories. BCPHD used the findings of this analysis to conduct a targeted intervention to decrease diagnostic delays for patients with positive HCV Ab results.

METHODS: Medical records were reviewed for patients who had a positive HCV Ab test result reported to BCPHD between July 2015 and September 2016 without NAT results reported within 30 days. HCV test results were evaluated to distinguish patients who never received confirmatory NAT from patients that received confirmatory NAT but whose results were never reported to BCPHD. For patients who never received confirmatory testing, information on the provider, facility and laboratory where the patient received HCV Ab testing were analyzed to identify 3 local hospital laboratories where the majority of HCV Ab testing was conducted. BCPHD worked with these laboratories to implement a reflex testing policy to ensure that when a patient receives a positive HCV Ab results, the patient automatically receives confirmatory NAT.

RESULTS: Between July 2015 and December 2016, an average of 6 patients per month with positive HCV Ab results and no confirmatory NAT were newly reported to BCPHD. By January 20th, 2017, 3 major hospital laboratories and their affiliated laboratories in Butte County adopted reflex testing. Between January 2017 and November 2017, only 2 patients with positive HCV Ab results without confirmatory NAT were reported to BCPHD, resulting in a 96% decrease in the average number of patients with positive HCV Ab results without confirmatory NAT reported monthly to BCPHD.

CONCLUSIONS: After 3 major facilities in Butte County adopted reflex testing, there was a 96% decrease in the number of patients with positive HCV Ab results without confirmatory NAT reported to BCPHD each month. Universal adoption of reflex testing can greatly increase the number of patients that receive confirmatory NAT and improve timely diagnosis of HCV infection.

Committee Infectious Disease

Topic Hepatitis

Keywords Barriers to Care; Hepatitis; Rural Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9409

Abstract Type Lightning

Abstract Title Increase in Syphilis and Hepatitis C Virus Co-Infection Among Women, California, 2012-2016.

Abstract

BACKGROUND: From 2012-2016, the annual rates of early syphilis and newly reported hepatitis C virus (HCV) infection among women of childbearing age (15-44 years) in California increased 454% and 148%, respectively. Our objective was to assess trends in syphilis/HCV coinfection among women and determine if high-risk sexual or drug use behaviors are associated with coinfection.

METHODS: Cases of early syphilis infection (primary, secondary, and early latent stages) among women reported to the California Department of Public Health during 2012-2016 were matched to cases of probable and confirmed chronic HCV by name, date of birth, and demographics using a probabilistic algorithm. Coinfection was defined as HCV infection reported before or after syphilis infection. Annual rates were calculated for 2012-2016 and linear regression was performed to assess change in rate over time. Cases of syphilis/HCV coinfection were described in terms of race and age. High-risk sexual behaviors and injection drug use reported at the time of early syphilis case investigation were assessed by univariate logistic regression for association with syphilis/HCV coinfection.

RESULTS: During 2012-2016, 3,474 cases of early syphilis were reported among women, of whom 231 (6.6%) had HCV coinfection. The rate of syphilis/HCV coinfection among women increased 4-fold, from 0.10 per 100,000 (95% CI 0.06, 0.16 per 100,000) in 2012 to 0.44 per 100,000 (95% CI 0.35, 0.54 per 100,000) in 2016, $p<0.01$. Women with syphilis/HCV coinfection were older than women without HCV infection (median age 39 years vs. 29 years, $p<0.01$). A higher percentage of women with syphilis/HCV coinfection were non-Hispanic, White compared to those without HCV infection (56% vs. 27%, $p<0.01$). In counties where risk factors for syphilis were investigated, syphilis/HCV coinfection was associated with injection drug use (OR=6.3, $p<0.01$); exchanging sex for drugs (OR=4.9, $p<0.01$); and having a sex partner who used injection drugs (OR 4.1, $p<0.01$) compared to those without HCV infection.

CONCLUSIONS: This study found a steady increase in syphilis/HCV coinfection among women in California. Findings suggest there are overlapping risk factors for syphilis and HCV infection. Treatment is needed to prevent ongoing transmission of syphilis and HCV among people who inject drugs and who exchange sex for drugs. These findings should be considered in strategies to increase identification and treatment of both syphilis and HCV among women, such as offering integrated testing in syringe exchange and drug treatment programs.

Committee Infectious Disease

Topic Hepatitis

Keywords Sexually Transmitted Diseases; Surveillance; Hepatitis

**Consider for
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Submission Type Breakout/Quick/Lightning/Poster

ID 9062

Abstract Type Lightning

Abstract Title Shining the (Sun) Light on Hepatitis C: Prospects for Negative Reporting to Enhance Acute Hepatitis C Case Finding and Hepatitis C Linkage to Care in California

Abstract

BACKGROUND: In California, hepatitis C virus (HCV) surveillance relies on laboratory reporting of positive test results and provider reporting of symptomatic individuals for acute HCV. Barriers to surveillance and linkage to care efforts exist because most cases are asymptomatic, and negative test results are not readily available to identify recent seroconversion, treatment status, and viral suppression. To inform deliberations on whether to request negative HCV test results from all labs reporting electronically despite anticipated challenges (including information technology resources and privacy concerns), California Department of Public Health (CDPH) assessed the potential to identify acute and resolved HCV infection by analyzing available negative HCV electronic lab reports (ELRs).

METHODS: CDPH used patient identifiers to match positive and negative HCV antibody and nucleic acid test (NAT) ELRs received from October 1, 2013 to October 30, 2017. Acute HCV cases were identified using the 2016 CSTE case definition, which includes seroconversions within 12 months. Using surveillance definitions for HCV treatment and sustained virologic response (cure) validated by New York City Department of Health and Mental Hygiene, CDPH identified HCV cases who met public health surveillance definitions for persons “on treatment” and “cured”.

RESULTS: Since ELR began in October 2013, CDPH has received more than 1.46 million HCV ELRs, including 50,212 (3.4%) negative HCV ELRs (352 antibody; 49,860 NAT) representing 29,445 unique persons whose negative results were voluntarily reported on a limited basis. Using available negative ELRs, CDPH identified 206 confirmed acute HCV cases (seroconversions), of which only one had been previously reported to CDPH. With the additional 205 confirmed acute HCV cases, there would have been 411 total confirmed acute HCV cases reported during the analysis period—a two-fold increase. Using available negative NAT ELRs, CDPH identified 10,863 individuals with HCV infection who met the surveillance definition for “on treatment,” and 3,800 individuals who met the definition for “cured.”

CONCLUSIONS: Although California does not currently mandate electronic reporting of negative HCV antibody or NATs, this analysis demonstrates that negative ELR data can be effectively used to enhance acute HCV case finding and HCV linkage to care efforts, and improve estimates of acute HCV burden in California. Health departments can use this information to prioritize HCV cases for investigation and follow up with medical providers, improve outbreak detection, monitor treatment coverage, and develop more accurate testing and treatment cascades. These public health benefits will be considered when CDPH deliberates whether to implement negative HCV reporting in California.

Committee Infectious Disease

Topic Hepatitis

Keywords Informatics; Electronic Laboratory Reporting (ELR); Hepatitis

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9278

Abstract Type Poster

Abstract Title Seropositive Hepatitis C and Associated Risk Factors in Knox County Tennessee

Abstract

BACKGROUND: The Knox County Health Department (KCHD) is a metropolitan public health department in Eastern Tennessee that sees approximately 100,000 patients annually. We face the public health challenge of serving patients in a high-risk area for Hepatitis C (HCV) infection due to the opioid drug addiction epidemic. In June 2016, KCHD launched a HCV screening, counseling, and linkage to care program as a FOCUS partner with Gilead Sciences and as one of the three pilot sites to begin HCV screening for the state.

METHODS: Integrated, universal, opt-out HCV screening is offered at five clinics for all persons over 14 years of age. RNA negative patients with ongoing risk factors may return for repeat testing every 6 months; however, repeat tests were excluded from this data set. Patients with documented previous lab-confirmed chronic HCV are likewise excluded. Risk factors were assessed at the time of testing with the exception of homelessness, which was determined by the patient's reported permanent address. Using SAS 9.3, logistic regression modeling was completed to evaluate the independent outcome of HCV antibody seropositivity adjusting for self-reported risk and demographic factors.

RESULTS: Between June 1, 2016 and September 30, 2017, 10,386 patients received an HCV test; 1,304 (12.6%) were found to be antibody positive (Ab+) and 877 (8.4%) were found to be RNA positive (Ab+/RNA+). A history of injection drug use (PWID) was reported in 1,116 (10.7%) of the total tested population, of which 754 (67.6%) tested Ab+. In comparison, of the 8,372 that denied injection drug use, 409 (4.9%) were Ab+ but of the 898 PWID not reported 141 (15.7%) were Ab+. PWID demonstrated the highest significance in a predictive model of each variable for Ab+ demonstrating an odds ratio of 40.6 (95% confidence interval: 34.6-47.6). A history of incarceration was reported in 3,050 (29.4%) of which 917 (30.1%) tested Ab+. Homelessness was identified in 1,316 (12.7%) of which 399 (30.3%) tested Ab+. Within the 1,304 Ab+ cases, 78.8% reported incarceration, 68.7% reported INDU, 64.8% reported PWID, and 30.6% were identified as homeless.

CONCLUSIONS: Limitations include incomplete reporting, relying on single-point self-report for risk factors and using address to identify homelessness. While PWID is the most significant risk factor in modeling antibody seropositivity, many of the other variables collected including homelessness, history of intranasal drug use, birth cohort, history of incarceration, race, ethnicity and gender were also identified as contributing factors.

Committee Infectious Disease

Topic Hepatitis

Keywords Local Epidemiology; Hepatitis; Risk Factors

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9139

Abstract Type Poster

Abstract Title Don't Get Stuck with Hepatitis

Abstract

BACKGROUND: Hepatitis C is not only a global issue but an increasing health threat in Tulsa County in Oklahoma. This project aimed to identify populations in Tulsa County most at risk for HCV, based on risky behaviors, demographics, and socioeconomic factors. Research was also conducted to illustrate the shift in populations most affected by HCV, as well as, factors that may influence its prevalence.

METHODS: The HCV rate for Tulsa County between 2013-2015 was calculated (per 100,000 population) by zipcode. Moreover, the U.S. Census data was used to identify other factors such as poverty, income, education, age, and race. Mental health and substance abuse data from the Oklahoma Department of Mental Health and Substance Abuse was also compared to HCV prevalence data.

RESULTS: Before screening of blood was implemented in 1992, HCV was spread predominantly through blood-borne routes resulting in a spike of HCV occurrences in "Baby Boomers" (individuals born between 1946-1964: ages 53-71). Between 2013-2015 in Tulsa County, 8.8% of individuals infected with HCV were in the 55-64 age group and 1.3% were in the 65+ age group as associated with the "Baby Boomer" era. Furthermore, only 12.1% in the 50+ age group who were infected with HCV in Tulsa County between 2013-2015 reported receiving blood/blood products. However, as intravenous drug use has increased more recently in younger individuals, HCV is more often spread via IV drug paraphernalia. For example, in Tulsa County between 2013-2015, 19.5% of individuals diagnosed with HCV were between the ages of 15-24 and 38.0% between 25-34. Of 20-24 year olds who were reported with HCV in Tulsa County between 2013-2015, 77.8% reported using IV drugs. Factors such as education, poverty, and mental health, can be a barrier for having the tools to reduce risky behaviors. For example, in the zipcode 74110 from 2013-2015, 2430 individuals sought help for mental health, substance abuse, or both. Moreover, that same zipcode had a rate of 125.4 for HCV, as compared to 75.0 for all of Tulsa County. Also, in 2015 only 66.8% of individuals in that zipcode had a high school diploma or higher and 38.8% live below poverty with 8.0% unemployed.

CONCLUSIONS: In conclusion, the populations being targeted for HCV testing, treatment, and education do not align with the populations most affected by HCV. Moreover, eliminating HCV as a public health threat can only be achieved when attainable education and affordable testing are linked to care, treatment, and resources.

Committee Infectious Disease

Topic Hepatitis

Keywords Data Collection; Disease Prevention; Hepatitis

Consider for Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9846

Abstract Type Poster

Abstract Title Estimating Hepatitis B Virus (HBV)-Exposed Births at Metro-Atlanta Hospitals Using the Mother's Country of Birth, Race, and Ethnicity to Increase Prenatal Testing

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) estimates that approximately 700 infants are born annually to hepatitis B-infected mothers in Georgia. Historically, the Georgia Perinatal Hepatitis B Prevention Program (PHBPP) has identified only half of these births, leaving hundreds of infants without critical post-exposure prophylaxis (PEP) intervention with hepatitis B immune globulin and hepatitis B vaccine at birth. Infants who fail to receive PEP are at higher risk for acquiring HBV perinatally. To ensure case identification, CDC recommends that hospitals perform HBsAg testing of women admitted for delivery with unknown HBV status. PHBPP data suggest that testing is not performed consistently at Georgia hospitals and among all demographic groups. The PHBPP sought to identify hospitals with large discrepancies between expected and identified HBV-exposed births for education about prenatal HBV testing protocols.

METHODS: In 2015, 65% of identified Georgia HBV-exposed births were among mothers from five of Georgia's 159 counties, all in metro-Atlanta. The PHBPP selected the largest birth hospital from each of these five counties for the project. The expected number of HBV-exposed births was calculated using vital records data and HBsAg-positive prevalence data from CDC's Expected Births Table, based on mother's country of birth, race and ethnicity. The number of HBV-exposed births identified by the PHBPP was obtained from Georgia's notifiable disease database. Percentages of expected births identified by the PHBPP were calculated, and results were stratified by hospital and by mother's birth country/region and race/ethnicity.

RESULTS: In 2015, 37,471 births occurred in the five metro-Atlanta hospitals. Based on our projections, 252 HBV-exposed births were expected at these hospitals. The PHBPP identified 135 (54%) of these births. The percentages of facility-specific expected births identified by the PHBPP ranged from 40%-70%, with two facilities identifying <50%. Results also varied by mother's birth country/region and race/ethnicity. The PHBPP identified ≥96% of HBV-exposed births to Southeast Asia-born mothers delivering at the five hospitals. Among US-born whites and blacks, the percentages were ≤35% for all five hospitals.

CONCLUSIONS: Expected and Observed Birth Tables showed that the percentage of estimated births identified by the PHBPP varies by hospital and by mother's race/ethnicity and birth country/region, suggesting that gaps in prenatal testing and case identification may exist among specific hospitals and demographic groups. Hospitals where >50% of estimated HBV-exposed births are missed should be targeted for education about HBV testing. Improved education may help narrow the gap between expected and identified HBV-exposed births.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Epidemiology; Maternal and Child Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9701

Abstract Type Poster

Abstract Title Hepatitis C Testing at Facilities Serving High Risk Clients in Allegheny County, PA

Abstract

BACKGROUND: Hepatitis C is a liver disease that results from infection with the hepatitis C virus (HCV), which is spread primarily through contact with the blood of an infected person. Persons who inject drugs (PWID), persons infected with HIV, hemodialysis patients and children born to HCV positive mothers are particularly at risk for HCV infection. To assess access to testing for individuals in Allegheny County who are at higher risk for hepatitis C infection, and to better understand barriers to testing, the Allegheny County Health Department (ACHD) conducted a survey of community organizations that work with individuals at high risk for hepatitis C infection.

METHODS: In 2017, ACHD staff identified facilities that work with high risk individuals to assess HCV testing protocols. Facilities included dialysis clinics, federally qualified health centers, HIV and STD clinics, drug and alcohol treatment facilities, neonatal abstinence syndrome programs, correctional institutions and syringe exchange programs. ACHD staff developed a survey to capture information related to testing, referral and patient education. ACHD staff conducted the survey with each partner organization over the phone. Data were entered and analyzed in Epi Info.

RESULTS: Of 85 partner organizations identified, 67 (79%) completed the survey. Of facilities completing the survey, 46 (67%) reported offering HCV testing and 27 (40%) reported having a written testing protocol. Of facilities who offer HCV testing, 16 (35%) offer testing to all their clients while the remainder offer testing based on risk. Although 100% of participating dialysis clinics, syringe exchange, FQHC and NAS clinics reported offering HCV testing, less than half of drug and alcohol treatment centers reported offering HCV testing. Testing was not offered at the county's correctional facility. Eight facilities that reported offering HCV testing reported that they did not offer venipuncture; thus, persons with a positive screening test were required to go elsewhere for confirmatory testing. Of the 21 facilities that did not offer testing, 5 would like to if resources were available. Reported barriers to testing included cost, staff capacity and absence of a testing requirement.

CONCLUSIONS: Many facilities in Allegheny County with clients at high risk for HCV infection do not currently offer HCV testing, and some offer only rapid testing but no confirmatory testing. Lack of resources was reportedly the main constraint. A concerted effort by the state and local health departments, facility management staff and other partners is needed to increase HCV testing of persons at risk.

Committee Infectious Disease

Topic Hepatitis

Keywords Surveillance; Hepatitis; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9947

Abstract Type Poster

Abstract Title HIV and Viral Hepatitis Co-Infection in Indiana: Beyond Scott County

Abstract

BACKGROUND: The Centers for Disease Prevention and Control (CDC) estimates that 25% of persons living with HIV nationwide are co-infected with hepatitis C virus (HCV), and that 75% of those co-infected are people who inject drugs. The co-infection rate of those with hepatitis B virus (HBV) and HIV is approximately 10%. To ascertain co-infection rates in Indiana, persons living with HIV were matched with HBV and HCV cases using parallel and distributed computing.

METHODS: All Indiana residents living with HIV reported in the Enhanced HIV/AIDS Reporting System (eHARS) as of December 2016 were matched with HBV and HCV patients reported in the Indiana National Electronic Disease Surveillance System (I-NEDSS). Using Python's Dask library for dynamic task scheduling, similarity scores were calculated for all combinations of HIV and viral hepatitis records. The returned records were filtered to high similarity sets by score. Results were then reviewed and validated.

RESULTS: Among the 12,203 people living with HIV in Indiana, 1,137 are co-infected with HCV (9.3%) and 292 are co-infected with HBV (2.4%). Approximately 50 of those infected with HIV are co-infected with HCV and HBV (0.41%). Fifty-four percent of those co-infected with HIV and HCV report injected drug use compared to only 9.1% of those with HIV alone.

CONCLUSIONS: Since 2015, Indiana has been in the spotlight for the HIV and HCV outbreak that occurred in rural Scott County due to injection drug use. While the rate of HIV and HCV coinfection for the Scott outbreak was approximately 94% (as of October 2017), Indiana has overall a lower number of individuals co-infected with HIV and HBV or HCV based on this analysis than the national average, despite. These data highlight the fact that any town, county or state is at risk of increasing rates of infection due to injection drug use being a strong risk factor for HIV/HCV co-infection. It is important to note that HIV positive individuals may not be tested for HBV or HCV and vice versa, thereby the co-infection rates are likely underreported.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; HIV/AIDS; Informatics

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9265

Abstract Type Poster

Abstract Title Implementation of an Integrated Hepatitis C Rapid Testing Initiative in Manatee County, Florida

Abstract

BACKGROUND: Rates of Hepatitis C infection have risen nationwide over the last decade. In Manatee County, Florida, the rate of infection with chronic Hepatitis C has increased from 13.4 per 100,000 population in 2006 (n=42) to 151.6 per 100,000 population in 2016 (n=545). Additionally, from 2013-2016 rates of infection were significantly higher for Manatee County than for the state of Florida. In order to combat morbidity and mortality related to undiagnosed chronic Hepatitis C infection, in 2015 the Florida Department of Health in Manatee County (DOH-Manatee) piloted the use of free rapid Hepatitis C testing services administered in conjunction with HIV/STD screenings during targeted community outreach at free clinics, churches, and local businesses in Manatee County with the following aims: 1) To test hard-to-reach individuals at high risk for contracting Hepatitis C who had never previously been tested, and 2) To use demographic and risk assessment data collected from tested individuals to identify opportunities for service expansion based on need.

METHODS: Over a 12-month period, the DOH-Manatee HIV/STD Mobile Outreach Unit (MOU) offered free Hepatitis C testing to clients seeking HIV/STD screenings at various outreach locations within the county. Prior to testing, clients were asked to complete a risk assessment form that included questions about demographics, Hepatitis testing, vaccination, and diagnosis history, and engagement in risk behaviors. Data from the risk assessments were analyzed in Excel to determine whether tests offered through the DOH-Manatee MOU were reaching untested and at-risk populations.

RESULTS: In total, 2,838 rapid Hepatitis C tests were conducted over the 12-month pilot study period. Of the clients tested, 244 were reactive for Hepatitis C antibodies and 22 clients were identified as having previously tested reactive for Hepatitis C. Over 70% of all clients (n= 2070) were being tested for the first time for Hepatitis C. Of the clients who tested reactive for Hepatitis C antibodies, 66% (n=160) were being tested for the first time. Out of all tested clients, 96% (n=2722) reported engagement in at least one risk behavior, the most common of which included 1) Having multiple sexual partners, 2) having a tattoo, 3) having a body piercing, and 4) inhaling drugs.

CONCLUSIONS: This initiative serves as a model for expanding access to Hepatitis C screenings for at-risk and under-tested populations using previously established community outreach efforts.

Committee Infectious Disease

Topic Hepatitis

Keywords Screening; Hepatitis; Risk Factors

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9609

Abstract Type Poster

Abstract Title Investigating Acute Hepatitis C Seroconversions in Dialysis Facilities, Georgia, 2016-2017

Abstract

BACKGROUND: From July 2016 to January 2017, the Georgia Department of Public Health (GDPH) received reports of acute hepatitis C (HCV) seroconversion among patients undergoing hemodialysis at 3 separate facilities, prompting epidemiologic investigations. The objectives of these investigations were to assess the potential for healthcare-associated HCV infection (HAI), prevent HCV transmission among patients, and determine best practices for epidemiologic investigations in dialysis facilities.

METHODS: The GDPH Hepatitis Program, HAI Program, and District Public Health staff collaborated to conduct these investigations, with guidance from CDC's Division of Viral Hepatitis (DVH) and Division of Healthcare Quality Promotion (DHQP). The GDPH Hepatitis Program developed a response plan to assist District Public Health staff in determining potential source(s) of exposure for hemodialysis patients with acute HCV seroconversion. Based on these findings, dialysis facilities were contacted for onsite investigations, including chart abstraction of epidemiologic data for all HCV-positive patients, an infection control assessment by the HAI Program, and specimen collection for HCV genotype determination and quasispecies analysis by CDC to identify linkages between patients.

RESULTS: Epidemiologic evidence revealed potential HAI at all 3 investigated dialysis facilities. Only one investigation resulted in phylogenetic linkage among HCV-infected patients from the same facility (indicating a match between 2 acute HCV seroconversions and 1 known chronic HCV infection). The average time to complete each investigation was approximately 21 weeks. Challenges included non-compliance with HCV testing among household contacts; inconsistencies in HCV/ALT testing policies within the dialysis facilities; lack of timeliness in specimen collection for molecular testing; and limited public health capacity to conduct these extensive investigations.

CONCLUSIONS: These investigations showed the importance of collaboration among local/district, state, and federal public health partners. Timeliness of specimen collection and lab submission was a key factor, since some specimens were deemed non-viable for molecular testing due to the start of HCV treatment or freeze-thaw cycles that occurred during shipping. Studies have estimated that 15-30% of acute HCV patients spontaneously clear the virus, which further emphasizes the importance of timely viral sequencing during these investigations. Furthermore, the varied frequency of HCV testing (annually vs biannually) and sporadic ALT testing among patients within the investigated dialysis facilities made it difficult to adequately identify a timeframe of potential exposure. Although these investigations were time-consuming and labor-intensive, epidemiologic investigations in dialysis facilities can be completed with the appropriate plans and collaborations in place, despite limited capacity.

Committee Infectious Disease

Topic Hepatitis

Keywords Infectious Diseases; Epidemiology; Hepatitis

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9731
Abstract Type	Poster
Abstract Title	Mortality Risk Among HCV/HIV Co-Infected and Mono-Infected Individuals in Chicago, 2001-2015

Abstract

BACKGROUND: Since 2007, annual Hepatitis C Virus (HCV)-related deaths have surpassed Human Immunodeficiency Virus (HIV)-related deaths in the US. In Chicago, deaths among residents with reported HCV surpassed the number of deaths among residents with HIV since 2010. This analysis compares mortality risk among those co-infected and mono-infected.

METHODS: Chicago HCV cases reported in the Illinois National Electronic Disease Surveillance System (I-NEDSS) and HIV cases reported in the Enhanced HIV/AIDS reporting system (eHARS) were used in the analysis. To identify co-infected individuals, HCV and HIV cases were matched using composite keys based on name and date of birth. Data were limited to records with diagnoses made between 2001 and 2015 for both diseases, and deaths were reported through 2015. Odds ratios (OR) and 95% confidence intervals (CI) were calculated to assess associations between vital status and co-infection/mono-infection. Adjustments were made for age at diagnosis, race/ethnicity, sex, transmission risk (HIV only) and year of diagnosis while evaluating interactions between these variables and co-infection status using multivariable logistic regression analysis.

RESULTS: Through the match, 1,241 individuals were identified as having both an HCV and HIV diagnosis between 2001 and 2015. Of the co-infected, 281 (23%) were known to be deceased compared to 19% with only an HCV diagnosis (4,751/24,720) and 14% with only an HIV diagnosis (2,657/19,103). Significant interaction by diagnosis year was found when comparing co-infected persons to HIV mono-infected and HCV mono-infected persons. Among those diagnosed with HIV from 2001-2005, co-infected individuals had an increased risk of dying over HIV mono-infected (OR: 1.46, CI: 1.21-1.77), while those diagnosed from 2011-2015 had a decreased risk of dying (OR: 0.79, CI: 0.55-1.15). Among those diagnosed with HCV from 2001-2005, co-infected individuals had a decreased risk of dying over HCV mono-infected (OR: 0.47, CI: 0.26-0.86), while those diagnosed from 2011-2015 had an increased risk of dying (OR: 1.64, CI: 0.96-2.81).

CONCLUSIONS: Year of diagnosis seems to play an important role in terms of mortality. Differences in the association between co-infection status and mortality over time may be explained by improved efficacy of antiretroviral medications and access to care for those with HIV and enhanced awareness and detection of HCV infections. Mechanisms to deliver effective medications and access to care for HCV lag behind HIV. By understanding the changes in mortality for HCV and HIV mono-infected individuals over time we can better target efforts that focus on linkage to care and disease management.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Co-Morbidity; Hepatitis; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10067

Abstract Type Poster

Abstract Title Perinatal Hepatitis C Surveillance in Kentucky

Abstract

BACKGROUND: Kentucky (KY) has historically had one of the highest rates of acute hepatitis C (Hep-C) cases in the US. In 2015, Kentucky ranked third in acute Hep-C cases with a rate of 2.7 per 100,000 (US rate of 0.8). Since 2012, hepatitis C virus (HCV) laboratory testing of at-risk individuals has revealed a large number of positive tests in persons aged 20-29 years, and has heightened concerns about the potential for perinatal HCV transmission. In 2013, the KY Viral Hepatitis Prevention Program requested voluntary reporting by healthcare providers of all HCV-positive pregnant women; all infants born to HCV-positive women; and all HCV-positive children aged 0 to 5 years to monitor geographic and temporal trends of perinatal Hep-C transmission. This reporting was mandated by law in February 2015.

METHODS: Perinatal hepatitis reports were collected from December 2013 through December 2016 for hepatitis markers, laboratory information, risk factors and vaccination history of pregnant women or children under the age of 5 years. These data were entered and maintained in Epi Info. Kentucky Office of Vital Statistics (OVS) reports were used to estimate how rigorously perinatal Hep-C cases have been reported.

RESULTS: From December 2013 through December 2016, 1,890 mothers or pregnant women were reported; 1,500 were HCV-antibody positive, five were HCV-antibody negative and 385 had no HCV antibody result. Of the 1,500 HCV-antibody positive women, 16.2% (243) were HCV RNA-positive, 4.1% (62) were HCV RNA-negative; and 79.7% (1,195) lacked confirmatory testing results. An additional 75 women had positive HCV RNA results; one had a negative HCV-antibody test, and 74 had no reported antibody test result. The total number of HCV RNA-positive mothers or pregnant women was 318. OVS reports showed that 2,997 of 166,199 births from 2014 to 2016 had a history of maternal HCV infection recorded on the birth certificate. That number was over 1,000 more than the number of HCV-positive pregnant women reported by clinics and medical providers.

CONCLUSIONS: This report demonstrates the importance of perinatal Hep-C surveillance in Kentucky. The comparison between maternal HCV infections reported to public health and on the birth certificate demonstrated substantial underreporting. More complete reporting from local health departments and healthcare providers can enhance perinatal Hep-C surveillance and may help target resources and prevention services more appropriately throughout the Commonwealth.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9335

Abstract Type Poster

Abstract Title Pregnancy Status and Risk Factors in Women of Reproductive Age with Chronic Hepatitis C in Tennessee

Abstract

BACKGROUND: Tennessee has one of the highest reported case rates of acute Hepatitis C (HCV) infection in the nation, and rates are on the rise. Birth certificate data reveals that the rate of HCV among women giving birth in TN increased 163% from 2009-2014. However, little is known about pregnancy status or risk factors (RFs) for women testing positive for HCV outside health departments (HDs). We sought to ascertain pregnancy status and RFs among reproductive aged women with newly reported chronic HCV in TN.

METHODS: We conducted a prospective cohort study among women aged 18-45 years residing in TN with a newly reported case of chronic HCV between May 1st and October 31st, 2017. We excluded participants tested through HDs or without provider or patient contact information. Investigation occurred in two steps: 1) faxing forms to providers requesting testing reason and pregnancy status at time of testing; then 2) mailing letters to the patients requesting they call the Tennessee Department of Health. When patients called, we provided information regarding test results, access to confirmatory testing, and linkage to care. We also asked patients about pregnancy status and RFs for HCV. We allotted 30 days each for provider and patient responses.

RESULTS: We identified 1,548 eligible participants. As of December 13, 2017, all participants completed the provider follow-up period and 985 participants completed the patient follow-up period. Complete contact information was available for 1,132 (73%) providers and 687 (70%) patients, yielding 59% (n=671) and 28% (n=191) provider and patient response rates, respectively. Of the 757 women with provider and/or patient responses, 30% (n=230) reported being pregnant when tested. Among these, 56% (n=129) had positive HCV RNA test results, denoting current infection. Of the 191 patients providing responses, 58% (n=111) reported a history of injection drug use, 65% (n=124) intranasal drug use, 64% (n=122) prior incarceration, 55% (n=106) were referred to their local HD for linkage to care, and 38% (n=73) for confirmatory HCV RNA testing.

CONCLUSIONS: Strengths of this study included the large study population, high provider response rates, and information obtained from providers and patients. Limitations included missing contact information and possible patient response bias. Given the high rates of pregnancy reported among women with newly diagnosed HCV, hepatitis surveillance efforts should be expanded to include identifying HCV-positive reproductive aged women in attempts to promote informed reproductive planning and reduce the risk of HCV vertical transmission.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Risk Factors; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9552

Abstract Type Poster

Abstract Title Prioritizing Programmatic Efforts to Determine the Burden of Hepatitis C Among High-Risk Populations

Abstract

BACKGROUND: The key to determining the prevalence of hepatitis C (HCV) in a community is screening those at highest risk for HCV infection. Despite limited resources, the Georgia Department of Public Health (DPH) Hepatitis Epidemiology Program leveraged funds to establish a HCV testing initiative within health departments in areas of the state demonstrating high prevalence of HCV and community-based organizations (CBOs) targeting populations at high risk for HCV transmission. These efforts have helped inform programmatic priorities and determine the burden of HCV in Georgia.

METHODS: In 2015, five CBOs targeting high-risk populations and four Public Health Districts were identified to participate in a HCV testing pilot program. Based on results from pilot testing, the HCV Testing Initiative was established in 2016, implementing rapid HCV antibody and HCV RNA/PCR testing in health departments in communities with burdens of injection and non-injection drug use and increases in HCV transmission among young adults ≤ 30 years of age, including the four Georgia counties identified in CDC's *County-level Vulnerability to Rapid Dissemination of HIV/HCV Infection among Persons who Inject Drugs*. DPH Hepatitis Epidemiology Program developed a HCV data collection form used to analyze demographic and risk factor data from all tested patients/clients.

RESULTS: From 2015-2016, 3,315 clients were rapid-tested for HCV antibody, with a 6% positivity rate; males comprised 56% of those positive. While 36% of participants with positive HCV antibody results were between ages 50 and 59 years, 38% were under the age of 40. Of HCV-positive patients between ages 12 and 39 years, 73% were White. In contrast, of the positive patients aged 40 and older, 70% were Black/African American. Of all who tested positive, 28% had engaged in high-risk behaviors within the six months prior to being tested; 58% reported a current or past IDU history; 47% admitted to sharing drug equipment; and 50% were baby boomers. Further, 33% of those with an IDU risk factor reported initiating IDU between the ages of 19 and 24 years; 29% between 25 and 40 years; and 23% by age 18 years.

CONCLUSIONS: While Georgia's resources for HCV testing are limited, the HCV Testing Initiative results show that targeted testing for those at highest risk can not only inform programmatic planning, but also provide a better understanding of the epidemiology of HCV.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10093

Abstract Type Poster

Abstract Title Rapid Hepatitis C Testing in Local Health Department (LHD) Sexually Transmitted Disease (STD) Clinics in Illinois, 2015-2017

Abstract

Rapid Hepatitis C Testing in Local Health Department (LHD) Sexually Transmitted Disease (STD) Clinics in Illinois, 2015-2017 Lesli Choat, B.S., MT (ASCP) Danucha Brikshavana, M.P.H., Eduardo Alvarado, M.P.H., MPAP, AAHIVS, Illinois Department of Public Health (IDPH)

BACKGROUND: Hepatitis C Virus (HCV) is a growing public health concern with infection rates predicted by the Centers for Disease Control and Prevention (CDC) to peak in the year 2033. It is estimated by CDC that 75% of persons with HCV infection remain unaware of their status. Effective screening programs are urgently needed to provide undiagnosed HCV infected individuals with therapy. With the introduction of direct-acting antiviral (DAA) therapy, there are now even greater opportunities for widespread treatment and cure for patients with chronic HCV infection. On January 1, 2015 IDPH began supporting rapid HCV testing in select STD clinic sites.

METHODS: HCV rapid antibody screening at select STD clinics was supported (12 in 2015, 13 in 2016, and 16 in 2017). Participating clinics are geographically distributed across all regions of the state and offered HCV screening to clients seeking STD services. Any clients testing antibody positive were offered educational information and referred to a clinician to receive follow-up testing and treatment as needed. Descriptive statistics of clients consenting for HCV screening including risk and positivity rates of those screened were performed.

RESULTS: In 2015, 12.0% (804) of STD clients at participating sites were screened for HCV with a 4.5% (36) positivity rate. In 2016, 14.1% (690) were screened with a 6.2% (43) positivity rate. In 2017, 18.4% (722) were screened with a 9.8% (71) positivity rate.

CONCLUSIONS: LHD STD clinic sites offer extremely effective HCV screening opportunities. Over the project period, the number of clinics participating increased and the overall positivity rates also increased, demonstrating HCV screening offered in STD clinics can provide for otherwise missed opportunities among clients seeking STD services. This resulted in Illinois residents previously unaware of their HCV antibody positive status referred for clinical follow-up testing and treatment if appropriate.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Screening; Sexually Transmitted Diseases

Consider for Different Presentation? No

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Submission Type Breakout/Quick/Lightning/Poster

ID 9615

Abstract Type Poster

Abstract Title Tennessee Department of Health's HCV Community Based Organization Rapid Testing Project

Abstract

BACKGROUND: The U.S. Preventive Services Task Force recommends one-time HCV testing for all Baby Boomers and ongoing risk-based HCV testing, including persons with histories of injection or illicit intranasal drug use, incarceration, tattoo or body piercing, sexual contact with an HCV positive individual, or history of an STD or multiple sex partners.¹ Despite these recommendations, approximately half of the estimated 3.5 million individuals infected with HCV in the U.S. are unaware of their infection.² The Tennessee Department of Health (TDH) partnered with Community Based Organizations (CBOs) to increase HCV testing among populations at increased risk of acquiring HCV who are infrequently engaged in traditional health care settings.

METHODS: CBO partners were identified through existing relationships with HIV prevention program testing sites. The CBOs were vetted to confirm that they serve populations at-risk of acquiring HCV, and that they fulfill the requirements for testing (CLIA Waived, internal quality assurance and training programs and verification of proper storage). Approved CBOs received HCV rapid antibody (Ab) test kits in exchange for monthly data reports (aggregate testing reports plus line-item reports for those testing positive). Individuals testing positive were referred to local health departments for confirmatory HCV RNA testing and linkage to care.

RESULTS: Data was collected for all individuals testing by participating CBOs from January 2016 through August 2017. A total of 4,371 HCV Ab tests were performed with a 33.4% (n=1,462) positivity rate. Expanded individual demographic and risk factor information was available for the 532 Ab positive clients detected from January through August 2017. Of the 532 Ab-positive clients: 53.7% were male; 94.2% white; and self-reported risk factors included histories of injection drug use (90.9%), illicit intranasal drug use (79.4%), incarceration (72.4%), tattoo or body piercing (62.8%), sexual contact with HCV positive individual (36.4%), or STD or multiple sex partners (29.9%).

CONCLUSIONS: TDH's partnership with CBOs resulted in substantial HCV Ab positivity rates among high-risk individuals which otherwise may not have been tested for HCV or linked to care. The positivity rates demonstrated the need for increased HCV screening in both clinical and non-clinical settings, as well as mechanisms for patient referral for confirmatory HCV testing and care and treatment.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Infectious Diseases; Risk Factors

Consider for Different Presentation? Yes

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State Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	9555
Abstract Type	Poster
Abstract Title	Tennessee Department of Health's Viral Hepatitis Case Navigators: Linkage to Care and Treatment Services

Abstract

BACKGROUND: Hepatitis C (HCV) infections are increasing nationwide and are of particular concern in Tennessee[1],[2]. Without treatment, individuals living with HCV may develop liver cancer, cirrhosis, or other life-threatening HCV-related diseases, and may transmit the disease to others. Unfortunately, HCV infected individuals face significant barriers to accessing HCV treatment and related medical services[3]. In order to facilitate linkage to HCV treatment and other available medical services, the Tennessee Department of Health has built capacity to navigate HCV-positive clients to care by establishing eight regional Viral Hepatitis Case Navigator (VHCN) positions. VHCNs are primarily responsible for identifying acute or chronically infected individuals residing in their region and subsequently referring clients to HCV treatment or other medical services based on client-centered goals.

METHODS: A Routine Electronic Data Capture (REDCap) database was established to track navigation efforts/referrals. All health department (HD) clients testing HCV RNA-positive are imported into this database weekly to populate each navigator's queue. Any additional clients navigated (i.e. acute, self-referred, etc.) are manually entered by the navigator. Contact attempts were made via phone call, text message, and/or letter. Clients were considered contacted if they were spoken to by a navigator.

RESULTS: Formalized data collection of navigation efforts began July 3, 2017. As of December 19, 2017, 1,381 clients were identified for VHCN follow-up, of whom 55% (n=755) were male, 24% (n=335) were less than 30 years of age, and 90% (n=1,246) were Non-Hispanic White. Of the 1,340 (97%) clients who reported risk factor information at the time of testing, 68% (n=910) reported a history of injection drug use, 63% (n=850) history of snorting drugs, and 66% (n=883) history of incarceration. VHCNs made at least one contact attempt for 846 (61%) clients. Of the 536 (39%) clients successfully contacted by the navigator, 72% (n=386) were referred to HCV treatment, 16% (n=84) were referred to substance abuse treatment, 3% (n=14) were referred to mental health services, and <1% (n=2) were referred to HIV care.

CONCLUSIONS: Though not all clients identified for VHCN follow-up were contacted, a large proportion of clients who spoke to a navigator received a referral to an appropriate service. VHCNs can be a crucial component in helping clients access the care they need to navigate towards successful outcomes. Intensive efforts to provide linkage to treatment and supportive services to HCV-infected clients are critical to ensure increased access to treatment and reduce the risk of HCV disease progression and transmission.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Capacity / Capacity Building; Hepatitis
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9797
Abstract Type	Quick
Abstract Title	Acute Hepatitis B Cluster Associated with Injection Drug Use in Southeastern Massachusetts

Abstract

BACKGROUND: In October 2017, the Massachusetts Department of Public Health (MDPH) observed an increase in cases of acute hepatitis B virus (HBV) infection reported from a city of about 95,000 in southeastern Massachusetts. Our objective was to characterize the cases to prevent and control additional cases.

METHODS: All suspect acute HBV infection cases are reportable to MDPH and investigated by local health departments using the Massachusetts Virtual Epidemiologic Network (MAVEN) as a surveillance and case management tool. MAVEN was queried for HBV cases since January 1, 2010. Cases defined as “acute confirmed” or “acute suspect” were included. The cluster area was defined as the initial city and the towns directly surrounding. Data are accurate as of November 29, 2017.

RESULTS: In the first 11 months of 2017, there were 130 acute HBV cases reported in Massachusetts. Fifty-nine percent of cases were male. The median age was 46 years. Of the cases for which race data were available (N=76), 68% were white. Of the cases for which ethnicity was available (N=49), 84% were non-Hispanic. Of the cases with drug use data available (N=32), 22% reported injecting drugs within the incubation period. There were 17 acute HBV cases in the cluster area, an 83% increase over the annual average number reported between 2010 and 2016. There were 13 cases with injection drug use or laboratory evidence of hepatitis C virus (HCV) infection; further analyses focus on these cases. There were 8 males and 5 females, with a median age of 40 years. Of the 10 cases for which race data were available, all were white. Of the 6 cases for which ethnicity data were available, 1 was Hispanic and 5 were non-Hispanic. Of the 10 cases for which drug use history was available, 9 reported injecting drugs within the incubation period. One case was coinfectd with HIV, and the other 12 had laboratory evidence of HCV infection. Of these 12 cases, 5 cases tested positive for HBV and HCV on the same day, and 7 tested positive for HCV prior to testing positive for HBV. One case was experiencing homelessness and one was incarcerated.

CONCLUSIONS: MDPH identified a cluster of 13 cases of acute HBV infection among individuals with high rates of injection drug use and HCV coinfection. As HCV infection likely preceded HBV infection, our ongoing investigation highlights the need to vaccinate persons with HCV infection to prevent HBV and hepatitis A virus infection.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Substance Use; Hepatitis; Co-Morbidity
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9205

Abstract Type Quick

Abstract Title Assessing the Impact of the 2016 Acute and Chronic Hepatitis C Case Definitions

Abstract

BACKGROUND: Hepatitis C virus (HCV) infection is one of the highest volume reportable conditions, causing significant morbidity and mortality. In 2016, revised surveillance case definitions were implemented for acute and chronic HCV infection. They contained significant differences from prior definitions, primarily focusing on improving acute case capture and restricting confirmed cases to those with evidence of infection. We aimed to retroactively apply the 2016 case definition to 2007-2015 surveillance data and describe case count changes.

METHODS: Over 700,000 laboratory test results from this period, along with case report form data, were extracted from the Massachusetts Virtual Epidemiologic Network (MAVEN). An algorithm was developed in SAS categorizing laboratory test results into positive or negative for antibody tests and nucleic acid tests (NATs), and continuous values for ALT results. As the definition is applied for surveillance purposes, utilizing a twelve-month reporting period, results collected more than one year after the case's first positive result were disregarded. Results were ordered chronologically, and the first and last test results of each type were identified, along with evidence of seroconversion. Clinical data were added, and indicator variables were created for HCV-related symptoms and elevated ALTs. Case definitions were assigned based on types of laboratory results available and presence of clinical criteria. Finally, antibody positive cases with negative NAT results were revoked.

RESULTS: Compared with case counts from the prior case definitions, the total number of reported confirmed and probable cases decreased 7.1% from 76,958 to 71,507 over the period. Confirmed cases decreased 33.4% from 53,702 to 35,779, while cases with a confirmed status according to the new definition increased from 42.4% in 2007 to 60.0% in 2015. Acute cases decreased 76.9% from 1,951 to 449, though there was now a seven-fold, versus three-fold, increase in acute cases over the period.

CONCLUSIONS: The case count decrease began accelerating in 2013, as reporting of negative NAT results began. The decrease in confirmed cases is due partially to the removal of high signal-to-cutoff antibody results as confirmatory, while the increasing proportion of confirmed cases can be attributed to reflex NAT testing. The effect of the more liberal acute definition was outweighed by the automated requirement for at least one HCV-related symptom to be reported. This finding will inform improvements in internal case review procedures. Our analysis provides an important tool for describing reported HCV incidence and prevalence, and highlights the need for consistent interpretation and application of case definitions across jurisdictions.

Committee Infectious Disease

Topic Hepatitis

Keywords Infectious Diseases; Surveillance; Hepatitis

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9467

Abstract Type Quick

Abstract Title Curing People Who Inject Drugs of Hepatitis C in Non-Specialty Care Settings

Abstract

BACKGROUND: People who inject drugs (PWID) have high rates of hepatitis C virus (HCV) infection yet face many barriers to medical care. In March 2016, the California Department of Public Health (CDPH) funded organizations in three local health jurisdictions (LHJs) to conduct intensive client navigation and to increase the number of providers treating HCV in non-specialty care settings, including primary care clinics, methadone clinics, and shelters. Funded sites included two urban federally qualified health centers (FQHCs) and one safety-net primary care and behavioral health network administered by an urban health department. This abstract describes these grantees' HCV treatment outcomes.

METHODS: Funded sites used electronic health records (EHR) to identify clients in their EHR systems diagnosed with current HCV infection. Each site collected data outside their EHR on demographics, HCV test results, treatment initiation, treatment completion, and sustained virologic response (SVR, or cure). Grantees provided CDPH with client level data monthly in Excel or Access via secure file transfer protocol. CDPH produced aggregate statistics on HCV treatment outcomes across all sites using SAS 9.4. Analysis was limited to clients who started treatment by February 28, 2017. Treatment outcomes were tracked through September 30, 2017. Chi-square analyses were conducted for associations between achieving SVR and lifetime injection drug use.

RESULTS: From March 1, 2016 through February 28, 2017, grantees initiated HCV treatment for 277 clients in non-specialty care settings. Among clients who started treatment, 164 (59 percent) were known to have ever injected drugs, of whom 156 (95 percent) completed treatment and were eligible for 12 week post-treatment SVR testing, 129 (79 percent) received SVR testing, and 123 (75 percent) achieved SVR. Among the 113 clients who initiated treatment and who were not known to have injected drugs, 102 (90 percent) completed treatment and were eligible for 12-week post-treatment SVR testing, 80 (71 percent) received SVR testing, and 77 (68 percent) achieved SVR. There was no significant difference between PWID and clients not known to inject drugs in achieving SVR ($p=0.2$).

CONCLUSIONS: Seventy-five percent of PWID who initiated treatment were known to achieve SVR as were 68 percent of clients who initiated treatment and were not known to inject drugs. The difference in the achieving SVR between these two groups was not statistically significant. This outcome suggests hepatitis C can be effectively treated and cured among both PWID and people without a known injection drug use history in non-specialty care settings.

Committee Infectious Disease

Topic Hepatitis

Keywords Health Care; Hepatitis; Substance Use

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9940

Abstract Type Quick

Abstract Title Impact of Electronic Lab Reporting and Automated De-Duplication on Hepatitis C Surveillance in Michigan

Abstract

BACKGROUND: Hepatitis C Virus (HCV) surveillance is complicated by the chronic nature of infection and the volume of laboratory results; therefore, having automated systems to report and process HCV labs and de-duplicate patients/cases is critical. This is particularly true for jurisdictions receiving negative HCV laboratory results to capture seroconversions and/or HCV clearance. The Michigan Disease Surveillance System (MDSS) receives both manual and electronic lab reports (ELR). Built-in algorithms flag incoming results for patient and then case de-duplication. Historically, these potential matches have required manual adjudication. We monitored trends in manual versus ELR submission of HCV labs reported to the MDSS over time and its impact on patient and case de-duplication. In addition, recent enhancements to automate de-duplication were evaluated.

METHODS: Monthly HCV lab counts were extracted from MDSS between 2013 and 2017. These data were categorized relative to how the lab results were entered (manual vs. ELR), whether a new case was created, whether the incoming patient was de-duplicated, and (for labs that matched existing cases) whether those case matches were manually or automatically merged. Descriptive analysis was then conducted to identify gaps in current functionality, to inform needs relative to anticipated changes in HCV surveillance, and to highlight where key potential for additional system development may lie.

RESULTS: The number of HCV results reported to MDSS increased from 14,272 in 2013 to 34,638 in 2017. The proportion reported via ELR increased from 40.5% to 62.3% during this same time frame. Over the study period the number of these HCV labs that matched an existing patient in MDSS remained relatively constant at approximately 80%. In 2013, two-thirds of all HCV labs matched an existing HCV case, while in 2017 that proportion grew to 74.3%. Automated patient de-duplication enhancements greatly reduced the number requiring manual resolution. Approximately 85% of all patient merges occurred automatically and 67% of case merges occurred automatically.

CONCLUSIONS: While continued system development and increased automation in the MDSS have made significant inroads in alleviating some burdens common to disease surveillance systems, additional improvements are still necessary to support anticipated changes in HCV reporting (such as receipt of negative HCV lab results) while minimizing manual intervention. Implementation of automated patient de-duplication and auto-case merging have significantly reduced the burden of manual intervention for these events, especially in the “ELR era”, however de-duplication algorithms might be optimized to better capture patient/case matches and further reduce reliance on manual processes.

Committee Infectious Disease

Topic Hepatitis

Keywords Surveillance; Electronic Laboratory Reporting (ELR); Hepatitis

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9767

Abstract Type Quick

Abstract Title Increase in Hepatitis A Virus Infections — Colorado, January–July 2017

Abstract

BACKGROUND: During April 2017, the Colorado Department of Public Health and Environment noted an increase in reported hepatitis A virus (HAV) cases, predominantly among men, over baseline rates (median, 27.5 cases/year during 2007–2016). Men who have sex with men (MSM) are routinely recommended to receive hepatitis A vaccination because of their higher risk. We sought to describe the epidemiology to launch targeted prevention efforts.

METHODS: We defined a confirmed case as clinical symptoms consistent with acute viral hepatitis, jaundice or elevated liver enzymes, and laboratory-confirmation of immunoglobulin M antibody to hepatitis A virus or an epidemiologic link to a laboratory-confirmed case. Cases were identified through routine surveillance. CDC performed molecular sequencing on available specimens.

RESULTS: During January 1–July 31, 2017, a total of 51 confirmed HAV cases were reported. Cases were among patients aged 19–83 years (median age 46 years); 38 (75%) were male. Twenty-seven patients (53%) were hospitalized, and 1 death was reported. Among the 38 males, 18 (47%) self-identified as MSM or reported sexual contact with other men. Sequencing revealed 7 distinct strains, 3 associated with outbreaks occurring outside of Colorado. The 2 most common strains, accounting for 13 (68%) of 19 sequenced isolates, were predominantly among MSM or their household contacts in 2 Colorado metropolitan areas.

CONCLUSIONS: Multiple HAV strains among the 19 HAV cases with known genotype do not support a single chain of transmission linking these cases. Public health response included social media messaging, outreach to providers and media, and hepatitis A vaccination efforts focusing on the MSM population. However, continued outreach and increased vaccination efforts among this population are needed.

Committee Infectious Disease

Topic Hepatitis

Keywords Underserved Populations; Hepatitis; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9571

Abstract Type Quick

Abstract Title Measuring the Impact of the 2016 Case Definition Change on Acute and Chronic HCV Surveillance Numbers

Abstract

BACKGROUND: In 2016, the CDC/CSTE Hepatitis C Virus (HCV) case definition was revised; largely lowering the threshold for inclusion as an acute or chronic HCV case. Our study looks to measure the impact the case definition change had on HCV surveillance numbers reported in Michigan post-implementation of the new case definition.

METHODS: All acute and chronic HCV cases meeting the new HCV case definition were extracted from the Michigan Disease Surveillance System between January 1, 2016 and June 30, 2017. These cases were then evaluated against the old CDC/CSTE HCV case definition (2012). Case counts in 2016 and 2017 were compared utilizing the old versus the new case definitions.

RESULTS: Using the 2016 CDC/CSTE case definition, 241 acute HCV cases were recorded during the study period. Of those, 146 would have satisfied the 2012 case definition criteria. Therefore, the change in the case definition was responsible for an increase of 95 (65.1%) acute HCV cases, 16 of which were counted as a result of extending the seroconversion window from 6 to 12 months, 34 as a result of including HCV antibody test results with a low or missing signal to cut-off ratio (S/CO), 35 were included as a result of lowering the alanine aminotransferase (ALT) threshold from greater than 400IU/L to 200IU/L, and 10 were included despite a positive Hepatitis A IgM. During the study period MDHHS recorded 18,090 chronic HCV cases using the 2016 CDC/CSTE case definition. Of those, 12,328 would have satisfied the 2012 case definition criteria. Therefore, the change in the case definition was responsible for an increase of 5,762 (46.7%) chronic HCV cases. Of those 5,762 cases, 222 were counted as a result of having a low S/CO ratio and 5,540 due to an unknown S/CO ratio and normal or unknown ALT.

CONCLUSIONS: Michigan saw its acute HCV case count rise from 84 cases in 2015 to 154 cases in 2016. Whether this represented a true increase in acute HCV cases or was partially a result of the change in the case definition was unknown. The same was true for chronic HCV cases which increased from 7,833 to 11,883 between 2015 and 2016. This analysis shows that a large proportion of Michigan's acute and chronic HCV cases counted post-implementation of the 2016 case definition was the result of less stringent inclusion criteria. This understanding will help inform interpretation of both local and national acute and chronic HCV surveillance trends.

Committee Infectious Disease

Topic Hepatitis

Keywords Hepatitis; Surveillance; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9063

Abstract Type Quick

Abstract Title Perinatal Hepatitis C Infections in California, 2007-2014

Abstract

BACKGROUND: From 2007-2015, rates of newly reported chronic hepatitis C virus (HCV) infections in California increased 37% among women 20-29 years of age. This trend raises the possibility of increased mother-to-child HCV transmission—a trend that has been observed in other U.S. jurisdictions. California Department of Public Health (CDPH) sought to describe the number of California children at-risk for, and reported with, perinatal HCV, and to assess the accuracy of maternal HCV reported on infant birth certificates.

METHODS: Positive HCV lab test results are reportable in California, and CDPH maintains a person-level registry containing cumulative case reports and lab testing history for Californians reported with chronic HCV infection. Using a probabilistic matching algorithm, CDPH matched cases in the HCV registry with state birth records to identify California mothers who had a live birth during 2007-2014 and HCV detection (reported as a confirmed or probable chronic case, or having antibody or ribonucleic acid (RNA) positivity). Among matched births, CDPH assessed the number with maternal HCV infection status indicated on the birth certificate. CDPH subsequently matched births among RNA-positive mothers with the HCV registry to identify children reported as a confirmed chronic case or having RNA positivity. The observed number of lab-confirmed perinatal HCV cases was compared to the expected number (5.8% of births to RNA-positive mothers).

RESULTS: California residents had more than 4.1 million live births from January 2007-December 2014. The HCV registry contained 241,604 individuals of female, transgender, or unknown sex with HCV detection. CDPH identified 18,256 births (less than 0.5% of total live births) to mothers with HCV detection, 5,649 (31%) of which were to mothers with history of HCV RNA positivity. Among 5,649 births to RNA-positive mothers, 748 (13%) had maternal HCV infection reported on the birth certificate. Among the RNA-positive mothers, CDPH identified 167 children reported as a confirmed chronic HCV case or having RNA positivity; only 18 tested RNA-positive between 2-36 months of age. Using the expected 5.8% vertical transmission rate, 328 children were expected to have acquired HCV perinatally, but only 18 were reported to public health.

CONCLUSIONS: This analysis describes the number of California children who were potentially at-risk of acquiring HCV perinatally during 2007-2014, and demonstrates a need to improve HCV testing among children born to HCV-infected mothers. Maternal HCV infection was often underreported on birth certificates, underscoring a need for improved reporting on live-birth certificates, and possibly improved HCV screening of pregnant women.

Committee Infectious Disease

Topic Hepatitis

Keywords Surveillance; Hepatitis; Maternal and Child Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10275

Abstract Type Quick

Abstract Title Predictors of Chronic Hepatitis C Treatment Among Patients of a Multi-Site Collaboration Project

Abstract

BACKGROUND: Patients with chronic hepatitis C virus (HCV) are at risk of liver-related morbidity and mortality. It is recommended that nearly all infected patients receive treatment using direct-acting antivirals (DAA). The HCV Test and Cure (TAC) Project partners Public Health – Seattle & King County with six healthcare organizations to increase HCV diagnosis and treatment. Using TAC data, predictors of HCV treatment were examined.

METHODS: Electronic health record data (9/30/13-9/30/17) of lab-confirmed HCV patients were examined to identify factors associated with HCV treatment including demographics (gender, race/ethnicity, and high-risk birth year cohort [between 1945-1965]), insurance (private insurance, Medicaid, Medicare, or other/uninsured), comorbidities (HIV, hepatitis b, cirrhosis, liver transplant, diabetes, kidney disease, dialysis), substance use history (history of injection drug use [IDU], alcohol use, or opioid use), and time from diagnosis to follow-up visit. Bivariate relationships were examined between HCV treatment and each factor using chi-square tests. Stepwise logistic regression modeling was used to determine which factors were associated with HCV treatment.

RESULTS: Of 8917 HCV patients, 4186 were prescribed HCV treatment. Females (adjusted odds ratio [aOR]=1.17; 95% confidence interval [CI]=1.06-1.28) and those born between 1945-1965 (aOR=1.71; 95%CI=1.55-1.88) were more likely to receive HCV treatment, as were patients with cirrhosis (aOR=1.26; 95%CI=1.12-1.40), liver transplant (aOR=2.49; 95%CI=1.56-3.95), or HIV (aOR=1.25; 95%CI=1.04-1.50). Compared to non-Hispanic whites, Asians were more likely to be treated (aOR=1.38; 95%CI=1.12-1.69). Compared to those on private insurance, Medicaid patients were less likely to be treated (aOR=0.75; 95%CI=0.67-0.84) as were uninsured patients (aOR=0.29; 95%CI=0.23-0.38). History of IDU (aOR=0.80; 95%CI=0.70-0.91) or opioid use (aOR=0.81; 95%CI=0.72-0.91) was associated with a decreased likelihood of treatment. Each 90-day delay in returning for follow-up visit resulted in a 13% decreased odds of receiving treatment (aOR=0.87; 95%CI=0.86-0.89).

CONCLUSIONS: HCV patients with severe liver damage or co-infection with HIV were more likely to be treated, while other comorbid conditions like diabetes and co-infection with hepatitis B had no association with HCV treatment. This likely reflects the effect of initial criteria restricting insurance coverage of DAA to patients with more advanced disease. Patients with documented history of IDU or opioid use were less likely to receive treatment. Although females comprised 36% of all HCV patients, they were more likely to be treated compared to males. Delays in returning for a follow-up visit after diagnosis were associated with decreased odds of treatment, highlighting the importance of linkage to care.

Committee Infectious Disease

Topic Hepatitis

Keywords Epidemiology; Hepatitis

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9466
Abstract Type	Quick
Abstract Title	Testing and Linkage to Hepatitis C Care Outcomes Among People Who Inject Drugs in California

Abstract

BACKGROUND: Hepatitis C virus (HCV) infection is a leading cause of liver cancer and liver transplantations, yet most people with HCV are unaware of their infection. People who inject drugs (PWID) compose 68 percent of new HCV infections and frequently face barriers to medical care. In March 2016, the California Department of Public Health (CDPH) funded community based organizations (CBOs) in three local health jurisdictions to conduct outreach, HCV antibody (anti-HCV) testing, HCV ribonucleic acid (RNA) testing, and linkage to HCV medical care. Grantees comprised of one urban syringe exchange program, one rural AIDS service organization, and one urban federally qualified health center (FQHC). This abstract describes these organizations' HCV testing and linkage to care outcomes.

METHODS: HCV testing was conducted in drug treatment facilities, syringe exchange programs, shelters, and single room occupancy hotels. CBOs used new or existing data collection systems to record demographics, HCV test results, attendance at first HCV medical appointment, and barriers to accessing medical care. Grantees provided CDPH with client level data monthly in Excel or Access via secure file transfer protocol. CDPH used SAS 9.4 to summarize outcomes across all three organizations.

RESULTS: From March 1, 2016 through September 30, 2017, grantees screened 3,963 clients for anti-HCV. Among screened clients, 2217 (56 percent) reported ever injecting drugs, and 947 (24 percent) tested anti-HCV positive. Among those with positive anti-HCV results, 627 (66 percent) received HCV RNA testing, 464 (74 percent) of whom tested HCV RNA positive. Among those with RNA positive results, 328 (70 percent) were referred to HCV care, of whom 190 (58 percent) were known to have attended their first medical appointment. Among clients who attended their first medical appointment, 168 (88 percent) reported ever injecting drugs. Clients also reported the following structural barriers in the past year: unstable housing (56 percent); incarceration (39 percent).

CONCLUSIONS: In three state-funded projects, CBOs testing PWID in drug treatment, syringe exchange, and residential settings yielded high rates of HCV positivity (24 percent). Sixty-six percent of clients with positive anti-HCV results received RNA testing, and 58 percent of clients with positive RNA results who were referred to care attended their first medical appointment, in spite of reported structural barriers such as unstable housing and incarceration. Health departments can use these findings to identify settings in which to support HCV testing and linkage initiatives.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Barriers to Care; Hepatitis; Substance Use
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9506
Abstract Type	Quick
Abstract Title	Using Surveillance Data to Implement Mandatory Hepatitis C RNA Reflex Confirmatory Testing in New York City

Abstract

BACKGROUND: Testing for hepatitis C virus (HCV) involves two steps: antibody screening, indicating whether a person has ever been infected, and, if positive, a confirmatory RNA test to establish current infection. If an RNA test is not ordered at the time of the initial test, the person must return for complete diagnostic testing. From 2006-2013, nearly one-third of people with a positive HCV antibody test in NYC did not have an RNA test to confirm their infection. Since 2013, confirmatory testing has been increasing; however, in 2016, 21% still did not have confirmatory testing. To improve the proportion of people infected with HCV who are aware of their status, linked to care, and cured, the NYC Health Department used the low confirmatory rate finding based on NYC surveillance data as justification for a proposed amendment to the NYC Health Code requiring laboratories to routinely perform reflex HCV RNA testing when the antibody test is positive.

METHODS: HCV antibody and RNA test results reported to the NYC Health Department were used to generate RNA confirmatory and reflex testing rates. Reflex testing was defined as when the RNA test was performed on the same specimen as the antibody test using the specimen dates. Reflex testing was assessed for unique individuals by diagnosis year and as a proportion of all antibody tests performed.

RESULTS: From 2006-2016, there were 436,331 positive antibody tests reported for 138,240 NYC residents. Among the 109,712 people newly reported with HCV during this time period, confirmatory testing increased from 72% in 2006 to 79% in 2016. Reflex testing also increased from 7% among people diagnosed in 2006 to 43% in 2016. Among those without reflex testing, the median number of months from the first positive antibody test to first RNA test was 6 months (IQR: 1, 39). In September 2017, the NYC Board of Health adopted the amendment requiring laboratories to perform reflex RNA testing. A “Dear Colleague” letter was sent to all NYC laboratory directors notifying them of the change. Preliminary findings indicate that in 2017, for the first time, over 50% of antibody positive tests were reflexed to an RNA test.

CONCLUSIONS: Robust HCV surveillance registries allow programs to determine confirmatory and RNA reflex testing rates and advocate for improved testing practices. We anticipate that reflex testing will increase throughout 2018 as more laboratories implement reflex RNA testing. Plans for monitoring compliance and reporting back to laboratories are being developed.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Surveillance; Screening; Hepatitis
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9736

Abstract Type Quick

Abstract Title Using Surveillance Data to Understand Hepatitis C Testing Practices at New York City Hospitals

Abstract

BACKGROUND: According to national guidelines, patients with a positive hepatitis C virus (HCV) antibody test result require a confirmatory HCV RNA test to establish current infection status. However, in 2016, almost one-quarter of patients newly reported to the New York City (NYC) Department of Health and Mental Hygiene (DOHMH) with a positive antibody test did not have a RNA test within three months. Using surveillance data from patients of the Hepatitis C Clinical Exchange Network (HepCX), a DOHMH-facilitated provider-to-provider learning collaborative comprised of 38 NYC hospitals, we created a HCV testing dashboard for the goal of improving the rates of HCV confirmatory RNA testing. The dashboard, a report of RNA testing rates of HCV antibody positive patients by HepCX facility, allows visualization of gaps in RNA testing, and is used to work one-on-one with facilities to increase RNA testing.

METHODS: The DOHMH receives positive HCV antibody and positive and negative HCV RNA results for NYC residents, which were used to assess rates of confirmatory RNA testing. Confirmatory RNA testing can be ordered at a follow-up provider visit, or done as reflex testing (automatically performed on same specimen as positive antibody test). Test results were assigned to a standardized facility by evaluating health care facility data for matches to key values of name, address and phone number of HepCX facilities. Dashboards displaying percentage of patients with a positive antibody test in 2016 who received a RNA confirmatory test ordered by the same facility within 3 months was generated using Microsoft Excel.

RESULTS: In 2016, there were 15,493 patients with a positive antibody test ordered by a HepCX hospital and 67% (10,332) had RNA test within 3 months of their antibody test. The median facility RNA confirmatory testing rate was 77% (range 10-100%). HepCX hospitals with reflex RNA testing had a median RNA testing rate of 90% (range 72-100%). Variability of data used to standardize health care facility was a limitation of this analysis which could underestimate confirmatory testing rates. Dashboards were emailed to each HepCX facility, and high volume facilities will be displayed on the DOHMH website.

CONCLUSIONS: HCV facility dashboards can be used to illustrate differences in HCV testing practices among high volume HCV facilities. By sharing the dashboards with hospitals, we aimed to highlight the benefit of implementing reflex RNA testing. Future dashboards could display surveillance-based HCV treatment initiation and cure rates to assess linkage to care and treatment.

Committee Infectious Disease

Topic Hepatitis

Keywords Chronic Disease; Surveillance

Consider for Different Presentation? Yes

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Submission Type	Roundtable
ID	9232
Abstract Type	Roundtable
Abstract Title	Drawing from State Experiences to Launch Formal Guidance for Developing Viral Hepatitis Epidemiologic Profiles

Abstract

Key Objectives:

The Association of State and Territorial Health Officials (ASTHO) and the Centers for Disease Control and Prevention (CDC) will engage partner organizations, national, state, and local stakeholders to:

- Share ASTHO and CDC's guidance document and supporting tools for developing viral hepatitis epidemiologic profiles.

- Collect feedback from stakeholders to inform future revisions/adaptations of the guidance and tools.
- Discuss alignment with complementary hepatitis surveillance and capacity-building initiatives.

Brief Summary:

Since 2014, ASTHO, with support from CDC, has funded 22 health departments to develop and use viral hepatitis epidemiologic profiles. These profiles incorporate an array of routine and novel data sources (e.g., notifiable disease surveillance, vital records, hospitalization records, cancer registries, organ transplant registries) to describe the burden of viral hepatitis within a jurisdiction. State grantees have used their profiles to raise awareness, engage new partners, and target public health interventions. With the explosion of the opioid epidemic and related increases in hepatitis infections, augmenting surveillance data to identify at-risk populations is critical – and viral hepatitis epidemiologic profiles can be an important tool towards this end. In an effort to provide support to other jurisdictions for the development and use of viral hepatitis epidemiologic profiles, ASTHO and CDC are launching a guidance toolkit. The toolkit is informed by lessons learned and implementation experience from previous grantees and includes tips on assembling a profile development team, setting the scope of the profile, identifying and using data sources, engaging stakeholders, and launching and evaluating the profile. Participants in the roundtable will have the opportunity to review the guidance toolkit, provide feedback, and discuss how this guidance can align with and complement other national initiatives around building hepatitis program capacity and developing definitions for core hepatitis surveillance.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Local Epidemiology; Hepatitis; Capacity / Capacity Building
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10364
Abstract Type	Roundtable
Abstract Title	Seeking Control of Hepatitis A Outbreaks Among People Experiencing Homelessness or Using Illicit Drugs and Men Who Have Sex with Men – California, 2016–2017

Abstract

Key Objectives:

- Identify successful methods and partnerships to reach at-risk populations for hepatitis A vaccination, including people experiencing homelessness or using illicit drugs and men who have sex with men
- Identify interventions to improve environmental sanitation to decrease risk of hepatitis A transmission among people exposed to settings with limited sanitation
- Understand uses of laboratory result data coupled with epidemiological information to assess the degree of local transmission of hepatitis A
- Identify lessons learned from the current outbreak response and steps for lasting prevention of hepatitis A transmission in the at-risk populations

Brief Summary:

Beginning in November 2016, hepatitis A cases began to rise in California among people experiencing homelessness and/or using illicit drugs in settings of limited sanitation, culminating in the largest outbreak of hepatitis A with person-to-person transmission in the United States since hepatitis A vaccination began in 1996. In addition, many jurisdictions began seeing multi-fold rises in hepatitis A cases among men who have sex with men (MSM), linked to outbreaks across other parts of the Americas and Europe. As multiple jurisdictions are seeing large outbreaks of hepatitis A from person-to-person transmission, we seek to share and obtain input about what works and what doesn't work to reach the at-risk populations with vaccine and interventions to improve environmental sanitation. Implementation of hepatitis A virus typing at CDPH accelerated case-linking efforts. We will share and obtain input in understanding about how the use of laboratory results has guided investigation and linking of outbreak cases. Multiple barriers have been encountered in this outbreak response. People experiencing homelessness and using illicit drugs can be especially difficult to reach given issues of lack of access to care, mistrust of government and sometimes mental illness. On the other hand, MSM have greater access to care and higher levels of insurance coverage, but face different challenges related to delivering targeted health messages. An additional challenge encountered during this outbreak is a constrained supply of single antigen adult hepatitis A vaccine. This session will provide an opportunity to exchange ideas on overcoming these barriers as well as to discuss successful strategies for providing lasting prevention of hepatitis A cases and outbreaks among these at-risk populations.

Committee	Infectious Disease
Topic	Hepatitis
Keywords	Hepatitis; Vaccine-Preventable Diseases; Environmental Health
Consider for Different Presentation?	No
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10189
Abstract Type	Breakout
Abstract Title	Behaviors Associated with Taking Pre-Exposure Prophylaxis Among a Sample of Participants in Washington State's HIV PrEP Drug Assistance Program
Abstract	BACKGROUND: Pre-exposure prophylaxis (PrEP) is a prevention strategy that involves prescribing HIV medication to people who are HIV negative. In 2014, the Washington State Department of Health (DOH) introduced the PrEP Drug Assistance Program (PrEP DAP), in which the state pays for the medication Truvada for persons that meet specific criteria indicating high risk of acquiring HIV. In an effort to collect information about participants' experiences with PrEP, DOH asked participants to complete a survey. METHODS: The survey was mailed in February 2017 to all PrEP DAP participants, including those who were no longer enrolled. The survey included a client identification number in order to match with client-level enrollment data and to STI surveillance data. Participants who completed the survey were entered in a lottery to win one of twenty \$50 visa gift cards. RESULTS: Two hundred and sixty four surveys were completed, for a response rate of 26%. Eighty-six percent reported current use of PrEP, 13% took it in the past and 1% never started PrEP. The distribution of demographic variables were similar between respondents and non-respondents. Nearly all respondents were male (96%), and 95% of males were MSM (men who have sex with men). The majority were white (72%), lived in King County (75%) and were middle aged (mean age of 43). There was a significant difference between STI testing frequency before versus after starting PrEP, with 98% reporting they tested every 3-6 months after starting PrEP, compared to 56% before taking PrEP ($p<.0001$). The majority reported no change in their behavior after starting PrEP for each of the sexual behavior change questions, with the exception of condom use. Among those who did report a change, we observed an increase in the number of sex partners in a typical month and in the frequency of anal sex, and a decrease in condom use and in discussing HIV status with partners (all p values $<.0001$). Adherence to PrEP appeared to be high, with 92% reporting they took PrEP on the day they completed the survey. Among those who discontinued PrEP, the most common reason for stopping was perceived lower risk for HIV. CONCLUSIONS: Current PrEP use and adherence to Truvada were high among respondents. While we observed a decrease in condom use, which could lead to an increase in STIs, the majority reported no change in risky sexual behaviors overall and testing regularly for STIs.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Sexually Transmitted Diseases; Prevention; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10098
Abstract Type	Breakout
Abstract Title	Characterizing HIV Stigma and Discrimination in Washington State from a Population-Based Sample of HIV-Positive Adults in Care
Abstract	BACKGROUND: Reducing stigma and discrimination is part of the National HIV/AIDS Strategy and is a primary goal of the End AIDS Washington Initiative. Stigma is an attitude of disapproval towards an individual or group based on an attribute perceived as undesirable. This can produce a discriminatory environment, where unfair actions are taken on the basis of stigma. There were three objectives of this analysis: (1) Characterize the experience of internalized stigma and discrimination among HIV-infected individuals in Washington State, (2) Identify populations experiencing the highest rates of stigma, and (3) Model the relationship between stigma and risk behaviors and disease management. METHODS: Patient demographics, perceived stigma and discrimination, and participant outcomes were collected between 2011 and 2014 as part of the Medical Monitoring Project, a national surveillance system used to learn about people living with HIV from representative annual interviews. This information was linked to state surveillance data representing the same time period. A stigma score was calculated by assigning one point for each positive answer to six stigma questions. Raw and adjusted mean stigma scores and the proportion of individuals facing discrimination were calculated across demographic factors, including age, gender, education, race, sexual orientation, and country of birth. Stigma was then modeled as a predictor of homelessness, depression, binge drinking, injection drug use, ART adherence, and AIDS status. RESULTS: The mean stigma score in the study population was 2.27 (SD=1.77). Across the population, the most common aspects of HIV stigma were difficulty in telling people about HIV infection (63%) and hiding HIV status from others (55%). The demographics most associated with stigma were age, race, and country of birth. Individuals between the ages of 35 and 54 reported higher levels of stigma (2.44 vs 2.00, $p<0.001$), as did non-white individuals (2.72 vs. 2.03, $p=0.002$). There were no significant differences stigma between urban or rural populations (stigma score: 2.28 vs 2.23, $p=0.905$). Stigma was significantly associated with homelessness (OR: 1.21, $p=0.012$) and depression (OR: 1.41 $p<0.001$), but not with ART adherence or AIDS. Seventy percent of participants provided answers suggesting experience with discrimination. Discrimination was most often perceived as a result of HIV status (90.2%) and sexual orientation (42.6%). CONCLUSIONS: HIV stigma and discrimination are perceived at high rates among people living with HIV in Washington State. Efforts to combat stigma may benefit from a focus on middle-aged and non-white populations, though the relative size of these populations should be taken into consideration.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Barriers to Care; Health Disparities; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9146
Abstract Type	Breakout
Abstract Title	Expedited Partner Therapy in Clark County, Washington: Baseline Rates, Provider Experience, and Implications for Provider Education

Abstract

BACKGROUND: Expedited partner therapy (EPT) refers to the practice of providing medications to sex partners of patients diagnosed with a sexually transmitted disease (STD) without a requisite medical examination. Randomized controlled trials have found that EPT increases rates of partner treatment and reduces the risk for recurrent gonorrhea or chlamydia infection. The Centers for Disease Control and Prevention (CDC) supports the use of EPT to treat sex partners of heterosexual patients diagnosed with uncomplicated chlamydia. Despite guidelines, most primary care providers do not routinely provide EPT to patients. Washington State provides free EPT partner packs for eligible patients and their partners to increase uptake of EPT. This research was conducted to understand current rates of EPT use in Clark County, Washington and to inform provider education about EPT.

METHODS: Phase 1 - Baseline rates of EPT use in Clark County, Washington were assessed through interviews with newly diagnosed heterosexual chlamydia cases between June and September 2017. Cases were interviewed by trained personnel using an established state reporting form that asked about treatment and EPT, reasons for testing, and timing of HIV testing. STATA and SAS software was used to assess selection bias and perform descriptive analysis. Phase 2 – Providers were surveyed with an online survey tool about their experience with EPT, including perceived barriers to use.

RESULTS: Investigators interviewed 237 newly diagnosed chlamydia cases from June to September 2017. There were 73 (24%) cases lost to follow up. There were no significant differences between those interviewed and those lost to follow up. Of those interviewed, mean age was 24.0 years, 69% were female, 81% were white, and 92% had insurance. Mean number of partners in the 60 days prior to testing was 1.4. EPT had been offered by a provider in 48% of cases. Provider responses from an online survey demonstrated familiarity with EPT, but concerns about liability and legality may limit EPT prescribing.

CONCLUSIONS: Clark County providers are prescribing EPT for partners of chlamydia cases. However, concerns about liability and legality may limit more complete utilization. Education should target these concerns to improve EPT prescribing in Clark County, Washington.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	Sexually Transmitted Diseases; Disease Prevention; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10182
Abstract Type	Breakout
Abstract Title	In Care but Not in Control: Characteristics of High Risk HIV Patients in Allegheny County, Pennsylvania, 2017

Abstract

BACKGROUND: New HIV infections are on the decline. However, some HIV positive individuals may pose a greater risk of transmitting HIV through unprotected sex with multiple partners. To better understand a local high-risk group, we examined a defined cohort in Allegheny County (AC), Pennsylvania (PA).

METHODS: The study group was identified using HIV surveillance data for individuals receiving HIV care in AC in 2017. The High-Risk Cohort (HRC) was defined as those HIV positive individuals that had multiple episodes of sexually transmitted diseases (STD) with at least one STD diagnosis in 2017.

RESULTS: The total study population included 4,491 individuals. 153 of those individuals were identified as the HRC. 111 of the 153 HRC patients had the same provider for both HIV care and their 2017 STD diagnosis. 42 of the HRC had different providers for their HIV care and 2017 STD diagnosis. Individuals who saw the same provider for HIV and STD care had higher rates of having viral load testing in the past two years (85% vs. 70%) than those who saw different providers. The HRC was overwhelmingly male at 97%. Compared to nonhigh-risk patients, the HRC included more Blacks/African Americans (45% vs. 39%) and were younger (68% in the 20 to 39 year age group vs. 24%). The HRC was more likely to be MSM (94% vs. 60%). They were more likely to have been diagnosed with HIV within the past 5 years than the nonhigh-risk patients. 62% of the HRC were HIV cases and 32% AIDS defined. 13 cases in this cohort had a confirmed diagnosis of shigella. The crude annualized rate for shigella among the HRC was approximately 500/100,000 while the crude rate for shigella among all adults in AC is 4.1/100,000. The HRC named 171 total primary contacts through partner service interviews. This was an average of 1.1 contacts per high risk patient versus 0.2 contacts among nonhigh-risk patients. The total number of STD-related encounters for the HRC prior to their HIV diagnosis date was 170, while the total number of STD encounters after the HIV diagnosis date was 659.

CONCLUSIONS: This investigation indicates some individuals may appear to engage in medical care, but may not maintain medication adherence and may experience treatment failure and/or engage in unprotected sex. Prevention efforts should include focusing on those individuals who may represent a greater risk of transmitting HIV to their partners.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	Local Epidemiology; Surveillance; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9635
Abstract Type	Breakout
Abstract Title	Mental Health Diagnoses and Service Needs Among an in-Care Population of Persons Living with Diagnosed HIV Infection in New York State, 2009-2014
Abstract	BACKGROUND: Mental health plays a critical role in a person's overall well-being. Studies suggest that adults infected with HIV are more likely than the general population to experience a mental health illness (MHI). The aims of this study were two-fold: 1) estimate the prevalence of select MHI in an in-care HIV diagnosed population in New York State (NYS), excluding New York City; and 2) assess the need for mental health services, as well as differences in service needs and utilization among those with a diagnosed MHI and those without. METHODS: Data were obtained from the Medical Monitoring Project (MMP), an expanded HIV surveillance project conducted by the NYS Department of Health in collaboration with CDC. From 2009-2014, data collection consisted of an hour-long survey with people living with diagnosed HIV (PLWDH) and a comprehensive medical chart review. Mental health information extracted from the medical records included diagnoses of: depression, bipolar disorder, anxiety, and any psychosis disorder. Needs and utilization of HIV related services were assessed via self-report. They included: HIV case management, AIDS Drug Assistance Program (ADAP) enrollment, adherence services, HIV peer group support, drug/alcohol treatment, shelter/housing, meal/food services, dental care, SSI/SSDI, and mental health services. Needs and utilization of services were scaled and individuals with high service needs were defined by the top quartile. Weighted adjusted logistic regressions were performed to determine the association between having a MHI and each individual service utilized and needed, as well as, MHI and high HIV service need and utilization. Statistical significance was set at $p < 0.05$. RESULTS: Among MMP participants, 50% had been previously diagnosed with a MHI. After adjusting for potential confounders, individuals with a MHI had significantly higher odds of needing and utilizing HIV peer group support, drug/alcohol treatment, SSI/SSDI, and mental health services. Those with MHI had 2.2 (aOR 2.2 (1.4-3.4)) times the odds of having high service needs compared to those without MHI. CONCLUSIONS: This in-care HIV diagnosed population had substantial MHI burden. There are significant differences in service needs between those with MHI and those without. This study found significant differences between the services needed and used by those with MHI and those without one. This may indicate the need to work closely with PLWDH with a MHI to ensure they are accessing the services they need and to provide tailored services to the population.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Health Care; HIV/AIDS; Mental Health
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10219
Abstract Type	Breakout
Abstract Title	Socio-Sexual Network Analysis to Identify Heterogeneity in Early Syphilis Networks: A Tool for Identifying Unique Populations at Risk
Abstract	BACKGROUND: In 2009, Louisiana had the highest rate of primary and secondary syphilis in the country. Recent partner notification approaches have been insufficient in addressing Louisiana’s deeply entrenched areas of syphilis infection. Prior research suggests surveillance systems may benefit from utilizing social network analysis in syphilis control efforts. Visualizing networks helps stress the need to focus on more heterogeneous groups instead of broad categories such as “gay men” or “sex workers”. METHODS: Utilizing state surveillance data, all cases of primary, secondary, and early latent syphilis that were diagnosed in 2009 and data on their sexual or needle sharing partners were analyzed using a combination of descriptive and network measures. Homogeneity by gender and race/ethnicity between cases and partners was assessed. RESULTS: A total of 1,574 cases and 3,422 partners were identified. Gender was known for 96.9% of the study population and race/ethnicity was known for 74.2%. In Louisiana, 96.0% of partners with known gender reported by female cases were male. Among male cases, 72.5% of partners were female and 27.3% were male. When partner race/ethnicity was known, 93.1% of partners among blacks were black and 6.1% were white. Among whites, 58.9% of partners were white and 37.6% were black. Sex of partner varied by region. New Orleans and Baton Rouge are Louisiana’s largest metro regions. In New Orleans, 47% of male cases reported male partners, and network visualization indicated the majority of these connections were among men who had sex with men (MSM) exclusively. In the Baton Rouge area, 28.5% of males reported male partners. Visualization of this network indicated a large amount of bridging between MSM and men who have sex with both men and women. CONCLUSIONS: The distribution and spread of syphilis among different demographic groups varies by region in Louisiana. The homogeneity of partnering among black persons with syphilis may serve to amplify disease spread in the community and keep prevalence high. Visualization of differences in partnering in New Orleans versus Baton Rouge by gender of partner show varying dynamics of disease transmission. Individuals who have sex with both men and women may not respond to MSM targeted messaging the same as persons who are strictly MSM, indicating a need for different prevention efforts between the two locales. This study demonstrates the feasibility of using network methods in state surveillance and prevention activities and how visualization of these networks can allow more precise targeting of populations at risk of syphilis infection.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Epidemiologic Methods; Minority Health; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9104

Abstract Type Lightning

Abstract Title Binge Drinking and Marijuana Use Are Associated with Non-Adherence to Antiretroviral Therapy (ART) in Persons Living with HIV (PLWH) in New York City (NYC): Findings from the Medical Monitoring Project (MMP)

Abstract

BACKGROUND: Adherence to antiretroviral therapy (ART) is critical for HIV viral suppression (VS) leading to better health outcomes for persons living with HIV (PLWH), and to the reduced risk of onward HIV transmission. Non-adherence to ART among substance users, including those who consume alcohol and marijuana in excess, has been shown to thwart VS and requires continued epidemiological examination. We examine the effect of binge drinking and marijuana use on ART non-adherence among PLWH in New York City (NYC) who participated in the Medical Monitoring Project (MMP) in 2015.

METHODS: The data come from a cross-sectional, probability sample of all adults aged ≥ 18 years living with HIV in NYC in 2015 who were interviewed and whose medical records for the 24 months prior to the interview were abstracted. Multivariate logistic regression was used to analyze the association of ART non-adherence (any dose missed in the past 30 days) with binge drinking (≥ 5 drinks per sitting, past 30 days) and marijuana use (past 12 months) in the subset of MMP participants who self-reported current ART use. Race/ethnicity, age and education were included in the model as covariates.

RESULTS: Of the 313 PLWH currently on ART, 66% were male with a median age of 49 years. The majority were black (45%) and Hispanic (33%). ART non-adherence was reported by 31% of current ART users. Binge drinking (aOR=3.0, 95%CI=1.4–6.3) and marijuana use (aOR=2.0, 95%CI=1.1–3.6) were independently associated with ART non-adherence.

CONCLUSIONS: One in three HIV-infected individuals in this NYC sample of PLWH reported ART non-adherence in the past month. Non-adherence was three times more likely among persons reporting recent binge drinking and twice as likely among those reporting marijuana use. Assessment of substance use behavior, including binge drinking and marijuana use should be included in patient evaluation at treatment initiation, with ongoing assessment and support services to improve treatment adherence.

Committee Infectious Disease

Topic HIV & STD

Keywords HIV/AIDS; Substance Use; Alcohol

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9924

Abstract Type Lightning

Abstract Title Pregnancy Ascertainment Among Syphilis Cases in Georgia, 2013-2015

Abstract

BACKGROUND: As of 2016, Georgia was ranked 4th in the United States for primary and secondary syphilis rates and 9th for the congenital syphilis rate. To prevent congenital syphilis, communicable disease specialists (CDS) investigate women with syphilis so that their pregnancy status can be ascertained. When women with syphilis are found to be pregnant, CDS ensure that they are treated according to CDC STD Treatment Guidelines, and retested in the 3rd trimester to detect potential re-infection. We sought to determine what percentage of women in Georgia who were diagnosed with syphilis during pregnancy between 2013 and 2015 were identified as pregnant as a result of programmatic activities.

METHODS: We matched Georgia STD surveillance data to vital records data using Link King to identify women who were diagnosed with syphilis between 2013 and 2015 and gave birth between September 2013 and December 2015. We restricted the matches to women with a syphilis diagnosis within 280 days (38 weeks) of delivery. For this group of women, we reviewed STD surveillance and field services data to determine the proportion correctly identified as pregnant.

RESULTS: During 2013 to 2015, there were 1434 female syphilis cases and 390,620 births reported to Georgia DPH. We determined that 238 women who were diagnosed with syphilis were linked to a birth between September 2013 and December 2015. Of these 238 women, 183 were diagnosed within 280 days of delivery. We determined that 150/183 (82%) of women who were diagnosed with syphilis during pregnancy were identified as pregnant in the STD surveillance and filed services data, while 27/183 (15%) were reported as not pregnant, and 6/183 had an unknown pregnancy status.

CONCLUSIONS: Conclusions: This analysis identified 18% of women with syphilis with incorrect or unknown pregnancy status in the STD surveillance and filed services data. When pregnancy status is not correctly ascertained, public health departments miss opportunities for treatment, third trimester testing, health education and reinfection prevention. Further work is needed to understand how to increase correct ascertainment of pregnancy status by STD program staff, before the women give birth, to maximize congenital syphilis prevention.

Committee Infectious Disease

Topic HIV & STD

Keywords Surveillance; Sexually Transmitted Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9431
Abstract Type	Lightning
Abstract Title	Prevalence and Predictors of Provider-Initiated HIV Test Offers Among Heterosexual Persons at Increased Risk of HIV in Virginia

Abstract

BACKGROUND: The CDC recommends routine, provider-initiated HIV screening for all patients aged 13–64 years, in all health-care settings. While there is evidence of the prevalence and trends of HIV testing, less is known about the prevalence or predictors of the provider’s HIV test offer to the patient. We examined the prevalence of receiving an HIV test offer and its association with select demographic and behavioral characteristics.

METHODS: We used data from Virginia National HIV Behavioral Surveillance, which collected data among heterosexuals with low socioeconomic status from September–December 2016 in the Eastern region of the state. We conducted descriptive statistics and, using log-binomial regression, examined the association between HIV test offer prevalence and the following variables: gender, age, race, current relationship status, health insurance coverage, non-injection drug use, binge drinking, and high-risk sexual activity.

RESULTS: There were 333 persons who visited a health care provider in the past 12 months. Among persons who did not receive an HIV test offer during the 12-month window (n=194, 58%), only 16% reported HIV testing during the 12-month window, while 71% of persons who received an HIV test offer reported HIV testing during the window. Additionally, 71/194 persons (37%) who didn’t receive an offer reported never having an HIV test in their lifetime. In univariable regression, gender, age, health insurance, and non-injection drug use were associated with HIV test offer. However, only gender remained significant ($p<0.05$) in multivariable analysis: compared to females, males had significantly lower HIV screening offer prevalence [adjusted prevalence ratio, 95% confidence interval: 0.69, 0.51–0.93].

CONCLUSIONS: Provider-initiated HIV test offers are essential to increase HIV testing and diagnoses. In the current study, HIV testing during the 12 months prior to NHBS interview was over four times higher among persons who received a provider-initiated HIV test offer compared to those who did not. However, over half of health-care seeking heterosexuals at increased risk of HIV were not offered an HIV test. The results indicate a need for increased provider-initiated HIV screening among heterosexuals, especially among males, who were less likely than females to be offered HIV screening in this study.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	Screening; Prevention; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9808

Abstract Type Lightning

Abstract Title Utilizing Surveillance Data to Confirm Provider Assessed Care Status

Abstract

BACKGROUND: Data to Care (D2C) is a public health strategy that aims to use HIV surveillance data to identify HIV-diagnosed individuals not in care, link them to care, and support the viral suppression goal of the HIV Care Continuum. Since 2014, NYS Public Health Law (PHL) has supported D2C in that patient specific information from the surveillance registry may be shared with healthcare providers with a verifiable diagnostic or clinical treatment interest in the patient for purposes of patient linkage and retention in care.

METHODS: In response to the PHL change, NYSDOH developed a secure tool to facilitate clinician inquiries regarding their presumed out of care (OOC) patients and for the NYSDOH to verify the patient-clinician relationship. The HIV/AIDS Provider Portal went live in 2016. The web-based application is available to licensed clinicians with a valid NYS medical license. The application is used to electronically submit inquiries of presumed OOC patients or patients who were diagnosed but never linked to care (DNLTC). Provider submitted files are reviewed and matched to the HIV Surveillance Registry. NYSDOH contacts the submitter and returns patient care status for matched patients verified to the clinician.

RESULTS: Since March of 2016, 25 files have been submitted via the NYS HIV/AIDS Provider Portal. Of the 98 individuals submitted, 43 (44%) were OOC according to NYS's definition. OOC individuals residing in NYS excluding NYC were assigned for Health Department Partner Services. 47 individuals were considered current to care, four were confirmed to be living out of state, three were not actually confirmed HIV infected, and one was deceased. Of the 47 in care, 34 (72%) were in care at a different provider, and 13 (28%) were in care with the provider submitting the file. Of the clinician identified and registry confirmed OOC patients living in NY excluding NYC, 78% are now current to care as of December 2017.

CONCLUSIONS: In response to PHL change, NYSDOH developed a secure portal for OOC and DNLTC requests. The HIV/AIDS Provider Portal empowers both clinicians and Health Department PS to focus efforts on a reduced number of HIV diagnosed and purportedly OOC or DNLTC patients, with documented improvements in viral suppression and care currency.

Committee Infectious Disease

Topic HIV & STD

Keywords HIV/AIDS; Public Health Law; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10129

Abstract Type Lightning

Abstract Title Who's Having Sex with Whom? Understanding Molecular HIV Transmission Partners in the District of Columbia

Abstract

BACKGROUND: With the increased availability of genetic sequence testing, molecular transmission networks have become a necessary complement to traditional partner contact tracing. This analysis provides a descriptive review of the molecular transmission networks of HIV diagnosis in the District of Columbia.

METHODS: People over the age of 12, diagnosed with HIV from 2012-2016 and reported to the DC HIV Surveillance system with a genetic sequence and at least one genetically-linked partner were included in this analysis (n=400). Network associations were established using Secure HIV TRACE with a maximum genetic distance of 0.015. Demographic factors, viral suppression at last known viral load test, and number of molecular transmission partners were analyzed. The number of molecular transmission partners was dichotomized as four or less partners compared with greater than four partners. Chi-square test was used to analyze differences by demographics between index cases and their molecular transmission partners. Multivariable logistic regression was used to analyze the relationship between demographic factors and the dichotomized number of molecular transmission partners.

RESULTS: This analysis found that among people age 30-39 at diagnosis, 56.5% had partners younger than their age group (n=62). This proportion increased to 69.0% among people age 40-49 at diagnosis (n=29; p<.0001). With respect to race, the majority of whites had partners who were not white (72.7%; n=33). Conversely, 89.7% of blacks had partners who were also black (n=381). Among Hispanics, 50.0% had partners who were also Hispanic (n=46; p<.0001). In reference to viral suppression, 59.2% of people not virally suppressed at last viral load were connected to people who were virally suppressed at last viral load (n=147; p<.0001). It was also found that people age 20-29 at diagnosis have a greater odds of having greater than four molecular partners than all other age groups combined (OR: 2.058 95% CI: 1.318-3.215). Additionally, people with a current residence outside of DC were found to have a greater odds of having greater than four molecular partners than those with a current residence of DC (OR: 1.950 95% CI: 1.218-3.120). No statistical difference was found among any other demographic category.

CONCLUSIONS: Among persons diagnosed with HIV from 2012-2016, older individuals were molecularly linked to younger partners, and differences in interracial linkages were observed. Younger individuals had a higher number of molecularly linked partners. As anonymous sex partners become more prevalent, partners identified through molecular linkage will be increasingly useful for supplementing traditional partner contact tracing and developing HIV prevention strategies.

Committee Infectious Disease

Topic HIV & STD

Keywords Sexually Transmitted Diseases; Epidemiology; HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10352
Abstract Type	Poster
Abstract Title	Associations between Sources of Information Used in HIV Care and Treatment, and Providers' Demographic and Medical Practice Characteristics
Abstract	BACKGROUND: HIV medical care providers (HMCP) need a wide range of evidence-based clinical information resources to manage their patients' health. Access to and effective use of these resources in their practice settings provide self-reliance and a better approach towards clinical decision-making and improved patients' health. The objectives of this study were to determine the associations between sources of information used in HIV care and treatment, and providers' demographic and medical practice characteristics. METHODS: Data used for this study were obtained from a probability sample of HMCP in 13 outpatient facilities in Houston/Harris County, Texas surveyed between June and September of 2009. HMCP were required to choose from a list of 12 medical information sources that they use in HIV care and treatment of patients. The differences and associations between the most common sources of medical information and providers' demographic and medical practice characteristics were determined using analysis of variance and chi-square tests. Selected characteristics that were associated with each source of information at the bivariate level ($p < .20$) were simultaneously entered into a multivariate logistic regression model. RESULTS: HMCP used on the average 5.83 (95%CI:4.04-7.88) of the sources ($n=12$) to obtain HIV care and treatment information with antiretroviral treatment guidelines (95.6%), medical Journals/textbooks (82.6%) and internet sources (69.5%) ranked first, second and third, respectively. Although there were no significant differences in the number of medical information sources used by providers' demographic and medical practice characteristics, 1-2 of the characteristics were distinctively significantly ($p \leq 0.05$) associated with six selected medical information sources. Providers who were physicians were 16 times more likely to obtain information from medical journals/textbooks than physician assistants and nurse practitioners. Similarly, male providers were 13 times more likely than females to source HIV care and treatment information from the internet. Providers who sometimes/always made referral to other HMCP for ART initiation were 96% less likely to use ART treatment guidelines. CONCLUSIONS: Following the heightened need for efficiencies in clinical care and decision-making process, HMCP are using various resources to satisfy their medical information needs. It is recommended that future research studies should focus on the quality of medical information sources and providers' information-seeking behaviors and preferences. Since providers require time and search skills to locate and access medical evidence, availability of these information will enhance efficiency through the integration of appropriate resources within clinicians' workflow.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Health Care; Evidence Based Practice; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9852

Abstract Type Poster

Abstract Title Demographics and Risk Factors of Mothers with Reported Congenital Syphilis Babies in Florida, 2012–2016

Abstract

BACKGROUND: From 2012 through 2016, reported cases of congenital syphilis (CS) increased 62% (n=37 in 2012 to n=60 in 2016). During this five-year span, 184 mothers infected with syphilis gave birth to 221 CS babies. We sought to elucidate if there were any characteristics shared among the CS mothers that could be the emphasis of future CS prevention tactics.

METHODS: The demographics and self-reported risk factors of the mothers of CS babies were extracted from Florida's sexually transmitted disease surveillance database for 2012 through 2016 and analyzed. The proportion of mothers reporting drug use, prior sexually transmitted diseases, incarceration, or prostitution was calculated as the number disclosing the behavior over the total number of mothers among babies with CS over the five-year span. Differences between the age and race of the mothers of CS babies were compared, using X^2 tests, to all mothers who delivered a live baby in Florida.

RESULTS: Most mothers (57%, n=105) did not report any risk factors. The highest self-reported risk factor was a prior STD history, with 38% (n=70) of mothers disclosing at least one previous STD in their lives. The lowest risk factor was mothers who exchanged money or goods for sex, with only 3% disclosing prostitution (n=5). Mothers between the age of 20–29 made up a significantly higher proportion than mothers without CS babies (64% versus 51%; p=0.0005). Conversely, CS mothers 30–39 years old comprised a significantly lower proportion than mothers without CS babies (27% versus 39%; p=0.0003). Mothers with CS babies were significantly more likely to be black or than mothers without CS babies (69% versus 30%; p=<0.0001).

CONCLUSIONS: Although fewer than half of the CS mothers disclosed a history of STDs, this was the risk factor most commonly communicated. Given the low percentage of risks reported, further review is warranted to determine if barriers to risk factor reporting are occurring or whether the prevalence of these risks are truly that low. Mothers in their twenties are at an increased risk of giving birth to a CS baby. Black mothers made up a disproportionately high number of CS births. Educational and other public health efforts focused on early and sustained prenatal care, syphilis screening, and timely treatment could reduce CS births.

Committee Infectious Disease

Topic HIV & STD

Keywords Sexually Transmitted Diseases; Infant Health; Infant Mortality

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10002
Abstract Type	Poster
Abstract Title	Describing the Geospatial Characteristics of HIV Antiretroviral Drug Resistance in Virginia

Abstract

BACKGROUND: Research suggests that HIV drug resistance mutations (DRM) and transmitted drug resistance mutations (TDRM) among treatment-naïve patients are associated with an increased risk of virologic failure and subsequent transmission. Analyzing the geospatial variations of TDRM and DRM prevalence are important tools in better understanding these risks from a state-wide perspective. The purpose of this analysis was to describe the geospatial characteristics of DRMs and TDRMs, and investigate the association between health region of residence and TDRM occurrence.

METHODS: HIV-1 nucleotide sequences reported to the Virginia Department of Health between 1/1/2013-6/30/2017 were included in this analysis. The most recent HIV sequence(s) collected and current residence were used to measure the prevalence of DRMs. Eligible baseline genotypes (EBG), defined as initial genotype(s) collected within 90 days following HIV diagnosis among ARV naïve individuals, and residence at diagnosis were used for TDRM analysis. Both sequences for patients with two genotypes (e.g., PR-RT and IN) collected at the same time were included. Mutations were inferred using the Stanford HIVdb and the spatial distribution was analyzed with ArcGIS. Bivariate logistic regression was used to measure the association between residence at diagnosis with the presence of TDRM.

RESULTS: A total of 1617 (41.5%) of 3896 most recent genotypes contained a DRM. The highest rate of PR mutations occurred in the New River health district (19.2 per 100 most recent genotypes). Rappahannock/Rapidan reported the highest rates of NNRTI and NRTI mutations (42.2 and 35.6 per 100 most recent genotypes, respectively) while Portsmouth had the highest rates of IN mutations (37.5/100 most recent genotypes). Of the 1650 EBGs, 475 (28.8%) contained a TDRM; Central Virginia displayed the highest rate of TDRMs (60.0 per 100 EBGs). Compared to patients residing in the Northern health region, those in Eastern (OR = 1.34, 95% CI 1.02 – 1.76), Central (OR = 1.53, 95% CI 1.12 – 2.07), Northwest (OR = 1.75, 95% CI 1.20 – 2.54) and Southwest (OR = 1.59, 95% CI 1.02 -2.49) were significantly more likely to have a TDRM ($p < 0.05$).

CONCLUSIONS: Findings suggest there is a significant association between health region and occurrence of TDRMs among patients living with HIV in Virginia. HIV-related stigma and limited access to care may contribute to higher rates of TDRMs and DRMs in rural areas, however, further investigation is needed to measure this effect. Prioritization of increased HIV nucleotide sequence testing in areas with limited numbers of genotypes reported is also needed.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	Geocoding; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9655
Abstract Type	Poster
Abstract Title	Evaluation of Neisseria Gonorrhoeae Interview Follow-up in Douglas County: A 2016 and 2017 Comparison

Abstract

BACKGROUND: On January 1, 2017, DCHD made it their goal to interview all gonorrhea cases that came into the department and obtain risk factor information. The objective of this evaluation is to compare 2016 and 2017 data and determine how well DCHD is following up on gonorrhea cases and partners while getting a better understanding of the risks associated with this disease.

METHODS: This cross-sectional analysis focused on interview completion and partner follow-up rates. Interview completion was determined by patients who completed full interviews and provided risk factor information. For partner follow-up, the likelihood of someone visiting an outside provider, giving us a full interview and partner names, was examined. Two groups were compared— external providers vs. internal- and the assumption was that patients seeing an internal provider will be more likely to give us partner information. Those living in Douglas County and tested positive for gonorrhea between January 1st and December 1st of 2016 and 2017 were included in this analysis. SAS statistical software was used for data analysis in this evaluation.

RESULTS: Of the total 1296 gonorrhea cases reported in between January 1, 2016 and December 1, 2016, 287 (22.1%) gonorrhea cases were interviewed. Of those interviewed cases, 167 (58.2%) completed full interviews. Approximately one third of interviewees were 24 years or younger and over two-thirds (67.1%) were male. Majority identified as either African-American (45.5%) or White (46.1%). Between January 1, 2017 and December 1, 2017, there were a total of 1473 gonorrhea cases reported with 905 (61.4%) cases being interviewed. Of those interviewed cases, 880 (97.2%) completed full interviews. Approximately 44% of interviewees were 24 years or younger and 51.3% were male. Like 2016, majority identified as either African-American (49.1%) or White (42.4%). Pending analysis, partner follow-up and risk association will be assessed.

CONCLUSIONS: The disease investigators at DCHD increased the number of interviews in 2017 due to the follow up of all gonorrhea cases. Through this comparison, we hope to find out if following up on all cases, rather than just untreated, will ultimately impact community health.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	Evaluation; Risk Factors; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9637

Abstract Type Poster

Abstract Title Extragenital *Neisseria Gonorrhoeae* Testing and HIV Co-Infection in Douglas County, 2016-2017

Abstract

BACKGROUND: Extragenital *Neisseria gonorrhoeae* testing has shown to capture positive patients that would have been missed for treatment if urine-only screening tests were implemented, especially among high risk populations such as men having sex with men (MSM). Rectal gonorrhea has been examined as an independent risk factor for HIV among MSM. The objective is to examine extragenital gonorrhea testing within Douglas County while focusing on HIV acquisition among persons with a positive rectal gonorrhea test, specifically among MSM.

METHODS: A descriptive analysis was conducted for gonorrhea testing sites. Data was collected between January 1, 2016 and December 1, 2017 from the Sexually Transmitted Diseases Management Information System (STD*MIS) database system. SAS statistical software was utilized to assess positive gonorrhea cases in Douglas County and analyze the positivity rate for extragenital testing sites during 2016-2017. Further analysis to determine among those who tested multiple specimen sources and had a positive extragenital test result, how many individuals tested negative or had a missing urine test result. This was to account for any potential person that could have been missed if urine-only screening was implemented.

RESULTS: Of the total 2879 positive gonorrhea cases reported in Douglas County between January 1, 2016 and December 1, 2017, 401 (13.9%) gonorrhea cases may have been missed if extragenital testing was not conducted. Of these cases, 84 (20.9%) were positive for rectal gonorrhea. Sixty-nine percent of those cases identified as White, 11.9% as Black, and 19.1% as another race. Most cases were among the 18-24 (39.3%) and 25-34 (45.2%) age groups. When examining gonorrhea among MSM, 52 (61.9%) of the positive rectal gonorrhea cases were among this population with 86.5% of MSM being between the ages of 18-34 years. Analysis showed that there were no HIV co-infection cases among MSM during this time.

CONCLUSIONS: Increasing extragenital STD testing is crucial to providing adequate treatment, among populations that would have been previously missed, while reducing the spread of diseases such as gonorrhea. Although HIV co-infection was not found in this analysis, the risk of HIV acquisition and/or co-infection is still a major concern and implementation of extragenital testing has shown to be beneficial in capturing many gonorrhea cases among high risk populations such as MSM.

Committee Infectious Disease

Topic HIV & STD

Keywords Screening; Sexually Transmitted Diseases; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10183

Abstract Type Poster

Abstract Title Increased STI Screening in HIV-Positive Patients in Virginia, 2009 to 2014

Abstract

BACKGROUND: The Centers for Disease Control and Prevention (CDC) recommends that all sexually active persons be tested annually for sexually transmitted infections (STI), including syphilis, gonorrhea, and chlamydia. For people living with HIV (PLWH), regular STI testing is particularly important as STIs can increase viral load, which can result in HIV disease progression, increased mortality and morbidity, and increased risk of HIV transmission. The purpose of this analysis was to determine if STI screenings, testing, and diagnoses changed from 2009 to 2014 for in-care PLWH in Virginia.

METHODS: Data for this analysis included Medical Monitoring Project (MMP) participants in Virginia from 2009 to 2014 (N=1201) who attended at least one HIV medical care visit between January 1-April 30 of their respective MMP participation year. Data were collected by a structured interview and a medical record abstraction (MRA). Demographics and behavioral characteristics were self-reported and summarized. Syphilis, gonorrhea, and chlamydia screening, testing, and diagnoses rates in the past 12 months were collected by MRA. Trend linear regression analyses determined if STI screenings, testing, and diagnoses changed over the six-year time period. Results are reported where $p < .05$.

RESULTS: From 2009 to 2014, statistically significant increases in STI screenings were observed for syphilis ($\beta_{\text{trend}} = 0.2$, $p < 0.0001$), gonorrhea ($\beta_{\text{trend}} = 0.2$, $p < 0.0001$), and chlamydia ($\beta_{\text{trend}} = 0.2$, $p < 0.001$). Interestingly, chlamydia testing increased from 2009 to 2014 ($\beta_{\text{trend}} = 0.2$, $p < 0.0001$), while syphilis testing decreased ($\beta_{\text{trend}} = -0.5$, $p < 0.0001$) and no significant change was observed for gonorrhea testing. There were no significant changes in diagnoses for any of the three STIs over the six-year time period.

CONCLUSIONS: Findings suggest in-care PLWH in Virginia are receiving STI screenings more often than in the past. However, reported STI testing rates are below the recommended guidelines for all sexually active persons. The varied STI testing rates may explain why increases in STI diagnoses were not observed, considering that STI rates have increased in Virginia over the six-year time period. It is possible that the limited time frame of the MRA may not have captured accurate STI screening, testing, and diagnoses for patients; or patients could have tested for STIs in places other than their HIV medical care provider (e.g., local health departments, community-based organizations). The findings of this analysis support the use of MMP data to evaluate STI screening, testing, and diagnosis for in-care PLWH in Virginia.

Committee Infectious Disease

Topic HIV & STD

Keywords Epidemiology; Sexually Transmitted Diseases; HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10251
Abstract Type	Poster
Abstract Title	Linkage to HIV Care and Retention in Care Among Patients Selected for a Linkage to Care Initiative in Dallas, Texas

Abstract

BACKGROUND: The Texas Data to Care (D2C) program utilizes HIV surveillance data and healthcare provider data to identify HIV-positive persons who are out of care in several Texas cities, locate or contact these persons, and link them to care. Patients linked to care through the D2C program are monitored using HIV surveillance data for continued engagement in care and viral suppression. Since 2012, 1,807 patients have been selected for linkage to care by the Dallas County D2C program. This analysis attempts to determine the effectiveness of linkage efforts by the Dallas County Health Department based on source of patient identification (e.g. surveillance versus provider identification).

METHODS: Patient outcomes were stratified by source of patient identification (provider versus surveillance). Chi square tests for independence were used to assess whether likelihood of locating the patient, linkage of the patient to care, retention in care one year after linkage, and viral suppression one year after linkage were independent of patient identification source.

RESULTS: Patients identified through provider data were more likely to be located by program staff ($p < 0.0001$), and more likely to be relinked to care ($p < 0.0001$) than patients identified through HIV surveillance data. Among patients successfully linked to care, retention in care and viral suppression at one year after linkage were not significantly associated with identification source.

CONCLUSIONS: Linkage to HIV care through the Data to Care program is significantly more likely to occur when the patient is identified for linkage efforts by a medical provider.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9071

Abstract Type Poster

Abstract Title Prevalence of Mycoplasma Genitalium in Clinical Specimen Using a Nucleic Acid Amplified Test (NAAT)

Abstract

BACKGROUND: *M. genitalium* inhabits the epithelial cells of the urinary tract and is considered to be a sexually transmitted disease. In fact, the Centers for Disease Control estimate that the bacterium is actually more common than gonorrhea but less common than chlamydia. Because *M. genitalium* is a fastidious organism that can take up to 6 months to grow in a lab. This makes Nucleic Acid Amplified Tests (NAAT) the preferred method for detection, although the United States Food and Drug Administration (FDA) has not yet approved any of these tests for detection and diagnosis.

METHODS: Between January and June 2016, a total of 2,019 samples were collected from clinic patients for analysis. Sample types included urine (86.6%), throat swabs (6%), rectal swabs (5.6%), vaginal swabs (1.6%), and cervical swabs (0.2%). Samples were analyzed for *Chlamydia trachomatis*, *Neisseria gonorrhea*, *Trichomonas vaginalis* and *Mycoplasma genitalium* utilizing Analyte Specific Reagents (ASRs) from Hologic®. The Aptima assays isolate and purify the nucleic acid from the samples followed by a transcription-mediated amplification (TMA) to produce multiple copies of the RNA for easier detection. The laboratory modeled the use of these ASRs after several publications which describe Research Use Only products available from Hologic®.

RESULTS: During the first 5 months of analysis, the overall *M. genitalium* positivity rate was 10.75%. Females had a slightly higher rate (12.67% versus 9.18%) with the majority of those tested falling between the ages of 18 and 34. *M. genitalium* rates for black patients were significantly higher than for white patients (16.08% versus 9.85%, p=0.0018), even though black patients composed only 14% of the clinic demographics and 3.3% of the overall Greene County population. Positivity rates for sample source data were similar (10.75% - 18.18%) with the exception of throat swabs at 2.46% and cervical swabs at 0%. Finally, co-infection rates of *M. genitalium* with chlamydia, gonorrhea or trichomonas overall was 36.87%. Individual co-infection rates had large gaps for sexually transmitted infections and gender, with the exception of *Chlamydia trachomatis* (22.55% for men and 26.09% for women). Rates for *Neisseria gonorrhea* were 23.53% for males while only 8.70% for females. Similarly, the gender gap for *Trichomonas vaginalis* was 13.91% for males and 2.94% for females.

CONCLUSIONS: More data will be needed to strengthen the study, but initial results suggest that the implementation of the NAAT technology to test for *Mycoplasma genitalium* is of public health importance for identifying and treating previously undiagnosed sexually transmitted infections.

Committee Infectious Disease

Topic HIV & STD

Keywords Infectious Diseases; Sexually Transmitted Diseases

Consider for Different Presentation? No

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Submission Type Breakout/Quick/Lightning/Poster

ID 9471

Abstract Type Poster

Abstract Title Spatial Patterns of Gonorrhea Screening - Chicago, 2014-2016

Abstract

BACKGROUND: Like most other large urban areas, Chicago has experienced higher rates of Sexually Transmitted Infections (STIs). From 2014 to 2016, the Chicago Department of Public Health (CDPH) reported a 30% (8,306 to 10,836) increase in total gonorrhea (GC) infections, and a 46% (4,709 to 6,900) increase among men who have sex with men (MSM). To combat this trends, CDPH awarded a delegate agency located on the North side of city, in the Roger Park community area, to expand extra-genital GC screening in MSM. Between 2015 and 2016, rectal GC screening at this delegate agency increased by 66% (from 7,446 to 12,377), with an increase by 59% (from 1,020 to 1,620) in Black MSM and 74% (from 1,517 to 2,635) in Hispanic MSM. Our study aims to determine if the expanded GC screening and treatment efforts contributed to the increase in GC infections in 2016.

METHODS: From 2014-2016, we analyzed year-end incidence data for GC infections from the Illinois National Electronic Disease Surveillance System (INEDSS). Using the Getis-Ord GI* statistical tool, we conducted an optimized hot spot analysis to identify statistically significant spatial clusters of high and low values of GC infections at the Chicago census tract level using ArcGIS 10.2.2. We mapped the 2014 economic hardship index values by Chicago community areas to determine if the high and low values of GC infections occurred in areas experiencing economic hardship.

RESULTS: From 2014 through 2016, clustering of GC infections increased on the North side of the city. In 2014, significant clustering of GC infections ($P < 0.05$) occurred in nine census tracts, involving Edgewater and Uptown community areas. In comparison, in 2016, the number of census tracts with significant clustering of GC infections ($P < 0.05$) increased five-fold to 60 in 2016, involving seven communities areas (Rodgers Park, West Ridge, Uptown, Lincoln Square, North Center, Lake View, and Edgewater) outside of the hardship index areas.

CONCLUSIONS: This spatial analysis allowed for CDPH to detect a significant increase in clustering of GC infections on the North Side, suggesting that this may be due to an increase in case ascertainment through increased extra-genital screening that occurred at the funded delegate agency. Ongoing assessment of screening practices for extra-genital infections is necessary for interrupting transmission among persons with exposures at these sites, and has shown to detect substantial number of cases that would be missed by urogenital screening alone.

Committee Infectious Disease

Topic HIV & STD

Keywords Geographic Information Systems (GIS); Sexually Transmitted Diseases; Epidemiology

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10040
Abstract Type	Poster
Abstract Title	Temporality of HIV Viral Suppression Among HIV-Positive Persons in Care in Washington State in 2013 and 2014

Abstract

BACKGROUND: The Medical Monitoring Project (MMP) is a federal surveillance project designed to produce nationally representative data on people living with HIV/AIDS (PLWH). MMP has two components: an interview and medical record abstraction. This analysis describes the demographic, behavioral and socioeconomic characteristics of HIV-positive persons in care who achieved HIV viral suppression and who subsequently became unsuppressed.

METHODS: MMP data from years 2013-2014 were used for this analysis. During these years, medical record data were obtained and recorded for the two years prior to the patient interview. Patient interview data were used to describe demographics, use of medical and social services and risk behaviors and medical record data were used to describe HIV viral suppression (≤ 200 copies per ml). Chi square measures of association were calculated using SAS v.9.4.

RESULTS: In 2013 and 2014, 13% (60 of 454) of the MMP participants had achieved and lost viral suppression in the two years prior to their interviews. Of those, the median number of days between the lab date of viral suppression and the next lab date without viral suppression was 126 days, the minimum days between suppressed and unsuppressed labs was 16 days and the maximum was 374 days. The median viral load of the first unsuppressed lab was 8235 copies/ml, and the distribution of the first unsuppressed lab was the following: > 200 and ≤ 400 , $n = 12$; > 400 and ≤ 4000 , $n=13$; ≥ 4000 and < 50000 , $n=19$; ≥ 50000 , $n=16$. Loss of viral suppression was associated with the following factors: race/ethnicity other than White, non-Hispanic ($p=0.05$); sexual orientation other than homosexual or gay ($p=0.03$); not being 100% dose adherent in the three days prior to the interview ($p=0.003$); lower education ($p=0.003$); and lower income ($p=0.0003$).

CONCLUSIONS: Achieving HIV viral suppression is an important personal health and public health outcome for PLWH. It not only prevents or delays serious medical conditions, such as opportunistic infections, but also significantly reduces the likelihood of transmitting the virus to others. The data from this analysis demonstrate that some people who achieve viral suppression subsequently become unsuppressed. The number of days between suppression and loss of suppression can differ significantly, as can the first unsuppressed viral load after suppression. Health promotion campaigns, healthcare providers and HIV case managers should communicate in ways that inform individuals of the value of viral suppression as well as the need to take measures to monitor and maintain it.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	HIV/AIDS; Communication; Health Disparities
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9069

Abstract Type Quick

Abstract Title Disparities in HIV Care in Small and Large Cities in Georgia, 2009-2014

Abstract

BACKGROUND: HIV surveillance data show disparities in treatment outcomes for people living with HIV (PLWH) in rural areas nationally and in Georgia. We used data from the Georgia Medical Monitoring Project (GA MMP) to characterize disparities among PLWH receiving care in small and large cities in Georgia during 2009-2014.

METHODS: The GA MMP is a surveillance system which produces representative data for HIV-infected adults receiving medical care in Georgia. From 2009-2014, MMP participants were sampled from HIV care facilities in Georgia. This analysis was limited to persons sampled from Ryan White HIV/AIDS Program-funded (RWHAP) facilities. Location of HIV care was dichotomized as a small (< 100,000 people) or large ($\geq$ 100,000 people) city based on facility address. Durable viral suppression (DVS) was defined as all viral load results < 200 copies/mL in the previous 12 months. Negative beliefs about antiretroviral therapy (ART) were measured by self-reported doubt in ability to take ART as directed or its positive effect on health. Characteristics were compared among participants in care in small and large cities; adjusted odds ratios (aOR) with DVS were assessed with logistic regression. Data were weighted to adjust for non-response and unequal selection probabilities.

RESULTS: Among 720 participants, one-third (225 (31%), 95% Confidence Interval (CI): (13.8-48.2)) received outpatient HIV care at RWHAP clinics in small cities in Georgia. A lower proportion of PLWH receiving care in small, compared to large, cities had a high school degree (77% vs. 86%, respectively, $p < 0.01$), and a greater proportion expressed negative beliefs about ART (20% vs. 12%, respectively, $p < 0.001$). A higher proportion of PLWH in care in small, compared to large, cities had at least one viral load test every six months (81.9% v. 71.8%, respectively, $p = 0.03$). Fewer PLWH in care in small cities were on ART (91% v. 94.7%, respectively, $p = 0.08$) and achieved DVS (59.3% v. 65.6%, respectively, $p = 0.33$), though differences were not significant. Participants with negative beliefs about ART were significantly less likely to achieve DVS than those with positive beliefs in small city facilities (34% vs. 69% DVS, respectively, $p < 0.01$), but not in large city facilities; this association remained in small city facilities after adjusting for age, race, gender, education, and time since diagnosis (aOR: 0.20, 95% CI (0.06-0.60)).

CONCLUSIONS: Negative beliefs about ART may contribute to poorer HIV treatment outcomes in small cities and rural areas. Further understanding and addressing this disparity would promote progress towards the updated National HIV/AIDS Strategy goals.

Committee Infectious Disease

Topic HIV & STD

Keywords Surveillance; Rural Health; HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10256

Abstract Type Quick

Abstract Title Evaluating Health Disparities in HIV Linkage to Care Using the High Impact Prevention Data to Care Initiative in Florida, 2015–2016

Abstract

BACKGROUND: Engaging people living with HIV in habitual care is paramount to reducing transmission. Furthermore, HIV is a reportable disease where routinely collected surveillance data are used as a strategic tool to trigger high impact prevention (HIP) activities. The Data to Care (D2C) initiative is a HIP activity that relies on the use of surveillance data to generate lists of persons living with HIV not in care. Linkage services are offered to those not receiving treatment by connecting them with HIV care. Florida is a high morbidity state that has implemented a statewide D2C program since 2015, with the goal of reaching individuals who were not linked to HIV care within three months of diagnosis.

METHODS: Demographic characteristics and laboratory test results reported to the Florida Department of Health HIV Surveillance reporting system and HIV care indicators (clinic visits or receipt of antiretroviral medications) captured in the Ryan White program databases from 2015–2016, were used to evaluate health disparities in initial linkage to HIV care and D2C linkage health outcomes twelve months from initial HIV diagnosis.

RESULTS: During 2015 and 2016, 9,680 new cases of HIV were diagnosed in Florida. Of those, 16% (n=1,547) were not linked to care within three months of diagnosis. Blacks were less likely to be linked to care (79.6%), compared to whites (88.3%) and Hispanics (86.5%) ($p<0.0001$). Removing those who moved out of state or died, 1,412 cases (2015–2016) were added to the D2C list for linkage to care. Of those diagnosed in 2015, and on the D2C list (n=678), 33.3% were linked to care, however, blacks were still less likely to be linked to care through D2C ($p=0.01$). In 2016, 40.5% of the 2016 D2C list (n=734) were linked, with blacks ($p=0.003$) again less likely to be linked to care. The number of months from diagnosis to linkage to HIV care improved from 2015 to 2016, with 2015 diagnoses taking an average of 10.9 (10.2–11.8 95% CL) months to obtain initial HIV care, compared to 6.4 (5.9–6.9 95% CL) months ($p<0.0001$) for 2016.

CONCLUSIONS: The D2C initiative in Florida provides a safety net for those not initially linked to care within three months of diagnosis as it increases the numbers of those eventually linked in care. The initiative needs to address health disparities associated with initial linkage and direct future HIP activities towards populations at risk in Florida.

Committee Infectious Disease

Topic HIV & STD

Keywords Surveillance; Infectious Diseases; HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10276

Abstract Type Quick

Abstract Title HIV Surveillance: Managing Loss to Follow-up Using External Data Sources

Abstract

BACKGROUND: Individuals living with HIV infection are routinely followed in Louisiana's enhanced HIV/AIDS Reporting System (eHARS). One purpose of this system is to monitor individuals who have fallen out of care by utilizing laboratory results received at the Louisiana Office of Public Health as a proxy for the receipt of care. Current laboratory results also provide indications of vital status and last known address. The objective of this project is to use Accurant LexisNexis batch matching to capture current address, missing social security numbers (SSN), and indications of death for persons in eHARS who have been lost to follow-up. The process involves providing Accurant with demographic information on persons of interest and receiving their most current information on a large scale.

METHODS: Persons over 12 years of age, living with HIV infection in Louisiana, whose most recent lab result was received on or before 12/31/2014 were included in this study (n=3,432). Using SAS 9.3 a dataset was created that contained first name, last name, date of birth, last known address, SSN (if available), and phone number. The dataset was then securely uploaded to Accurant for batch matching. Accurant subsequently provided best SSN, last known address, and vital status on individuals who satisfied the matching algorithm.

RESULTS: Of the 3,432 persons submitted to Accurant, 2,527 (73.6%) persons returned a most recent address. 1,347 (53.3%) addresses were still in Louisiana while the remaining 1,180 (46.7%) addresses were outside the state of Louisiana. The most common states of residence included California, Georgia, Florida, and Texas. In addition, 66 persons were identified as deceased. After importing 40 best SSNs for persons missing an SSN, eight profiles previously thought to be unique individuals living with HIV were deduplicated.

CONCLUSIONS: Accurant batch matching, although an added expense, allowed for the import of 40 SSNs that were otherwise missing, the deduplication of eight profiles, the closing of 66 profiles with accurate death data, and indications for follow-up with the remaining persons out of care. Additional investigations will include contacting health departments of corresponding states and exchanging data for more current and complete profiles on these individuals. This data matching will expedite tracking persons who have moved to other jurisdictions, reduce unnecessary workloads of the linkage coordinators, and provide a more precise estimate of disease prevalence on both a state and national level.

Committee Infectious Disease

Topic HIV & STD

Keywords Data Sharing; Surveillance; Data Collection

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9744

Abstract Type Quick

Abstract Title HIV Viral Suppression – Multiple Measurements Identify Disparities in Sustained Viral Suppression in New York State, 2016

Abstract

BACKGROUND: Sustained HIV viral suppression is the key pillar of the Undetectable equals Untransmittable (U=U) public health campaign. At the population level, the last HIV viral load reported in a calendar year is often used to evaluate viral suppression. However, published HIV literature indicate that a single point in time measure may overestimate viral suppression. This study uses population-based data to compare viral suppression based on the number of tests reported in a calendar year among persons living with diagnosed HIV infection (PLWDHI) in New York State (NYS).

METHODS: NYS HIV surveillance data were used in this retrospective cohort study to identify PLWDHI in NYS as of December 2016. HIV viral suppression (<200 copies/mL) was computed for three groups: 1) people with one viral load test in 2016; 2) people with two viral load tests; and 3) people with 3 or more tests. The relationship between the number of tests and level of viral suppression achieved (suppressed on all tests during the calendar year, yes or no) was evaluated.

RESULTS: In 2016, there were 109,862 PLWDHI in NYS; 87,161 had ≥ 1 viral load test within the calendar year. The median number of tests was 3 (Interquartile Range 2-4). A total of 16% had one viral load test, 29% had two tests and 55% had three or more tests. Within these groups, 79% of those with one test achieved viral suppression, 83% of those with two tests were suppressed on both tests and 72% of those with three or more were suppressed on all tests during the year. Those with two tests were slightly more likely to be suppressed than those with one test (unadjusted Risk Ratio [uRR] 1.05 (95% Confidence Interval [CI] 1.04-1.07)) while those with three or more tests were less likely to be suppressed (uRR 0.92 (95% CI 0.91-0.93)).

CONCLUSIONS: Multiple measurements over time identified disparities in sustained viral suppression among people living with diagnosed HIV infection in NYS in 2016. As the U=U campaign is more widely endorsed, it is imperative to understand the motivation for care and treatment, the context of care, and structural barriers to achieving sustained viral suppression.

Committee Infectious Disease

Topic HIV & STD

Keywords HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9387
Abstract Type	Quick
Abstract Title	Improving Access to HIV Prevention Services, Medical Care, and Supportive Services for MSM and Transgender Persons of Color in DC, Maryland, and Virginia
Abstract	BACKGROUND: In 2017, DC Department of Health (DOH) funded 10 community-based organizations to develop a culturally sensitive health system for HIV negative and positive MSM and transgender persons of color in DC, Maryland, and Virginia (IMPACT). This system ensures equitable access to screening, prevention services (PrEP/PEP), care, and behavioral health/ supportive services. The purpose of this analysis is to evaluate the newly created system of care and determine the effect of demographic characteristics on receipt of services. METHODS: Individual-level demographic and service (clinical and supportive care) utilization data were submitted to DOH from June-September 2017 via REDcap or Sharefile. The data were analyzed in SAS and linked with HIV surveillance data. Chi-square analysis was used to calculate Odds Ratios and compare the effect of race, ethnicity, gender, and age on screenings, services, and health outcomes. RESULTS: IMPACT enrolled 3,180 clients, including 2,584 (81%) MSM and 359 (11%) transgender persons of color. Most clients were Black (54%) or Hispanic (30%). IMPACT provided 2,076 HIV tests (78% lab-based/22% rapid), tested 1,527 people (84% of HIV-), and identified 22 new infections. Among clients living with HIV (n=1,354), 82% were virally suppressed at most recent viral load. Of the 2,043 (64%) clients screened for STIs, 792 tested positive (39%) and 332 (42%) were treated. Approximately 17% of clients were screened for behavioral health/supportive services and 84% were provided services. Black clients were less likely to be tested for HIV (OR: 0.592, CI: 0.467-0.751, p<0.0001) and STIs (OR: 0.622, CI: 0.535-0.724, p<0.0001), and more likely to test positive for an STI (OR: 1.74, CI: 1.44-2.08, p<0.0001). Hispanic clients were less likely to be prescribed PrEP (OR: 0.537, CI: 0.362-0.792, p=0.000166) and ARVs (OR: 0.718, CI: 0.521-0.996, p=0.0435). Transgender and gender non-conforming clients were less likely to be screened for PrEP (OR: 0.711, CI: 0.531-0.945, p=0.0195), tested for HIV (OR: 0.279, CI: 0.213-0.366, p<0.0001) and STIs (OR: 0.405 CI: 0.329-0.498, p<0.0001), and be virally suppressed (OR: 0.578, CI: 0.383-0.882, p=0.00886) compared to cisgender individuals. Clients < 30 years living with HIV were less likely to be prescribed ARVs (OR: 0.398, CI: 0.295-0.539, p<0.0001) and be virally suppressed (OR: 0.330, CI: 0.249-0.438, p<0.0001) compared to those over 30. CONCLUSIONS: IMPACT successfully enrolled clients in the focus population (MSM and transgender persons of color), but STI and behavioral health/supportive services screening and PrEP provision must be improved. DOH will use these results to develop activities to improve service delivery for all clients.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Prevention; Minority Health; HIV/AIDS
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9722

Abstract Type Quick

Abstract Title Indicators of Injection Drug Use Suggest Increasing Risk for Idu-Related HIV Outbreaks — Indian Health Service , 2010 –2014

Abstract

BACKGROUND: Little is known about the risk of an HIV outbreak linked to injection drug use (IDU) among the American Indians/Alaska Natives (AI/AN) living in the U.S. We aimed to characterize the risk of IDU-related HIV transmission among AI/AN by describing conditions commonly found among people who inject drugs (PWID) as a proxy for IDU.

METHODS: We analyzed 2010-2014 data from the Indian Health Service (IHS) National Patient Information Reporting System, to include all AI/AN persons eligible for service at an IHS facility. As there are no ICD-9- CM codes specific to IDU, we enumerated IDU-related ICD-9- CM codes of hepatitis C (HCV) in 18-35 year olds, arm cellulitis, opioid use disorder (OUD), and opioid poisoning in ≥ 18 year olds. For each outcome, we determined the number of persons with at least one ICD-9-CM code in the year, and calculated annual prevalence per 10,000 adults. HCV among 18-35 year olds was used because younger people with HCV are more likely to be PWID. We estimated average annual percentage change in prevalence of these outcome variables and determined p-values for trend using Poisson regression. For the 18-35 year old individuals with HCV during 2010 – 2014, we also assessed co-occurrence of OUD, opioid poisoning, and arm cellulitis diagnoses in the same period for those 18 years or older at diagnosis.

RESULTS: During 2010 – 2014, an average of 1.06 million adults per year were eligible for analysis (median age = 39 years, Interquartile Range 27-54 years, 46% male). The annual prevalence of HCV diagnoses increased 9.41% per year from 2010 to 2014 ($p < 0.0001$); and OUD increased 13.19% per year from 2010 to 2014 ($p < 0.0001$). Opioid poisoning remained constant and arm cellulitis diagnoses decreased 2.97% per year from 2010 to 2014 ($p < 0.0001$). There was substantial overlap of the IDU-related conditions, and among the 18 – 35 years old with HCV during 2010 - 2014, 26% also had OUD, 1% had opioid poisoning, and 8% had arm cellulitis.

CONCLUSIONS: The increasing trend in HCV diagnoses in young AI/AN adults and opioid use disorder among all AI/AN adults suggests increasing risk for IDU-related HIV outbreaks in this population. These data can be used at a local level to ensure that access to OUD treatment and syringe service programs matches the community's need.

Committee Infectious Disease

Topic HIV & STD

Keywords Outbreaks; HIV/AIDS; American Indians / Alaska Natives

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9429
Abstract Type	Quick
Abstract Title	Interim Assessment of CDC's Improving STD Programs through Assessment, Assurance, Policy and Prevention Services (STD-AAPPS) Surveillance Strategies
Abstract	BACKGROUND: STD-APPPS is a CDC-funded, 5-year co-operative agreement (FY2014–FY2018) that supports 59 state, territorial, and local health departments for STD surveillance, prevention, and control activities. We conducted an interim assessment of STD-AAPPS implementation and report recipient's perceptions of their program's strengths and weaknesses in implementation of required and recommended surveillance strategies. METHODS: STD-APPPS recipients completed a quantitative assessment tool and participated in semi-structured interviews with a non-CDC interviewer during January–May, 2017. For each of the seven STD-AAPPS surveillance strategies, the recipients scored themselves on perceived strength (very strong, somewhat strong, somewhat weak, very weak, don't do much) and perceived improvement during the first few years of STD-AAPPS (strengthened a lot, strengthened some, no change, weakened some, weakened a lot). Qualitative interviews included discussions of their quantitative responses and their reported barriers and facilitators to accomplishing strategies. Content analysis was used to identify themes related to surveillance strategies, and basic descriptive analysis was used to summarize survey data. RESULTS: Fifty-three (90%) recipients completed the quantitative assessment and 52 (88%) completed a qualitative interview. One-third (34%) of recipients completing the assessment considered themselves very or somewhat strong in all of the 5 required surveillance strategies (security & confidentiality; geocoding; quality and timeliness of case data; matching STD and HIV data; data dissemination) and 74% reported having strengthened in three or more of these strategies. Only 17% considered themselves very or somewhat strong in both recommended strategies (electronic laboratory/case reporting; sentinel surveillance); however, 85% reported that they has strengthened electronic reporting and 25% reported strengthening sentinel surveillance. During the qualitative interviews, switching to new/enhanced data systems was identified as both a barrier and facilitator; in some jurisdictions, new data systems supported activities such as improving case data quality, while in others, the time and resources needed to implement new systems posed a barrier to making progress. Similarly, infrastructure was reported as both a facilitator (e.g., the ability to hire new staff; enhanced collaborations) and a barrier (e.g., hiring freezes; lack of data integration with HIV). CONCLUSIONS: The majority of STD-AAPPS recipients reported improving surveillance objectives in the first few years of implementation; however, additional support, including targeted technical assistance, may be needed to help recipients overcome barriers, particularly for jurisdictions transitioning to new data systems. Additional evaluation could link objective metrics (e.g., percent of STD cases matched to HIV data) to recipients' perceptions to further assess implementation of surveillance strategies.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Surveillance; Sexually Transmitted Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9949

Abstract Type Quick

Abstract Title Prevalence and Characterization of HIV and Hepatitis C and Hepatitis B Virus Coinfections — Alabama, 2007–2016

Abstract

BACKGROUND: HIV, hepatitis C virus (HCV), and hepatitis B virus (HBV) share transmission risk factors; persons infected with HIV are also at risk for hepatitis C or B, which both independently increase a person's risk for serious liver-related complications. Among HIV-infected persons in the United States, an estimated 25% are coinfecting with HCV, and 10% are coinfecting with HBV. HIV coinfection with HCV or HBV has not been previously described in Alabama; therefore, we characterized prevalence and risk factors to guide future interventions.

METHODS: We conducted a case-control study using Alabama HIV, HCV, and HBV surveillance data during 2007–2016. Persons with HIV and known HCV or HBV coinfection were classified as case-patients; persons with HIV only were classified as control subjects. Keeping HIV/HCV and HIV/HBV case-patients separate, we compared case-patient and control subject demographics using univariate analysis. Multivariable regression compared case-patient and control subject risk factors while controlling for age, sex, race, and ethnicity.

RESULTS: Of 6,380 persons infected with HIV, reported coinfection prevalence was 5.4% for HIV/HCV and 2.9% for HIV/HBV. Persons coinfecting with HIV/HCV had an increased odds of reporting injection drug use (IDU) (adjusted odds ratio [aOR] 10.4; 95% confidence interval [CI]: 7.0–15.4) and combined IDU and male-to-male sexual contact (aOR; 7.4; CI: 4.3–12.6). Persons coinfecting with HIV/HBV had an increased odds of reporting male-to-male sexual contact (aOR: 1.6; CI: 1.1–2.3).

CONCLUSIONS: Compared with national estimates, Alabama has a lower prevalence of HIV and hepatitis coinfections reported through the state surveillance system, which likely underrepresents actual HCV and HBV cases. Significant differences in risk factors were reported between case-patients and control subjects, particularly a history of IDU among HIV/HCV coinfecting persons and male-to-male sexual contact among HIV/HBV coinfecting persons. These results are important for planning targeted interventions and prevention efforts among at-risk groups.

Committee Infectious Disease

Topic HIV & STD

Keywords Hepatitis; HIV/AIDS; Risk Factors

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9273
Abstract Type	Quick
Abstract Title	Shigella Infections with Decreased Susceptibility to Azithromycin and Association with Bacterial Sexually Transmitted Infections in New York City, 2014–2016
Abstract	BACKGROUND: <i>Shigella</i> is a common cause of bacterial enteric infection in the United States. Transmission occurs via the fecal-oral route; anal sex is a risk factor. Antibiotics may be prescribed to reduce illness duration and severity. Rising rates of decreased susceptibility to azithromycin (DSA) have been observed in New York City (NYC), with high proportions of patients identifying as men who have sex with men (MSM). Given that azithromycin is a common treatment for other bacterial sexually transmitted infections (STI), we sought to examine the relationship between DSA-shigellosis and recent history of bacterial STI. METHODS: Shigellosis cases are required to be reported to the NYC Department of Health and Mental Hygiene (DOHMH), and isolates are forwarded to the Public Health Laboratory (PHL) where antimicrobial susceptibility testing (AST) is conducted. DSA is defined as a minimum inhibitory concentration ≥ 16 ug/ml (<i>S. flexneri</i>) and ≥ 32 ug/ml (<i>S. sonnei</i>). NYC residents ≥ 18 years-old who were diagnosed with <i>Shigella</i> during 2014–2016 with AST results for azithromycin from PHL were matched to the DOHMH Bureau of Sexually Transmitted Diseases Control (BSTD) registry to identify patients diagnosed with <i>Chlamydia trachomatis</i> or <i>Neisseria gonorrhoeae</i> infection within one year prior to shigellosis diagnosis. RESULTS: During 2014–2016, 1,319 shigellosis cases were diagnosed. Of those, 669 were ≥ 18 years-old at diagnosis and 665 had AST results for azithromycin; 274 (41%) exhibited DSA. The proportion of interviewed DSA-shigellosis patients ≥ 18 years old (N=326) who identified as MSM increased from 74% in 2014 to 87% in 2016. A recent bacterial STI was identified among 80 (29%) DSA-shigellosis patients ≥ 18 years old, compared with 54 (14%) among patients with isolates susceptible to azithromycin (RR=2.1, 95% CI: 1.6, 2.9). CONCLUSIONS: <i>Shigella</i> infections exhibiting DSA in NYC occur disproportionately among MSM. DSA-shigellosis is significantly associated with recent bacterial STI. Provider education should emphasize the importance of using AST results and recent STI history to guide treatment if indicated for shigellosis.
Committee	Infectious Disease
Topic	HIV & STD
Keywords	Sexually Transmitted Diseases; Antimicrobial Resistance; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9994

Abstract Type Quick

Abstract Title Shigellosis and Giardiasis Among People Living with HIV in Washington, DC, 2012-2016

Abstract

BACKGROUND: Shigellosis and giardiasis are transmitted via food, water, and fecal-oral contact. CDC has recently reported increased shigellosis among men who have sex with men (MSM) and among people living with HIV (PLWH), particularly stage 3. Our goal was to characterize the incidence and risk factors associated with shigellosis and giardiasis among PLWH in Washington, DC, in an era of robust availability of antiretroviral treatment.

METHODS: We conducted a retrospective analysis of HIV, shigellosis and giardiasis cases reported to the District of Columbia Department of Health from 2012 to 2016. We used LinkPlus to probabilistically match individuals with reported HIV and *Shigella* or *Giardia*. We conducted bivariate analysis on gender, race/ethnicity, and age for Shigella-HIV, Giardia-HIV and HIV alone. Among men, we conducted bivariate analysis for HIV transmission risk factors. Among those with Shigella-HIV or Giardia-HIV, we compared CD4 cell count, HIV stage, HIV viral load, and viral suppression (VS) using laboratory data within 8 weeks before or after the incident enteric infection. We compared the incidence of shigellosis and giardiasis in the general population versus among those living with HIV in 2016.

RESULTS: During 2012-2016, 250 DC residents were reported with shigellosis (2.1 per 100,000 in 2016) and 412 with giardiasis (7.3 per 100,000 in 2016). The proportion with HIV coinfection was 20.4% for shigellosis and 10.6% for giardiasis. Incidence rate ratio (PLWH versus general population) was 25.8 for shigellosis and 9.6 for giardiasis. 40.9% of coinfection cases, versus 15.9% HIV alone, were ages 25-34 at the end of 2016 ($p < 0.0001$). White race was more common among Shigella-HIV (19.6%) and Giardia-HIV (27.3%) versus HIV alone (15.9%) ($p < 0.0001$). Nearly all (97.8%) coinfection cases occurred in men. MSM was the most common HIV risk factor among men with Shigella-HIV (80%) and Giardia-HIV (64.3%) compared to HIV without enteric disease (60.4%). Rates of stage 3 HIV and VS were similar between Shigella-HIV (stage 3 HIV 25%, VS 40%) and Giardia-HIV (stage 3 HIV 34.3%, VS 40%).

CONCLUSIONS: PLWH in DC disproportionately acquired shigellosis and giardiasis in 2012-2016. Factors associated with shigellosis and giardiasis among PLWH include male gender, white race, being in the 25-34 age group, and MSM. Among the Shigella-HIV and Giardia-HIV cases, most did not have stage 3 HIV, but we found low viral suppression rates. Our data supports the need for obtaining a thorough sexual history, focused HIV prevention and antiretroviral adherence counseling, and provides information to target high risk groups in DC.

Committee Infectious Disease

Topic HIV & STD

Keywords Enteric Infectious Diseases; Surveillance; HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9930

Abstract Type Quick

Abstract Title Spatial Analysis of Chlamydia: VD in 3D

Abstract

BACKGROUND: Reported rates of Sexually Transmitted Infections (STIs) have increased in the United States, including Vermont. Increased rates of STIs are associated with certain demographics and access to care. The Vermont Department of Health looked at chlamydia rates, representative populations, and service areas using geographic information systems (GIS) to describe the Vermont population infected with STIs and identify resource gaps.

METHODS: Esri GIS software analyzed 8,967 chlamydia cases from 2011 to 2016. Case addresses were geocoded, and incidence was calculated using a spatial join to a subcounty geographic layer. The GIS Pro Hotspot Getis-Ord Gi tool was used to identify chlamydia hot and cold spots. The incidence and the hotspot maps were compared to maps showing representative populations based on age and gender. Age was represented by the percentage of town population between 15 and 30 years of age – the most common age cohort for chlamydia. Gender was mapped by highlighting towns in which more than 50% of the 15 to 30-year-old population was female. Colleges and urban areas were also mapped and compared. The network analysis GIS tool, Service Area Creator, was used to show the areas of the state serviced by the sexual health care provider, Planned Parenthood of Northern New England (PPNNE).

RESULTS: Hotspot analysis showed hotspots in both Chittenden and Franklin counties, surrounding the major cities of Burlington and St. Albans, respectively. A cold spot was seen in northern Bennington and southern Rutland counties. Towns with a higher percentage of 15 to 30-year-olds did not always correspond with higher incidence for chlamydia. Towns with higher percentages of women did not correspond to higher incidence. Colleges correspond with some of the higher incidence areas. Urban areas corresponded with all higher incidence. When looking at the hot spot analysis, the cold spots were 15 minutes or greater outside of the PPNNE service areas.

CONCLUSIONS: In Vermont, there are higher incidence areas that do not correspond to areas with representative age groups as seen in previous literature. The analysis identified the need for continued research to describe the at-risk groups in these areas. Analysis showed that low incidence areas have limited health care coverage, and a few sporadic areas with higher incidence are not being served by PPNNE. Health care provider sexual health education should be targeted in areas of high incidence and limited PPNNE coverage. The visualization of this type of data provides a unique insight into the populations at risk.

Committee Infectious Disease

Topic HIV & STD

Keywords Risk Factors; Sexually Transmitted Diseases; Geographic Information Systems (GIS)

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9958

Abstract Type Quick

Abstract Title The Effects of STI Co-Infection on HIV Clinical Outcomes in the District of Columbia

Abstract

BACKGROUND: The use of antiretroviral drugs to treat HIV disease has proven to be effective in leading to viral suppression and reduce HIV transmission. Though treatment as prevention has been highly promoted, subsequent STI diagnoses may interrupt HIV treatment and enhance health negative outcomes. The purpose of this study is to evaluate STI diagnoses among people living with HIV (PLWH) and determine the association of these diagnoses on HIV clinical outcomes in Washington, DC.

METHODS: Data from the enhanced HIV/AIDS reporting System and STD surveillance data were matched. HIV cases diagnosed and living in DC through 2016 and STIs (Chlamydia, gonorrhea, and Primary & Secondary syphilis) diagnosed ≥ 3 months after HIV diagnosis between 2012 and 2016 were included in this analysis. Bivariate analysis was performed to identify differences by demographics, HIV disease stage, retention in HIV care (RIC), HIV viral suppression (VS) and time to VS. Adjusted Odds Ratios (aOR) were calculated.

RESULTS: Of 12,964 people diagnosed with HIV and living in DC at the end of 2016, there were 6,584 STI diagnoses among 4,216 HIV cases (32.5%) between 2012 and 2016. Compared to mono-infected cases, co-infected cases were more likely to be male (80.3% vs 68.6%, $p<0.0001$), have a mode of transmission of sexual contact (74.2% vs 71.1%, $p<0.0001$), and more likely to be RIC in 2017 (76.4% vs 73.7%, $p=0.0010$). Co-infected cases were more likely to ever have been virally suppressed (82.9% vs 71.0%, $p<0.0001$) but there was no difference in viral suppression in 2017. Co-infected cases were also more likely to first be virally suppressed two to five years after diagnosis (20.1% vs 18.7%, $p=0.0129$). HIV mono-infected cases were more likely to ever have a stage 3 HIV disease diagnosis (53.2% vs 50.3%, $p=0.0091$) and there were no difference in stage 3 HIV disease at the end of 2017. Adjusted results showed that co-infected cases who had fewer than 5 STI diagnoses were more likely to ever be virally suppressed (aOR: 8.21, CI: 7.93-8.59) and more likely to be suppressed within two years of HIV diagnosis (aOR: 2.33, CI: 2.05-4.86).

CONCLUSIONS: HIV/STD co-infected cases differed from HIV mono-infected cases. Though there were few adverse differences, interventions targeting PLWH are effective in promoting RIC and VS but should also include reducing unprotected sex and acquisition of sexually transmitted infections. STI prevention among PLWH remains a public health priority given established associations between STI co-infections and increased risks of HIV transmission.

Committee Infectious Disease

Topic HIV & STD

Keywords Co-Morbidity; HIV/AIDS; Sexually Transmitted Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10319

Abstract Type Quick

Abstract Title Trends in Causes of Death Among Females Living with HIV in Tennessee, 2001-2015

Abstract

BACKGROUND: The introduction of and increased access to antiretroviral therapy (ART) has improved health outcomes and increased life expectancy for people living with HIV (PLWH). Despite significant progress, routine surveillance of deaths among PLWH in Tennessee has revealed a sharper decline in deaths among males versus females. The objectives of this analysis are to: 1) identify the most commonly reported causes of death among female PLWH and 2) describe the extent to which causes of death (e.g., AIDS-defining vs. non-AIDS morbidities) among female PLWH in Tennessee have changed since the advent of ART.

METHODS: In Tennessee, causes of death among PLWH are collected via death records as part of routine HIV surveillance. HIV surveillance data from Tennessee's enhanced HIV/AIDS Reporting System (eHARS) were analyzed to identify trends in causes of death among female PLWH residing in Tennessee at time of death during 2001-2015. Frequencies of ICD-10 codes from death records were ranked, and top ten causes were assessed using annual and 5-year intervals.

RESULTS: From 2001-2015, 1,414 deaths were reported among female PLWH in Tennessee. During this time, the proportion of deaths among females aged ≥ 45 years increased from 33% to 62%. The most commonly reported cause of death among female PLWH each year was unspecified HIV disease, which decreased 23% during the reporting period. Pneumonia-related, septicemia, cardiac arrest, respiratory failure/distress, and renal failure were consistently reported among the top ten causes of death. During 2011-2015, wasting syndrome and chronic hepatitis C emerged as commonly reported causes of death and reports of urinary/renal conditions increased. Additionally, beginning in 2006, one-fifth of deaths among female PLWH were assigned a generic cause of death (i.e., other specified general symptoms and signs).

CONCLUSIONS: Reports of unspecified HIV disease decreased during 2001-2015; however, AIDS-defining conditions (i.e., pneumonia, septicemia, and wasting syndrome) continue to contribute to morbidity and mortality among female PLWH in Tennessee. Health outcomes among female PLWH in Tennessee may improve through HIV medical care and other services to prevent comorbidities and improve chronic disease management for conditions such as heart disease and hepatitis C. Future investigations into differences in causes of death by time of diagnosis, demographic characteristics, and geographic region would provide additional insight into the provision of these services. This study also shed light on the quality and utility of Tennessee's death data, including a need to better delineate changes in reporting versus true cause of death.

Committee Infectious Disease

Topic HIV & STD

Keywords Local Epidemiology; Co-Morbidity; HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9390
Abstract Type	Quick
Abstract Title	Using Surveillance-Verified Data to Identify Re-Engagement Opportunities in Texas Routine HIV Screening Programs

Abstract

BACKGROUND: The Texas Department of State Health Services (DSHS) supports opt-out routine HIV screening as a standard of care in health care settings, including emergency departments, community health centers, and correctional health facilities. It has been suggested that routine screening is an opportunity to identify previously diagnosed individuals out of care and re-engage these individuals to HIV care. DSHS verified data submitted by routine screening programs using the enhanced HIV/AIDS reporting system (eHARS) and analyzed care patterns of individuals to determine whether there were opportunities for re-engagement.

METHODS: The population evaluated were individuals who received routine HIV screening at a DSHS supported program in 2015 or 2016, previously diagnosed (diagnosis date ≤ 14 days before the test event), and diagnosed in Texas at least one year prior to testing. If an individual tested more than once, only the first test event was used in this analysis. Having no evidence of HIV care prior to testing is defined as not receiving a CD4 count or viral load ≤ 365 days prior to testing. Factors associated with having no evidence of HIV care prior to screening were assessed using chi-square tests and logistic regression.

RESULTS: A total of 1,341 previously diagnosed individuals were identified. The majority ($n = 1,123$; 83.74%) had evidence of care; 218 individuals (16.26%) did not have evidence of care ≤ 365 days prior to screening. Race, birth sex, and transmission category were not associated with having evidence of care before screening. Age and years since HIV diagnosis were found to have a significant positive association with having evidence of care ≤ 365 days prior to screening ($p < .0001$ and $p = .0095$, respectively). A significant interaction was found between age and type of screening facility ($p = .0172$). With each 5-year increase in age among those tested in emergency departments, there was a 27.1% increase in the odds of having evidence of care ≤ 365 days prior to screening. There were no significant interactions between age and being screened in correctional facilities or community health centers.

CONCLUSIONS: There were 218 individuals whom did not have evidence of HIV care at the time of screening. Those who were younger or more recently diagnosed were less likely to have evidence of care ≤ 365 days prior to screening. Routine screening may be an effective tool to re-engage out-of-care individuals to HIV medical care, particularly among younger populations screened in emergency departments.

Committee	Infectious Disease
Topic	HIV & STD
Keywords	HIV/AIDS; Prevention; Surveillance
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9492

Abstract Type Quick

Abstract Title Validation of Breastfeeding Data from the State Birth Registry for Perinatally HIV Exposed Infants in Pennsylvania, 2014-15

Abstract

BACKGROUND: Perinatal HIV transmission can happen at any time during pregnancy, labor, delivery, or breastfeeding. The objective of this project was to validate breastfeeding data obtained from the Pennsylvania birth registry for infants perinatally exposed (PE) to HIV.

METHODS: Feeding method is not always documented during the HIV surveillance investigation. Therefore, we opted to supplement our data with breastfeeding data collected by the Pennsylvania birth registry. During that process, 29 PE infants were documented as being breastfed. Since that practice would be contraindicated for the health of the infant, we did a reabstraction of feeding data with the birthing hospitals and the pediatricians providing follow up care.

RESULTS: 9 of the 29 mothers were born outside of the United States, with 3 (10%) from Central America and 6 (21%) from Africa. All 9 foreign-born mothers were documented as bottle feeding their infants in hospital records. Only 7 could be confirmed by their pediatrician. Feeding method was documented from all 29 of the birthing hospitals. The birthing records noted bottle feeding in 100% of the infants. Bottle feeding was confirmed with 27 of the 29 pediatricians. Seventeen of the pediatricians had notes documenting discussion with the mother about breastfeeding contraindications. We were unable to obtain feeding information from the pediatrician records for 2 of the infants. The 29 infants were born at 15 different hospitals.

CONCLUSIONS: The breastfeeding information contained in the birth registry could not be validated by this study. We suspected that the breastfeeding data could be reporting error from the birthing hospital. Following a child's birth, a worksheet is completed collecting demographic, birth history, prenatal care and parental information. It remains unclear whether the worksheet is completed by the mother or staff at the birth hospital utilizing the medical record data. We also were concerned that cultural pressures may lead some mothers to breastfeed their children even when medically contraindicated. We were specifically interested if this was true among the foreign-born mothers of PE infants. All 29 of the PE infants are documented as pediatric seroreverters. It is recommended that feeding data be collected from the birth or pediatric records during the surveillance investigation rather than utilizing the birth registry feeding information. The source of the registry information could not adequately be documented. Breastfeeding poses societal and cultural implications for the mother. However, to ensure the health of the perinatally exposed infant, it should be avoided.

Committee Infectious Disease

Topic HIV & STD

Keywords Breastfeeding ; HIV/AIDS

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9618

Abstract Type Breakout

Abstract Title Assessment of Respiratory Syncytial Virus Surveillance in the United States

Abstract

BACKGROUND: Vaccines and new prophylactic treatments are under development to prevent respiratory syncytial virus (RSV); however, RSV surveillance is not standardized and varies widely across jurisdictions. To understand the epidemiology of RSV and prepare to assess the impact of future RSV preventive measures, current RSV public health surveillance systems need to be better understood.

METHODS: In July 2017, the Council of State and Territorial Epidemiologists (CSTE) distributed an RSV assessment to 54 Influenza Surveillance Coordinators in state and select local and territorial health departments with the aim of identifying what RSV information is collected in the United States and how it is analyzed, interpreted, and disseminated. Questions asked about mandated and non-mandated surveillance systems used; how or if RSV seasonality is determined; how information is disseminated; and the funding available for these activities.

RESULTS: The assessment was completed by all 54 jurisdictions; 47 (87%) indicated that they conducted some RSV surveillance, either through required reporting of at least one RSV-related condition (40 [74%]) or using non-mandatory data sources (44 [87%]). Of the 40 jurisdictions indicating any required reporting, RSV outbreaks (35 [88%]), laboratory reporting of RSV-positive specimens (12 [30%]), and RSV-associated deaths (6 [15%]) were the most common. Case definitions for reportable RSV conditions were not standardized across jurisdictions; only 10/35 (29%) had a case definition for RSV outbreaks and 2/6 (33%) defined RSV-associated deaths. Of the 44 jurisdictions using non-mandated RSV surveillance data, public health laboratory testing (27 [61%]), the National Respiratory and Enteric Virus Surveillance System (NREVSS) (26 [59%]), sentinel clinical laboratories (23 [52%]), death certificates (12 [27%]), and syndromic surveillance (9 [20%]) were most frequently utilized. Among the 47 jurisdictions conducting any RSV surveillance, 33 (70%) provide public statements (routine or otherwise) about RSV activity, such as describing seasonality or severity. More than half (27 [57%]) of the 47 jurisdictions conducting RSV surveillance receive no specific funding for these activities.

CONCLUSIONS: Most health departments conduct RSV surveillance using a variety of surveillance systems, despite limited funding for these activities. The degree and scope of RSV surveillance differs greatly across jurisdictions, supporting the need for standardization of case definitions and surveillance methods. In addition, the assessment suggests underutilization of existing, available data sources like NREVSS and syndromic surveillance. Future efforts should focus on standardizing RSV surveillance across state, local, and territorial health departments and expanding RSV surveillance resources to better equip public health to measure the population-level impact of new prevention methods.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Epidemiology Capacity; Respiratory Diseases; Surveillance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9942
Abstract Type	Breakout
Abstract Title	Beyond the Human Cost: Quantifying the Financial Burden of Racial and Socio-Economic Disparities of RSV-Associated Emergency Department Visits and Hospitalizations in Children Less Than Five Years Old, Florida, 2010-2016
Abstract	BACKGROUND: Florida is home to over 1,000,000 children, half are Medicaid-receiving (MR), and 20% of the state's population is black. Roughly 25% of MR children are black. Florida's longer respiratory syncytial virus (RSV) seasonality leaves children at increased risk of RSV infection that can lead to severe illness, including hospitalization and death. Prophylactic treatment is available but often prohibitively expensive. This analysis describes the MR disparities among RSV-associated visits (RSV-visits) to emergency departments (ED), inpatient hospitalizations, and hospitalizations requiring ICU-level care by race and socio-economic status (SES), and quantifies the direct financial charges from that care. METHODS: Hospitalization data (both visits to EDs and inpatient hospitalizations) on children less than 5 with RSV infection between 2010 and 2016 were accessed through the Florida Agency for Healthcare Administration hospital discharge data set. These data include total charges, payer, intensive-care unit level (ICU-level) incurred diagnosis, age, admission, and discharge dates. Payer information, specifically whether or not the visit was charged to Medicaid, was used as a proxy measure of SES. Incurred ICU-level charges were used to measure severity. RESULTS: Between 2010 and 2016, 107,017 RSV-visits to EDs and inpatient hospitalizations were identified in children. These visits totaled \$1,586,800,706 in charges with an average of \$14,827 per visit. ICU-level care was used for 7,284 (7%) of the 107,017 visits. Visits requiring ICU-level care accounted for 37% of the associated charges. The average per-visit charge associated with ICU-level care was \$67,273. MR visits made up 78% of all visits (n=82,979). Regardless of MR or ICU-level care status, black children were significantly ($p<0.01$) disproportionately impacted (MR: 33% and 33%; ICU-level care: 27%, and 30%, respectively). CONCLUSIONS: RSV unduly burdens low SES children and their families. These impacts are even greater among low SES blacks. Those most heavily impacted are least able to afford it. The charges described here likely undercount the true financial burden of RSV-visits in children as they neglect the lost work time associated with one or more adults being absent from work to care for a child with RSV. To address the disparities in the socio-economic burden of RSV in children, these findings will be presented to Medicaid in conjunction with a review of current RSV prophylaxis prescribing policies to improve care, health outcomes and reduce costs among this medically underserved population. Improved access to prophylactic treatment and preventative care will save lives and improve good stewardship of public dollars.
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Health Disparities; Surveillance; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9938
Abstract Type	Breakout
Abstract Title	Comparison of Death Certificate Data to Hospital Discharge Data for Validation of New York City Pneumonia Deaths, 2010-2014

Abstract

BACKGROUND: Pneumonia is the eighth leading underlying cause-of-death (UCOD) reported on death certificates in the United States. However, in New York City (NYC), pneumonia is the third leading UCOD. To better understand this difference in ranking, it is important to assess the validity of pneumonia reporting on death certificates in NYC. Patients with pre-existing chronic conditions are at higher risk for developing pneumonia. In these cases, pneumonia should be documented as an intermediate condition in the chain of events leading from the pre-existing condition to death, and not as the UCOD on the death certificate. Utilizing hospitalization data, we aim to determine the accuracy of reporting pneumonia as the UCOD in NYC.

METHODS: NYC death certificate data from 2010-2014 were linked to Statewide Planning and Research Cooperative System hospitalization discharge data for discharges from 2009-2014. We analyzed death certificates linked to the hospitalization in which death occurred (i.e., a terminal hospitalization), restricted to adult NYC residents (n=101,520). A terminal hospitalization was categorized as pneumonia-related if the discharge record included any pneumonia diagnoses (International Classification of Disease (ICD), 9th revision, Clinical Modification codes 480-486, 487.0, 488.01, 488.11, 488.81, 507.0, 997.31), regardless of the reported UCOD on the death certificate. Descriptive statistics were used to validate the presence of pneumonia at time of death by comparing pneumonia reporting on the death certificate (ICD, 10th revision codes J12-18) to terminal pneumonia-related hospitalizations. To validate pneumonia as a UCOD, we identified pre-existing conditions reported in discharge data up to two years prior to the date of death which were not documented on the death certificate and may have been a more appropriate UCOD for pneumonia deaths.

RESULTS: Among all linked terminal hospitalizations, 42.1% (n=42,714) were pneumonia-related, while 8.7% (n=8,871) of deaths had pneumonia as the reported UCOD. Of deaths with a reported UCOD of pneumonia, 89.2% occurred during a pneumonia-related hospitalization. Among persons with a reported UCOD of pneumonia, 99.1% had ≥ 1 pre-existing condition. Heart disease (81.8%), hypertension (77.8%), nephritis/nephrotic syndrome/nephrosis (70.0%), diabetes (39.8%) and dementia (35.5%) were the most frequently reported pre-existing conditions.

CONCLUSIONS: The majority of linked inpatient deaths with a UCOD of pneumonia were validated as having pneumonia reported during the terminal hospitalization. However, almost all of these decedents had a diagnosis for a pre-existing condition that could have been a more appropriate UCOD. Pneumonia is likely over-reported as an UCOD, but remains a substantial mortality burden as an intermediate cause-of-death.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Hospital Data; Epidemiology; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9836

Abstract Type Breakout

Abstract Title Influenza-Associated Pediatric Deaths Identified Through Minnesota's Unexplained Critical Illness and Death Project — Minnesota, 2004-2017

Abstract

BACKGROUND: Since 1996, deaths investigated by medical examiners (MEs) that are unexplained and appear to be associated with an infectious cause are reportable to Minnesota Department of Health (MDH) Unexplained Critical Illness and Death Project (UNEX) with priority given to deaths <50 years of age with no significant underlying conditions. Influenza-associated pediatric deaths have been nationally notifiable since 2004 and MDH reporting guidelines call for all severe cases of suspect influenza to be reported, including specimen submission from patients with influenza-like illness (ILI) who were hospitalized or died. In addition, MDH has a robust influenza surveillance program consisting of surveillance for influenza-associated hospitalizations, outpatient ILI, influenza and ILI outbreaks, vital records data, and influenza testing data from MDH and clinical laboratories. We investigated influenza-associated pediatric deaths detected both by traditional influenza surveillance programs and by UNEX.

METHODS: We reviewed all influenza-associated pediatric deaths in Minnesota from 2004-2017. Influenza-associated pediatric deaths were defined as a death resulting from a laboratory confirmed, clinically compatible illness with no period of complete recovery between the illness and death in a patient <18 years. Deaths were identified through clinic and hospital surveillance, death certificates, and medical examiners reports to UNEX. Laboratory confirmation for influenza was performed at clinics, hospitals, MDH, and/or CDC.

RESULTS: From 2004-2017, 44 influenza-associated pediatric deaths were identified in Minnesota. Median age was 4.4 years, 61% were white/non-Hispanic, and 47% of influenza vaccine eligible cases with known vaccine status were vaccinated during the current influenza season. The most commonly identified strain was influenza A/H1 (36%), followed by influenza A/H3 (30%), influenza B (25%), and influenza A subtype undetermined (9%). Twenty-seven (61%) of the deaths were identified through UNEX. Deaths identified through UNEX were more likely to have shorter duration of illness (4 days vs. 7 days; $p=.04$), no underlying health conditions (69% vs. 19%; $p<.01$), and die outside of the hospital (48% vs. 12%; $p=.01$) compared to those not identified through UNEX.

CONCLUSIONS: The UNEX program identified over half of all influenza-associated pediatric deaths. Jurisdictions not including MEs or coroners in influenza surveillance may be significantly underestimating pediatric influenza mortality. While the denominator is small, our data suggest that influenza-associated pediatric deaths identified through UNEX may have different characteristics than those identified through traditional surveillance methods. Establishing consistent ME/coroner-based infectious disease surveillance efforts such as UNEX are needed to help fully recognize the burden of pediatric influenza mortality.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Epidemiology Capacity; Influenza Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9439

Abstract Type Breakout

Abstract Title Legionella Novella, a Surveillance Story

Abstract

BACKGROUND: Reported Legionellosis cases are increasing in Georgia, similar to national trends. Before 2017, Georgia Department of Public Health (DPH) conducted case interviews using the CDC Legionellosis Case Report Form (CRF), with few questions addressing potential exposure locations. These data were stored in multiple physical and electronic locations, which restricted data analysis capability. Cluster detection relied on manual review of cases and was limited to those data on the CDC Legionellosis CRF. There was not a clear threshold to trigger cluster investigations, potentially limiting additional case prevention. To better characterize potential sources of exposure, Georgia modified case and cluster investigation methods during 2016 and 2017. **METHODS:** In late 2016, Georgia developed a new CRF that gathers more complete exposure information. A case and cluster investigation manual was developed in 2017, and training was conducted for local epidemiologists with an emphasis on early, comprehensive interview. The case report form was added to Georgia's State Electronic Notifiable Disease Surveillance System (SendSS) to ensure centralized data availability and subsequent analysis. The threshold for cluster investigation was clearly defined as two or more possibly associated cases within 12 months or a single definite case for healthcare, residential, tourist, or recreational water facilities. Case and cluster investigation data were analyzed using Excel. **RESULTS:** The percentage of confirmed and suspect Legionellosis cases interviewed increased from 79% in 2016 to 88% in 2017. Case interviews yielded more specific potential exposure data, including workplace, plumbing disruptions or general construction, recreational water, and produce misters. The median time to attempt interview in 2017 was two days from local epidemiology notification. Interview data were entered into SendSS for all cases, and the state surveillance coordinator queried these data to identify clusters. The number of clusters detected in Georgia increased from five in 2016 to 13 in 2017. **CONCLUSIONS:** Georgia's updated Legionellosis case investigation methods emphasizes early case contact, expands assessment of potential exposures, channels data into a centralized database, and facilitates data analysis. By improving the quantity, quality, and accessibility of case investigation data, cluster detection has increased by more than 250%. Subsequent cluster investigations enable timely intervention to prevent additional cases of Legionellosis. Georgia plans to further enhance cluster detection by implementing expanded analytical methods, such as spatial temporal analysis. As more clusters are identified, increased state and local resources will be needed for public health investigation and intervention to prevent additional Legionellosis cases.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Respiratory Diseases; Surveillance; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9397

Abstract Type Breakout

Abstract Title Respiratory Enterovirus and Rhinovirus Circulation in the US: 2014-2017

Abstract

BACKGROUND: Enteroviruses (EV) and rhinoviruses (RV) circulate annually in the United States (US), peaking during summer and fall. Molecular panels cannot distinguish between the two virus groups and so positive results are reported as combined EV/RV detections. The contribution of different virus types to respiratory EV/RV activity is not fully understood. During an unexpected increase in severe respiratory illness between August and November, 2014, EV-D68 was detected in 49% of EV/RV-positive respiratory specimens submitted to CDC, and RVs were detected in 47%. During 2015-2017, improved detection methods and increased awareness of EV-D68 have led to continuing EV-D68 detections. We reviewed the national epidemiology of respiratory EV/RV circulation during 2014-2017.

METHODS: We assessed weekly EV/RV tests and detections reported to the National Respiratory and Enteric Virus Surveillance System (NREVSS), during 2014 – 2017, to determine the percentage of tests that were EV/RV-positive (%-positivity). We included EV/RV reports, based on molecular panels in respiratory specimens, from all contributing laboratories (n=340). To assess specific EV types circulating during this period, we reviewed data submitted to a second surveillance system, the National Enterovirus Surveillance System (NESS). NESS collects voluntary reports of specimen-level data from laboratories with specialized typing capabilities. We included respiratory specimen data from all contributing laboratories (n=11). NESS collects data on EV but not RV types.

RESULTS: The %-positivity of EV/RV tests reported nationally to NREVSS peaked annually during September – October, reaching 46% in 2014 and 32% in 2015, 2016 and 2017. There was also a period of increased activity during May of each year, with the weekly %-positivity reaching 24-27%. Testing volume increased annually across the time period. Based on EV types reported to NESS, there were 1240 EV-D68 detections (80% of all respiratory specimens) in 2014, 9 (12%) in 2015, 102 (62%) in 2016 and, to date, 8 (8%) in 2017. EV-D68 detections were reported throughout the year, but increased activity was observed during August – September in 2014 and 2016. Over the four year period, EV-D68 was the most frequently reported EV in respiratory specimens (70%), followed by coxsackievirus A6 (4.6%), coxsackievirus B3 (2.0%), Echovirus 11 (1.5%) and coxsackievirus A21 (1.0%).

CONCLUSIONS: EV-D68 predominated during a nationwide outbreak of respiratory illness in 2014, and continued to be reported during 2015-2017, although to a lesser degree. Seasonal peaks in EV/RV activity were observed annually, including in years with limited EV-D68 detection, representing the contribution of a broad range of EV/RV types.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Respiratory Diseases; Surveillance

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9522
Abstract Type	Breakout
Abstract Title	What You Should Know about Respiratory Syncytial Virus (RSV) Infections and Why You Should Know It

Abstract

BACKGROUND: Respiratory syncytial virus (RSV) is the leading cause of severe respiratory infections in young infants and is increasingly being recognized as a significant cause of severe respiratory infections in older adults and adults with chronic medical conditions. There are several vaccine and immunoprophylaxis products in development aimed at preventing RSV infections. The Advisory Committee on Immunization Practices (ACIP) has formed an RSV Work Group to consider recommendations for products that become licensed in the future. The session will review the 1) epidemiology of RSV infections; 2) landscape of prevention strategies; 3) current Centers for Disease Control and Prevention (CDC) RSV surveillance activities and 4) ways that health departments can contribute to filling knowledge gaps in understanding the epidemiology of RSV infections.

METHODS: An overview of the current landscape of RSV prophylaxis products will be presented with a focus on those in late stages of clinical development. The epidemiology of RSV infections will be reviewed, including seasonality, incidence and risk factors for disease. CDC surveillance activities designed to fill epidemiologic gaps will be reviewed. Finally, areas where health departments and CSTE can play a critical role in informing ACIP recommendations and developing the infrastructure to evaluate future prevention strategies will be highlighted.

RESULTS: Based on decades-old surveillance, RSV infections cause ~1.5 million outpatient clinic visits, ~500,000 emergency department visits, ~58,000 hospitalizations and ~140 deaths among children <5 years of age and 177,000 hospitalizations and 14,000 deaths among adults annually in the United States. There are over 45 vaccine and immunoprophylaxis products targeting RSV infections in development. There are products targeting newborns directly through passive immunization or indirectly through vaccination of pregnant women, products targeting infants and young children and products targeting older adults and adults with chronic medical conditions. In 2015 and 2016, CDC launched pediatric and adult surveillance platforms to update RSV burden estimates and inform recommendations for products licensed in the future and to create the infrastructure necessary to evaluate products post-licensure. Estimating RSV-associated mortality requires a larger catchment area than is possible under existing surveillance platforms and therefore a nationwide approach is needed.

CONCLUSIONS: RSV is a well-recognized cause of severe respiratory infections that has spurred development of several prevention products. CDC and health departments can contribute to developing the evidence base needed to determine populations that should receive vaccines and immunoprophylaxis products under development and to create the infrastructure needed to evaluate the products post-licensure.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Epidemiology; Infectious Diseases; Respiratory Diseases
Consider for Different Presentation?	No
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Submission Type Breakout/Quick/Lightning/Poster

ID 9806

Abstract Type Lightning

Abstract Title Appropriate Transfer of Recovering Influenza Patients from Hospital to Long-Term Care and Influenza-like Illness Outbreak Management: A Collaborative Approach to Education and Material Development

Abstract

BACKGROUND: The 2016-2017 influenza season was particularly severe in Washington state, with 278 lab-confirmed influenza deaths and 235 influenza-like illness (ILI) outbreaks in long-term care facilities (LTCFs) reported to the Washington state Department of Health (DOH). Some hospitals reported issues discharging recovering influenza patients to LTCFs, contributing to over-capacity at some hospitals. During the 2016-2017 season DOH hosted webinars targeted to hospitals, local health jurisdictions (LHJs), and LTCFs addressing appropriate care of recovering influenza patients. We recognized that a more proactive approach was necessary in order to prevent transfer and capacity issues in the future and sought to make improvements to our existing LTCF influenza materials.

METHODS: Over the summer of 2017 we convened a workgroup comprised of LTCF representatives, licensors, and LHJ partners to understand LTCF concerns regarding caring for recovering influenza patients and to update and improve our educational materials. Because many jurisdictions face similar issues communicating with LTCFs, the CSTE Influenza and Other Viral Diseases subcommittee had asked state influenza coordinators to share their existing materials on these topics and compiled a resource sheet of web-links. In the WA workgroup we reviewed this CSTE document and critically examined all of our existing LTCF ILI materials. We revised and updated all of these materials to ensure that they were as useful as possible to end users.

RESULTS: We discovered that some LTCFs were concerned about the regulatory aspects of admitting recovering influenza patients and some reported feeling pressure from hospitals to admit patients. We made it clear in the revised materials that each LTCF must assess its capacity to care for any given patient and provided information on how to safely care for recovering flu patients. We updated all LTCF ILI materials on our website, and created frequently asked questions documents, quick reference versions of the guidance, and signs LTCFs can post. We also hosted additional webinars to address transfer and patient care issues in advance of the 2017-2018 season.

CONCLUSIONS: Meeting directly with LTCF representatives allowed us to understand their needs around LTCF ILI outbreaks and patient care, and the representatives were very invested in making sure that the materials the workgroup created would be useful to end users. The materials available now at the WA DOH website are living documents that will be updated as needed per stakeholder feedback.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Occupational Exposure; Respiratory Diseases; Special/Vulnerable Populations

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9330

Abstract Type Lightning

Abstract Title Incidence and Temporality of Influenza-Related Parotitis — Arkansas, 2016–17

Abstract

BACKGROUND: During August 2016–July 2017, Arkansas experienced the second largest mumps outbreak in the last 30 years. Mumps virus is the most common cause of epidemic parotitis. However, other respiratory viruses, including influenza A, have been implicated in sporadic parotitis. Among ~4,000 buccal swabs taken from persons with clinical parotitis in Arkansas during the outbreak period, ~2,400 were negative for mumps by real-time polymerase chain reaction (RT-PCR). We tested mumps-negative buccal swabs available from January–July 2017 for presence of influenza virus.

METHODS: Up to 20 mumps-negative buccal swab samples from patients with clinical parotitis, but without epidemiologic links to mumps cases were randomly selected in each calendar month during January–July 2017 for influenza PCR analysis. Demographic information collected during the outbreak investigation was analyzed. The positive influenza results among mumps-negative cases were compared to Arkansas' reported influenza cases by month.

RESULTS: Eighteen of 122 (14.8%) mumps-negative samples tested were positive for influenza virus; all were influenza A. Eleven (61.1%) of those testing positive were male, 17 (94.4%) were white, and median age was 11 years (range: 4–25 years). Among mumps-positive cases, 1,688 (50%) were male, 688 (23%) were white non-Hispanic, and median age was 15 years (range 4 months–82 years). Monthly positive influenza test results were as follows: January, 3/20 (15%); February, 7/20 (35%); March, 6/20 (30%); April, 1/20 (5%); and July, 1/11 (9%); results that mirrored the local influenza season.

CONCLUSIONS: Influenza-associated parotitis was reported among a subgroup of mumps-negative patients during a mumps outbreak in Arkansas. Since buccal swabs are a suboptimal sample for influenza, reasonable inferences can be made that an even higher proportion of parotitis might have been attributable to influenza. Influenza vaccine could be considered to potentially reduce cases of mumps-negative parotitis in future outbreaks.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Infectious Diseases; Influenza Surveillance; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9262

Abstract Type Lightning

Abstract Title Methodology and Implementation of Pneumonia & Influenza (P&I) Mortality Surveillance in Texas' Influenza Surveillance System, 2015-16 Season & 2016-17 Season

Abstract

BACKGROUND: Historically, data collected through routine influenza surveillance in Texas has not been able to describe influenza mortality for people 18 years or older (i.e., adults) at a state or regional level. Although some local jurisdictions require influenza mortality reporting in all ages, only influenza-associated pediatric deaths (i.e., deaths in children <18 years of age) are reportable under state law. To address the lack of influenza mortality data for adults, the Department of State Health Services (DSHS) Influenza Team decided to supplement the mortality component of the state influenza surveillance system with pneumonia and influenza (P&I) mortality data.

METHODS: Texas' P&I mortality data comes from death certificates collected by the DSHS Vital Statistics Unit. The death certificates are sent to the National Center for Health Statistics where the cause of death and underlying causes of death on the death certificates are coded with ICD-10 mortality codes. Once coded, the information is returned to DSHS Center for Health Statistics (CHS). CHS provides a Weekly P&I Death Report to the State Influenza Surveillance Coordinator for inclusion in the Texas Weekly Flu Surveillance Report. P&I deaths in all ages are identified for the surveillance report based on ICD-10 multiple cause of death codes, and in particular, pneumonia and influenza mortality codes. Texas' P&I mortality data is also used for case finding. Pediatric deaths with any mention of influenza on the death certificate are further investigated to determine whether they are reportable under state law. The data is analyzed using Microsoft (MS) Excel and MS Access.

RESULTS: The total number of P&I deaths for the 2015-16 and 2016-17 seasons was 8470 and 10875. Adults ≥ 65 years of age had the highest number of P&I deaths for both seasons (15-16: 6685, 16-17: 8350). Comparing P&I death data by different areas of the state, Upper/Southeast Texas had the highest P&I mortality rate per 100,000 population for each season (15-16: 43.95, 16-17: 52.96). As for case finding, 49 suspected influenza-associated pediatric death cases were identified from the P&I mortality data for both seasons; of these, 10 children had already been identified as confirmed influenza-associated pediatric deaths and two additional confirmed influenza-associated cases were identified.

CONCLUSIONS: Texas P&I mortality data has provided a source for descriptive data for illness severity in adults for the 15-16 and 16-17 seasons. It has also identified influenza-associated pediatric mortality cases that would have not otherwise been reported through traditional surveillance.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Epidemiology; Influenza Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10125

Abstract Type Poster

Abstract Title Legionnaires' Disease Surveillance in Arizona 2006-2016

Abstract

BACKGROUND: The incidence rate of reported Legionnaires' disease has been on the rise nationally, increasing almost 3-fold during 2000-2009. In Arizona, the number of Legionnaires' disease cases has also shown an increasing trend from 38 cases in 2006 to 76 cases in 2016. Due to the increasing incidence and to the high case-fatality rate of healthcare-associated Legionnaires' disease cases, a better understanding of the disease epidemiology in Arizona is important.

METHODS: Legionnaires' disease data from Arizona's communicable disease database (Medical Electronic Disease Surveillance Intelligence System, or MEDSIS) for 2006-2016 was analyzed using SAS 9.3. Cases meeting the confirmed 2005 CSTE case definition were included. When examining test types, the first three reports received for each case were included, accounting for 87% of confirmed cases.

RESULTS: The demographic profile of confirmed Legionnaires' disease cases in Arizona for 2006-2016 mostly aligned with the national profile, being mainly elderly (52% over 65 years of age), male (56%), and non-Hispanic whites (65%). Cases tended to occur between June and October (50%), with peaks in August and October, for most years, but with a less-marked seasonality than seen nationally. On average, about 20% of cases had some travel away from home during the 10 days before onset, and 69% were hospitalized due to the disease. The serogroup most commonly reported through the entire period was *Legionella pneumophila* serogroup 1 (62%), followed by serogroup 6 (3%); this was true also among cases confirmed by culture. When looking at test types, urine antigen test was the most common test among confirmed cases from 2007 onwards, with culture second, whereas culture was the most common test type among confirmed cases in 2006 (46%). Despite serology being a very small fraction of the tests reported for confirmed cases, serological tests account for an average of 50% of all reported tests each year for this time period. This suggests that healthcare providers may be incorrectly using serological tests for diagnosing Legionnaires' disease.

CONCLUSIONS: Legionnaires' disease epidemiology in Arizona mostly reflects the national profile. The diagnostic tests used have changed through time, with urine antigen becoming more common in recent years. The use of serological tests is a problem detected during the entire period analyzed but more common in recent years. This is concerning as incorrect diagnosis is likely to cause underestimates of the real incidence of Legionnaires' disease in Arizona.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Surveillance; Waterborne Disease; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9780

Abstract Type Poster

Abstract Title Neurologic Complications Among Children Hospitalized with Laboratory-Confirmed Influenza, 2003-2015

Abstract

BACKGROUND: Influenza is associated with a range of neurologic complications in children, including acute encephalopathy, encephalitis, meningitis, acute disseminated encephalomyelitis, transverse myelitis, Guillain-Barre Syndrome and stroke. These complications may result in full neurologic recovery, chronic neurologic sequelae or death. However, there are limited population-based data on the prevalence, morbidity and mortality of influenza-associated neurologic complications among hospitalized children in the United States.

METHODS: We identified patients aged <18 years hospitalized with laboratory-confirmed influenza and diagnosed with neurologic complications from the Influenza Hospitalization Surveillance Network (FluSurv-NET), which conducted surveillance in 10 to 17 states during the 2003-04 through 2014-15 influenza seasons. We defined an influenza-associated neurologic complication as a medical record discharge summary diagnosis of acute encephalopathy/encephalitis or at least one ICD-9 discharge diagnostic code for acute encephalopathy, encephalitis, encephalomyelitis, myelitis, or viral meningitis. We excluded cases with other known viral or bacterial causes of meningitis/encephalitis. We described demographic and clinical characteristics and outcomes.

RESULTS: Among 14,185 pediatric patients hospitalized with laboratory-confirmed influenza, 173 (1%), with a median age of 5 years (IQR 1, 11), had an influenza-associated neurologic complication; 50 (29%) occurred before the pandemic (2003-2009 seasons), 24 (14%) during the pandemic (2009-2010), and 99 (57%) post-pandemic (2010-2015). One-hundred-and-three (60%) patients with neurologic complications were male and 110 (64%) had ≥ 1 underlying medical condition. The most common underlying medical conditions were asthma or chronic lung disease and chronic neurologic disorder. The median number of days from symptom onset to hospital admission was 1 day (IQR 0, 3) and 122 (71%) patients received antiviral treatment. Ninety-four (55%) patients were admitted to an intensive care unit, 51 (30%) required mechanical ventilation, 7 (4%) received extracorporeal membrane oxygenation, and 12 (7%) died during hospitalization. The median length of hospital stay was 5 days (IQR 3, 10), and among those discharged alive, 7 (5%) were discharged to a long-term care facility. Among 148 patients aged >6 months and with data on influenza vaccination status, 47 (32%) were vaccinated, 87 (59%) were unvaccinated and 14 (9%) had unknown vaccination status.

CONCLUSIONS: Influenza-associated neurologic complications, including acute encephalitis/encephalopathy, encephalomyelitis and viral meningitis were uncommon in children hospitalized with influenza. While these complications were rare, the majority of patients experienced severe disease. Influenza vaccination coverage was low indicating that efforts are needed to increase influenza vaccination, especially in children at high-risk for influenza complications. Providers caring for children should be aware of these rare yet serious neurologic complications associated with influenza.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Influenza Surveillance; Influenza / Pandemic Influenza

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9855

Abstract Type Poster

Abstract Title Prevalence of Influenza Vaccination in Adults with Asthma in Kentucky

Abstract

BACKGROUND: According to CDC, nearly 24 million people live with asthma in the United States. Infections in these patients often result in excessive morbidity and mortality. Prophylactic vaccinations such as influenza can help reduce complications, however current immunization rates are considered poor. The purpose of this study was to determine the prevalence and describe the epidemiology of influenza vaccination among Kentucky adults with asthma.

METHODS: Data from the 2016 Kentucky Behavioral Risk Factor Survey (KyBRFS) was used in this study. There were 1,227 adults who self-reported that they currently had asthma. Prevalence estimates were calculated using raking weights. Chi-square statistics were used to test for significant differences. Unadjusted and adjusted odds ratios were calculated using multivariate logistic regression models to control for socio-demographic factors. The results were considered statistically significant if the p value was less than 0.05. All percentages were weighted to population characteristics.

RESULTS: Overall, 38.4% of Kentucky adults reported that they had a flu shot in the past year. CDC recommends influenza immunization for all persons with asthma. However current immunization status among Kentucky adults with asthma showed that only 42.6% of them had flu shot in 2016. There were no significant differences in influenza immunization based on gender or race but it was significantly higher for respondents with a college degree compared with those with less than high school education (54.7% vs 34.7%, $p=0.012$). Black adults were slightly more likely to get influenza immunization as compared to white adults. It was less likely that Hispanics ($OR_{adj}=0.17$) and multiracial ($OR_{adj}=0.58$) adults with asthma to get a flu shot as compared to white adults. As expected, influenza immunization was significantly higher among respondents aged 65+ compared to young adults aged 18-34 (25.3% vs 61.1%, $p=0.0001$). Adults aged 50-64 and 35-49 years were also two times more likely to get influenza vaccination as compared to younger adults ages 18-34 years.

CONCLUSIONS: Findings suggest that health care professionals need to continue educating all patients with asthma about the importance of influenza vaccination. They need to especially focus on asthma patients who are less educated, Hispanic, and are multiracial to help improve vaccination rates in Kentucky adults with asthma.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Chronic Disease; Immunization; Asthma

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9666

Abstract Type Poster

Abstract Title Risk of Legionnaires' Disease Among Persons Receiving Hemodialysis, 2006-2015

Abstract

BACKGROUND: The incidence of Legionnaires' disease (LD) in New York City (NYC) has increased from 2.3 per 100,000 persons in 2006 to 4.8 per 100,000 persons in 2015. Although hemodialysis treatment has not previously been identified as a risk factor for LD, patients with chronic renal failure requiring hemodialysis are known to be immunocompromised. Biologically, immune systems of hemodialysis patients are compromised via the impairment of leukocyte phagocytosis, which can increase one's susceptibility to bacterial infections. The purpose of this study is to quantify the risk of hemodialysis treatment on the development of LD among NYC residents from 2006–2015.

METHODS: Data used was collected from surveillance conducted by the NYC Department of Health and Mental Hygiene's investigation of LD cases, the United States intercensal population estimates, and the United States Renal Data System 2006–2015. Populations included individuals over 18 and residing in NYC. Descriptive statistics and the chi-square test were used to determine differences between LD cases receiving hemodialysis and not receiving hemodialysis. The incidence of LD among hemodialysis patients compared to the general NYC population not on hemodialysis was calculated and stratified by age group, sex, and borough. Multivariable logistic regression on aggregate data was performed to determine the association between dialysis and LD adjusting for sex, year of diagnosis, age group, and borough.

RESULTS: From 2006–2015, there were 2,262 confirmed cases of LD in NYC, of which 58 (3%) were receiving hemodialysis. Persons with LD on hemodialysis did not differ significantly from persons not on hemodialysis in terms of age group, sex, neighborhood level poverty, race/ethnicity, borough, HIV status, or smoking status. LD patients on hemodialysis had a significantly higher case fatality rate than LD patients not receiving hemodialysis (31% vs. 11%, $p < 0.0001$). The unadjusted odds ratio for LD among hemodialysis patients was 9.1 (95% CI 7.0, 11.8) times the risk of LD in non-hemodialysis patients. Adjusting for sex, diagnosis year, age group and borough, the risk of developing LD among hemodialysis patients was 4.5 (95% CI 3.5, 5.9) times that of the general population.

CONCLUSIONS: There are significantly higher odds of developing LD among hemodialysis patients compared to the general population. Among LD cases, the CFR was higher among persons receiving hemodialysis. Increased awareness of these risks among hemodialysis patients and their physicians may facilitate earlier diagnosis and treatment of LD.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Infectious Diseases; Waterborne Disease; Diabetes

Consider for Different Presentation? Yes

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Affiliation Student

Submission Type	Breakout/Quick/Lightning/Poster
ID	9758
Abstract Type	Poster
Abstract Title	The Effect of Influenza Vaccination Coverage Among Health-Care Personnel (HCP) in Long-Term Care Facilities (LTCFs), 2016-2017 Influenza Season, Pennsylvania
Abstract	BACKGROUND: Residents of long-term care facilities (LTCFs) are at high risk of influenza complications including hospitalization and death. Influenza can be introduced into LTCFs by healthcare personnel (HCP), newly admitted residents and by visitors. During the 2016-2017 influenza season in the United States, 97.2% of influenza A subtyped at public health laboratories was A/H3N2, a subtype known to be associated with excess morbidity in the elderly. Nationally, HCP influenza vaccination coverage was 78.6% (0.4 percentage-points less than in 2015-2016). Higher influenza vaccine coverage among HCP has been associated with lower LTCF resident influenza-like-illness (ILI) and death. METHODS: Pennsylvania conducts systematic surveillance for influenza outbreaks in LTCFs, defined as one laboratory-confirmed influenza case plus one additional case of ILI, or 2 cases of ILI within 72 hours. Information is collected on the number of total and ill residents and employees, hospitalization of residents, and vaccination coverage of residents and employees. Influenza vaccination coverage during Oct 1, 2016-May 1, 2017 was categorized for residents (low: 0-79%; medium: 80-89%; high: 90-100%) and employees (low: 0-59%; medium: 60-80%; high: 90-100%). Outcomes and vaccination categories were compared using ANOVA/Welch's test with Bonferroni corrections for multiple comparisons. RESULTS: During the 2016-2017 influenza season, 436 outbreaks were identified in Pennsylvania LTCFs. Since many outbreak report forms were not complete, the percentages presented use the number of outbreaks with non-missing data for that field as the denominator. LTCFs with outbreaks had a median of 102 residents (range 8-724) and a median of 130 employees (range 7-1045). Sixty-five percent of outbreaks occurred in facilities with medium or high resident vaccination coverage (low: 92 facilities [35%]; medium: 82 [31%]; high: 90 [34%]). Facilities with higher resident vaccination coverage had fewer mean percent of residents hospitalized during the outbreak than did facilities with low resident vaccination coverage (low: 2.8%; medium: 2.2%; high: 1.6%; ANOVA p=0.03). Fifty-four percent of facilities had medium or high employee vaccination coverage (low: 111 [46%]; medium: 46 [19%]; high: 82 [34%]). These facilities also reported fewer mean resident hospitalizations than facilities with low employee vaccination coverage (low: 2.7%; medium: 2.4%; high: 1.3%; ANOVA p=0.04). CONCLUSIONS: Higher resident and particularly employee influenza vaccine coverage was associated with lower percentage of hospitalizations among ill residents in LTCFs with a reported influenza outbreak. However, vaccination coverage was missing for a substantial proportion of all outbreaks investigated. Improving vaccination coverage among LTCF residents and employees could help curb influenza-related complications among residents of LTCFs.
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Vaccine-Preventable Diseases; Influenza Surveillance
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10164

Abstract Type Poster

Abstract Title Trends in Screening Tests for Tuberculosis, Saint Louis County 2009 to 2016

Abstract

BACKGROUND: Traditionally, a Mantoux (i.e., PPD) test has been used as a screening tool to assess *M. tuberculosis* infection. PPD testing requires that patients return to their doctor 48-72 hours after injection for evaluation. This method can potentially lead to false positives if *M. tuberculosis* antigens from a previous Bacillus Calmette-Guérin (BCG) vaccine are identified. Interferon-Gamma Release Assays (IGRAs) mitigate these limitations by requiring only a single healthcare visit and distinguishes between latent tuberculosis infection (LTBI) and prior BCG vaccination. We examined trends in the number of PPD and IGRA tests, as well as reporter type, conducted on Saint Louis County residents from 2009 to 2016.

METHODS: Data were obtained from WebSurv, Missouri's system for surveillance and management of communicable diseases including tuberculosis. Saint Louis County residents, regardless of testing jurisdiction, who were diagnosed with LTBI between 01/01/2009 and 12/31/2016 were included in this analysis. Statistical analysis was conducted using Microsoft Excel 2013.

RESULTS: Among Saint Louis County residents, there were 4,899 positive PPD and IGRA tests between 01/01/2009 and 12/31/2016. Of these, 62.2% were PPDs and 37.8% were IGRAs. The number of PPDs per year ranged from 306 (in 2012) to 460 (in 2011), with a median of 380. The number of IGRAs ranged from 48 (in 2010) to 433 (in 2016) with a median of 235.5. The overall ratio of IGRAs to PPDs was 38.7% with the annual ratio increasing each year from 12.1% in 2009 to 54.4% in 2016. This change in ratio from 2009 to 2016 was statistically significant ($p < 0.01$). The three reporter types conducting the most IGRAs all performed more than 25 IGRAs per year – health departments (average $n=82.4$ IGRAs/year), labs (average $n=61.0$), and hospitals (average $n=26.8$). For these three reporters, as well as three of the remaining 8 reporter types, the change in percent IGRAs was statistically significant (all p -values < 0.01).

CONCLUSIONS: The relative proportion of IGRAs vs. PPDs among Saint Louis County residents changed significantly from 2009 to 2016. The three largest entities conducting IGRAs – health departments, labs, and hospitals – were the prime drivers of this change. As testing practices evolve, it is possible that this ratio, as well as the relative cost-benefits of each test, may similarly change.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Infectious Diseases; Respiratory Diseases; Screening

**Consider for
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Submission Type Breakout/Quick/Lightning/Poster

ID 9437

Abstract Type Quick

Abstract Title All Shook up: A Legionellosis Outbreak at a Graceland Hotel, Tennessee, 2017

Abstract

BACKGROUND: On June 26, 2017, the Tennessee Department of Health (TDH) was notified by CDC of two travel-associated cases of legionellosis with a common hotel exposure in Memphis, Tennessee. On June 27, the Shelby County Health Department (SCHD) identified a third case with the same hotel exposure. Initial interviews identified that all three patients reported use of the hotel hot tub. SCHD and TDH launched a joint investigation.

METHODS: The investigation involved epidemiologic, environmental and laboratory components. A guest roster from May 15 – June 27 was requested and used to conduct a case-control study through a web-based survey. Odds ratios (OR) and confidence intervals (CI) were calculated in SAS. Environmental health specialists conducted an assessment of the hotel aquatics area. Building and aquatics area water samples were collected and tested for *Legionella* and other water quality indicators.

RESULTS: Over 4,000 emails were sent to hotel guests on July 6, resulting in 983 survey responses. Through CDC reciprocal notification, calls received at the health department, and the web-based survey, a total of 92 cases were identified including nine confirmed (urine antigen positive), 19 probable (self-reported pneumonia), and 64 suspected (self-reported fever and ≥ 1 compatible symptom). Case-patients resided in 29 states, the United Kingdom, Canada and Australia. There were 16 hospitalizations and 1 death. Illness was strongly associated with exposure to the aquatics area (OR: 11.2; 95% CI: 3.4 – 37.4). Environmental assessment identified improper water treatment monitoring and low chlorine residuals in the aquatics area (0 ppm; acceptable range = 1–3 ppm). A public health directive was issued on June 28, which closed the aquatics area and required assessment, testing and remediation of the hotel water distribution system. Water testing isolated *Legionella pneumophila* serogroup 1 from the hot tub sand filter. There were no clinical isolates available for comparison with the environmental isolate.

CONCLUSIONS: Rapid and collaborative epidemiologic, environmental, and laboratory investigations ensured swift identification and remediation of a legionellosis exposure. The hotel aquatics area was closed within three days of notification and over 4,000 hotel guests were emailed within two weeks of notification. Streamlined communication between local, state, federal, and international partners was integral to outbreak case finding and follow-up. No clinical isolates were available, limiting the ability to identify any genetic link between case-patients and environmental *Legionella* isolates. This limitation highlights a need for provider education about the public health importance of culture testing when legionellosis is suspected.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Outbreaks; Waterborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9970

Abstract Type Quick

Abstract Title Characteristics of Respiratory Syncytial Virus Infection Among Hospitalized Adults, United States (2016-2017)

Abstract

BACKGROUND: The Influenza Hospitalization Surveillance Network (FluSurv-NET) conducts population-based surveillance for laboratory-confirmed influenza hospitalizations. With the current development of >40 respiratory syncytial virus (RSV) vaccine and monoclonal antibodies, several of which target adults, RSV surveillance was initiated using the FluSurv-NET platform to investigate characteristics of adults (≥ 18 years) hospitalized with RSV.

METHODS: Laboratory-confirmed RSV cases were identified in seven states (California, Georgia, Michigan, Minnesota, New York, Oregon and Tennessee) that participated in adult RSV surveillance during October 1, 2016–April 30, 2017. Laboratory-confirmed RSV cases were identified using hospital and state public health laboratory databases, hospital infection control practitioner databases/logs, and reportable condition databases. Medical charts were abstracted to collect demographic and clinical characteristics as well as ICD-10 discharge codes. We conducted a descriptive analysis and calculated frequencies using the number of responses for each characteristic as the denominator.

RESULTS: 1116 cases of laboratory-confirmed RSV in hospitalized adults were identified. The median age of cases was 71.0 years (IQR=24.0), and 63% (700/1110) were ≥ 65 years. Over half were female (629/1116, 56%), white (740/1108, 67%), and non-Hispanic or Latino (759/1106, 69%). Symptoms reported at admission included cough (895/1105, 81%), shortness of breath/respiratory distress (781/1105, 71%), and fever/chills (513/1105, 46%). Pre-existing medical conditions occurred in almost all cases (1069/1109, 96%) with cardiovascular disease being the most common (677/1105, 61%). Fifty percent (552/1109) of RSV cases were current or former smokers. Nineteen percent (214/1108) were admitted to the intensive care unit (median length of stay, 3 days; IQR=5 days). In-hospital deaths occurred in 4% (49/1109) of cases. Among cases who had additional viral testing, 4% (42/1052) had at least one other viral pathogen identified, influenza being most common (20/1052, 2%). RSV-specific ICD-10 codes (i.e., J12.1, J21.0, B97.4, and J20.5) in any position were listed for 51% (562/1103) of cases.

CONCLUSIONS: RSV is an important cause of hospitalizations in adults, specifically those ≥ 65 years and with pre-existing medical conditions. Our data also show that using ICD-10 codes to identify RSV cases might underestimate disease burden in studies using administrative data. Continued surveillance for RSV hospitalizations in adults is important to understand at-risk populations and to establish disease burden estimates in anticipation of future prevention and treatment strategies.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Epidemiology; Surveillance; Respiratory Diseases

**Consider for
Different
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Submission Type Breakout/Quick/Lightning/Poster

ID 9840

Abstract Type Quick

Abstract Title Influenza A (H3N2) Variant Virus Infections at County Fairs — Maryland, 2017

Abstract

BACKGROUND: In September 2017, multiple swine exhibited at Maryland county fairs were diagnosed with swine influenza A(H3N2) virus. Concurrently, state health officials were notified of influenza-like illness (ILI) among persons who attended agricultural fairs where swine were exhibited. We investigated to determine whether persons contracted an influenza virus that normally circulates in swine (variant influenza).

METHODS: Through active case finding (i.e. press releases, Epi-X alert, clinician notifications, and community meetings), we identified fair attendees with ILI onset (fever with cough or sore throat) within 7 days of swine exposure, and collected respiratory specimens for influenza testing. We interviewed patients by phone who tested presumptive positive for H3N2 variant (H3N2v) influenza using a novel influenza A virus case report form to collect demographic, health, and exposure information, where swine exposure was characterized as direct (e.g., touching swine) or indirect (e.g., walking through a swine barn).

RESULTS: In total, 80 fair attendees with ILI were identified, of whom 76 underwent influenza testing. H3N2v infection was confirmed among 40 patients who attended 1 of 3 co-occurring county fairs (A [15], B [1], and C [24]). Among these 40 patients, 24 (60%) were aged <5 years, 21 (53%) were male, 6 (15%) had chronic medical conditions, and 26 (65%) had direct and 14 (35%) had indirect swine exposure. Thirty (75%) patients were at high risk for complications from influenza (i.e., aged <5 or ≥65 years or chronic medical conditions). Two children were hospitalized; no deaths were reported.

CONCLUSIONS: This investigation highlights that even indirect swine exposure, such as walking through swine barns, can put persons at risk for contracting H3N2v. CDC recommends that persons at high risk for influenza complications avoid swine and swine barns, and publicizing this recommendation to fairgoers might help to prevent future variant influenza outbreaks among these vulnerable groups.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Zoonotic Diseases; Influenza / Pandemic Influenza

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9844

Abstract Type Quick

Abstract Title Influenza Outbreak at Senior Centers and the Efficacy of Influenza Vaccine

Abstract

BACKGROUND: During 2015-16 *influenza* season for age-group ≥ 65 years, the CDC estimated *influenza* related medical visits at 944,631; hospitalizations at 153,349; pneumonia and deaths at 7,639. In the fourth quarter of 2017, the Houston Health Department (HHD) experienced increased reporting of upper-respiratory illness among seniors at assisted-living facilities. Symptoms reported were mainly fever and cough. The Bureau of Epidemiology (BOE) discovered outbreaks caused by *influenza* A at two facilities. Senior residents at these facilities routinely received *influenza* vaccine. The two outbreaks were examined for *influenza* vaccine efficacy and herd immunity.

METHODS: The BOE investigated isolated reports of ill seniors at the assisted-living facilities. Epidemiologists conducted site visits and interviewed key personnel at the facilities to detect disease causation. Laboratory tests were performed to identify the disease etiology. Data was compiled to determine the demographics, vaccination status and severity of the outbreak. Preventative measures were emphasized to contain the outbreaks.

RESULTS: Laboratory tests performed at commercial labs detected *influenza* A either by PCR or antigen test. To contain the outbreaks preventative measures of droplet and contact precautions were applied. No mortality was reported at either facility. 1) Assisted-living facility A: Earliest onset of illness was 1/7/2017. Final attack rate was 36.2% (25/69). Age group 70 years and above comprised 96% of ill seniors. Eighty-eight percent reported symptoms of cough and 44% had fever. Sixty percent were females. Total of 81% ill seniors had received *influenza* vaccine. 2) Assisted-living facility B: Earliest onset of illness was 7/8/2017. Final attack rate was 17.3% (14/81). All ill seniors were above 70 years of age. One hundred percent reported symptoms of fever, 43% had cough and 57% had weakness. Seventy-nine percent were females. Total of 78% of ill seniors had received *influenza* vaccine.

CONCLUSIONS: *Influenza* outbreaks persist as a severe health risk to seniors at assisted-living facilities. Even facilities with extensive vaccination rates of 81% and 78% bear the brunt of *influenza* outbreaks. This reinforces concern regarding the efficacy of *influenza* vaccine in the senior population. *Influenza* vaccines particularly towards seniors are customarily executed per CDC guidelines every year, but results indicate *influenza* outbreaks continue to occur. Innovative strategy is essential to acquire herd immunity. Attention to preventative measures and collaboration with the health department is key to minimize the impact. **LIMITATIONS:** Both outbreaks also reported staffs with upper respiratory illness, but staffs were excluded due to non-availability of vaccination data and laboratory results.

Committee Infectious Disease

Topic Influenza & Other Respiratory Diseases

Keywords Infectious Diseases; Influenza Surveillance; Local Epidemiology

Consider for Different Presentation? Yes

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Submission Type	Roundtable
ID	9290
Abstract Type	Roundtable
Abstract Title	Assessing RSV-Associated Morbidity and Mortality—Creating a Strong Foundation to Evaluate the Potential Impact of Future Prevention Strategies in the United States

Abstract

Key Objectives:

- Discuss epidemiologic evidence gaps prior to potential vaccine and immunoprophylaxis introduction in the United States
- Discuss new and ongoing activities to assess RSV-associated morbidity and mortality
- Conduct strategic planning for future RSV-related collaborations between CDC, public health departments, and CSTE

Brief Summary:

Respiratory syncytial virus (RSV) is the most common cause of lower respiratory tract infections in children younger than 1 year of age in the United States and is being increasingly recognized as a significant cause of respiratory illness in older adults and adults with chronic medical conditions. With more than 45 immunization and therapeutic products in development, it is important to accurately document and assess RSV-associated morbidity and mortality prior to their introduction. In 2016, CDC convened an expert panel to identify epidemiologic gaps related to RSV infections. A better understanding of mortality and other severe manifestations of RSV infections across all ages was identified as an urgent need. While CDC has surveillance systems in place to assess RSV-associated hospitalizations and outpatient visits, a larger catchment area is required to assess the most severe disease outcomes. Over the past few years, CDC has engaged with health departments and CSTE to discuss strategies for collecting data on RSV-associated deaths. Through this collaboration, a case report form for pediatric RSV-associated deaths was created and piloted at several health departments. Having recently developed a mechanism for web-based reporting using RedCAP, CDC would like to continue working with jurisdictions to implement a system for reporting deaths of children <5 years of age and possibly expanding efforts to measure RSV-associated ICU admissions. These activities complement existing health department efforts within FluSurv-NET—a population-based surveillance platform for laboratory-confirmed RSV sponsored by CDC’s Emerging Infections Program and CSTE’s Influenza Population-Based Hospitalization Surveillance Project. With support from local and state partners, these activities will 1) guide future recommendations of RSV products in the pipeline by assessing their potential impact on severe infections, 2) identify risk factors for severe outcomes, and 3) create the infrastructure needed to assess post-licensure impact of new vaccines and therapeutics on severe RSV infections.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Surveillance; Epidemiology; Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9420
Abstract Type	Roundtable
Abstract Title	Development of Surveillance Systems for Respiratory Syncytial Virus in the United States

Abstract

Key Objectives:

- Define and discuss components necessary to standardize respiratory syncytial virus (RSV) surveillance across jurisdictions.
- Discuss how existing surveillance systems used by state and local health departments are currently using or could be leveraged to implement RSV surveillance in their jurisdictions.

Brief Summary:

There are several candidate respiratory syncytial virus (RSV) vaccines and prophylactic treatments that are expected to reach the market in the next few years. Measuring the impact that the introduction of these therapies can have on the population at large is of interest to public health. An assessment conducted in 2017 by the CSTE Influenza and Respiratory Diseases Subcommittee revealed that some RSV surveillance is being conducted at the state and local level; however, the surveillance is not standardized across jurisdictions and dedicated resources for this type of surveillance are limited. Additionally, the assessment results also identified opportunities to leverage existing surveillance systems (e.g., NREVSS, syndromic) for RSV surveillance. During this roundtable session, public health partners will discuss the next steps in standardizing RSV surveillance across jurisdictions, focusing on defining surveillance components (e.g., case definitions, forms, required surveillance elements). Since resources for conducting RSV surveillance are limited, this forum will also be used to discuss how existing respiratory surveillance systems might be leveraged to also capture information related to RSV.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Infectious Diseases; Surveillance; Respiratory Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9546
Abstract Type	Roundtable
Abstract Title	Improving Nationwide Surveillance of Legionnaires' Disease: A Discussion of the Evolving Landscape

Abstract

Key Objectives:

- Discuss the increased use of polymerase chain reaction (PCR) techniques as a confirmatory test for Legionnaires' disease (LD).
- Discuss the application of LD and Pontiac fever (PF) case definitions at the state and local levels.
- Discuss differences in surveillance definitions for definite and possible healthcare-associated LD cases at the state and local levels.

Brief Summary:

Due to an increase in LD incidence, the Centers for Disease Control and Prevention (CDC) has created new resources for building owners and managers to reduce *Legionella* growth and spread within complex water systems. Assessing the success of these efforts over time requires accurate LD case counts. Use of novel diagnostic methods, inconsistent interpretation of the current case definitions for LD and PF, and a lack of standard definitions for healthcare association create challenges for accurate surveillance. We have noted an increase in LD cases using PCR as the sole laboratory test for disease confirmation: this currently meets the criteria for a suspect case. Data reported to CDC suggest these cases have nearly doubled since 2014. As use of PCR assays becomes more widespread, the percentage of confirmed cases may decline artificially. We propose a discussion with our public health partners of how best to integrate PCR testing results into routine LD surveillance. Misclassification may also lead to an artificial decrease in reported LD cases, negatively impacting public health response to clusters. Previous discussions with state and local partners revealed that interpretations of the LD and PF case definitions may differ between jurisdictions. The current PF definition, "a milder illness without pneumonia," does not sufficiently describe the unique characteristics of PF to ensure accurate categorization. We would like to facilitate a conversation regarding the differences between clinical syndromes and how the definitions could be enhanced to improve reporting accuracy. Accurate identification of definite and possible healthcare-associated LD is essential for assessing risk associated with a healthcare facility's water system, and can affect public health response. Case definitions for possible and definite healthcare-associated LD are not consistent throughout the United States. We would like to examine the different definitions used by state and local partners to understand how healthcare-associated cases are identified and reported, and to determine if there are commonalities that could lead to more consistent categorization. A roundtable would be a great opportunity to solicit input from stakeholders on current LD reporting challenges and possible ways to reduce inconsistencies through improved guidance.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Surveillance; Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9100
Abstract Type	Roundtable
Abstract Title	Non-Influenza Respiratory Virus Outbreaks: CDC Resources, Approach and Priorities

Abstract

Key Objectives:

- Introduce CDC Respiratory Viruses Branch (RVB) resources and toolkits available for investigation of respiratory virus outbreaks
- Discuss challenges and needs of local and state health departments in investigating outbreaks of respiratory viruses and ways in which RVB support could help address challenges
- Discuss the RVB approach to outbreaks and priorities for investigation, including working with local and state health departments to better define the burden of human adenovirus (HAdV) respiratory disease

Brief Summary:

Respiratory viruses are ubiquitous and have temporal and geographic circulation patterns that vary by virus type. Given the diversity of respiratory viruses and their circulation patterns, outbreaks can occur throughout the year. Features of clinical illness typically overlap, making it difficult or impossible to determine viral etiology based on signs and symptoms alone. Understanding the etiology of respiratory virus outbreaks is important because infection prevention and control guidance and treatment options can vary by virus. CDC RVB is available to support local and state health departments in the investigation of respiratory virus outbreaks. Available laboratory support includes real-time RT-PCR testing, confirmatory testing or typing, and genome sequencing. Available epidemiologic support includes subject matter expert consultation, data collection tools, communications guidance, and field assistance, including EpiAids. In addition, RVB is developing outbreak toolkits for specific viruses, which include fillable templates and communications materials that can be readily adapted to meet the needs of a particular outbreak. A toolkit is currently available for Middle East respiratory syndrome coronavirus (MERS-CoV) outbreak response. Understanding the burden of respiratory viruses that are potentially vaccine preventable is a priority for RVB. For example, HAdV causes outbreaks in the community as well as congregate settings and has long been recognized as a major contributor to febrile respiratory illness among military recruits living in close quarters. The Department of Defense (DoD) currently administers a live, oral vaccine for HAdV types 4 and 7 to all incoming recruits. Since re-implementation of this vaccine in 2011, dramatic declines in overall rates of respiratory illness and incidence of HAdV infections among military recruits have been documented. During the past year, RVB has assisted with numerous respiratory adenovirus outbreaks, including in universities, skilled care facilities, dormitories, and hospitals, as well as among non-vaccinated DoD personnel.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Infectious Diseases; Outbreaks; Respiratory Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9324
Abstract Type	Roundtable
Abstract Title	Utilization of National Respiratory and Enteric Virus Surveillance System (NREVSS) Data for Respiratory Virus Surveillance in State and Local Health Departments
Abstract	Key Objectives: • Describe the different methods state and local health departments are using to analyze NREVSS data for respiratory virus surveillance • Devise an evaluation plan to identify and standardize optimal analysis methods across jurisdictions Brief Summary: The National Respiratory and Enteric Virus Surveillance System (NREVSS) is a laboratory-based surveillance system utilized to monitor viral seasons and patterns. Participating laboratories in the United States voluntarily report weekly the number of antigen, polymerase chain reaction (PCR), or culture tests performed for respiratory syncytial virus (RSV), human parainfluenza viruses (HPIV), human metapneumovirus (HMPV), adenoviruses, rhinoviruses/enteroviruses, and coronaviruses and the number of those tested that were positive. As interest in, and demand for non-influenza virus surveillance strategies at the state and territorial level grows, many health departments look to NREVSS first to strengthen those efforts; however, methods of analysis vary by jurisdiction. State and local health departments with NREVSS-participating laboratories who are not using these data to supplement their existing respiratory virus surveillance efforts could benefit from the experiences of jurisdictions using these data. During this roundtable session, public health partners will share their experiences with, and methods for using NREVSS data for respiratory virus surveillance. The methods shared during this roundtable will be evaluated and the results distributed by the CSTE Influenza and Viral Respiratory Diseases Subcommittee to inform members of best practices for programs using and considering using NREVSS respiratory virus surveillance data.
Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Respiratory Diseases; Surveillance
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10099
Abstract Type	Roundtable
Abstract Title	"How Much Disease Is There? How Bad Will It be?" New Approaches to Answer Old Questions in Influenza.

Abstract

Key Objectives:

- Discuss shared challenges to answering questions about influenza disease burden and severity during the influenza season at the local, state, and national levels
- Describe new approaches by CDC to describe influenza disease burden and severity at the national level and obtain feedback on what may or may not be useful at a state level

Brief Summary:

Influenza presents a major burden each year in the United States, with 3-11% of the population getting sick with the flu in any given season, resulting in hundreds of thousands of hospitalizations and tens of thousands of deaths. Consequently, influenza-related activities take up a substantial amount of effort every year by state and local health departments to collect information to monitor the influenza season; investigate and control outbreaks; and communicate with government and healthcare leadership, the public, and the media. During the season, epidemiologists and public health leadership at local, state, and national levels may be asked similar questions, including: "How much disease is there in the population?" or "How bad is the season going to be?" or "Is this year worse than other years?". These questions can be difficult to answer because no one source of data directly answers those questions and answers may require epidemiologists and surveillance officers to synthesize data from a variety of sources and make judgments based on a number of different factors. During this roundtable session, CDC epidemiologists will share examples of new ways they are synthesizing surveillance data at the national level to address questions about influenza disease burden and severity and will facilitate open discussion between local, state and national epidemiologists to share successes and gaps in effectively addressing similar types of questions.

Committee	Infectious Disease
Topic	Influenza & Other Respiratory Diseases
Keywords	Influenza / Pandemic Influenza; Influenza Surveillance
Consider for Different Presentation?	No
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Submission Type Breakout/Quick/Lightning/Poster

ID 9889

Abstract Type Lightning

Abstract Title Whole-Genome Sequencing Used to Link a Platelet Donor Colonized with *Clostridium Perfringens* to Two Fatal Cases of Sepsis after Transfusion — Salt Lake City, 2017

Abstract

BACKGROUND: Bacterial contamination of platelets, primarily from a donor's skin flora, results in substantial morbidity and mortality. In August 2017, the Utah Department of Health was notified of 2 patient deaths from *Clostridium perfringens* sepsis. Patient A expired 5 days and Patient B a few hours after receipt of apheresis platelets from the same donation. We investigated to determine contamination source and prevent additional cases.

METHODS: We reviewed blood collection facility and hospital records and infection prevention practices. Healthcare professionals at the hospital and blood collection facility and the donor were interviewed to assess risk factors. Whole-genome sequencing (WGS) was performed on specimens cultured from the donor (axilla, antecubital fossa, self-administered perianal swabs) and specimens associated with each patient.

RESULTS: Each patient received platelet units 4 days after collection and ~14 hours apart. *C. perfringens* was isolated from Patient B's platelet bag samples, and from anaerobic blood culture from Patient A 5 days post-transfusion. No blood collection or transfusion-related infection control breaches were identified. The blood collection facility confirmed the donor's initial platelet screening culture was negative. The donor reported no recent exposures to farm animals, children or travel; however, 2 household canines had had recent diarrheal illness. The donor was noted to have poor general hygiene. WGS identified 3 isolates from the donor's skin and 1 from each patient (Patient A's blood and Patient B's platelet bag residual) that were highly related. The donor was permanently deferred from donating.

CONCLUSIONS: This investigation is the first to use WGS to link bacteria on a donor's skin to a contaminated platelet product. It documents transmission by platelet transfusion of a rarely reported organism, *C. perfringens*, and highlights the urgent need for increased uptake of evidence-based bacterial contamination risk mitigation strategies.

Committee Infectious Disease

Topic Miscellaneous Infectious Diseases

Keywords Infectious Diseases; Infection Control; Local Epidemiology

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9501
Abstract Type	Poster
Abstract Title	Application of Whole Genome Sequencing to an Outbreak of <i>E. coli</i> O157:H7 in a Rural Community in Utah and Arizona

Abstract

BACKGROUND: Shiga toxin producing *Escherichia coli* subtypes, including *Escherichia coli* O157:H7 are responsible for an estimated 265,000 infections and 30 deaths annually in the United States according to the Centers for Disease Control and Prevention. In July of 2017, the Utah Department of Health and Utah Public Health Laboratory (UPHL) identified a cluster of *E. coli* O157:H7. During the course of the investigation, UPHL applied whole genome sequencing and molecular phylogenetic analysis to patient and environmental samples to aid in the investigation, to help identify the source of the outbreak, and to help prevent further illness.

METHODS: The Utah Public Health Laboratory performed whole genome sequencing, bioinformatic analysis, and molecular phylogenetics on 15 confirmed *E. coli* O157:H7 isolates linked to the outbreak, including 11 patient isolates and 4 environmental isolates (horse and bull manure). Bioinformatic and phylogenetic analyses were all performed using an analysis pipeline developed by UPHL (reference).

RESULTS: All 15 of the patient and environmental isolates form a single monophyletic clade with short branch lengths and high statistical support. This indicates all the isolates are highly related and share a common molecular evolutionary history lending evidence to the conclusion that exposure to animal manure may have been a potential source of infection.

CONCLUSIONS: The methods used during this outbreak provided the phylogenetic relationships of isolates as well as provided near complete genotypic information for each isolate in near real time. Additionally, the information generated by WGS could be further exploited to gain insights into virulence factors that may present in the outbreak associated isolates. This work demonstrates how WGS can be applied in near real time to an ongoing outbreak and highlights the benefits of WGS and advanced bioinformatic analyses for outbreak investigations.

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Informatics; Infectious Diseases; Genomics
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9411
Abstract Type	Poster
Abstract Title	Developing Tools for Infection Control in Group Care Facilities: The DOH-Manatee Outbreak Information Packet

Abstract

BACKGROUND: Epidemiology staff at the Florida Department of Health in Manatee County (DOH-Manatee) have identified a lack of accessible information regarding the importance of outbreak reporting and first steps for infection control in settings such as schools and assisted living facilities (ALFs). The development of an Outbreak Information Packet (OIP) aims to ease and encourage the reporting process, as well as provide high-risk facilities with information on common types of outbreaks.

METHODS: In order to determine what kinds of information would need to be included in the OIP, epidemiology staff reviewed outbreak reports from the previous three years and consulted with a Regional Epidemiologist from the Florida Department of Health to obtain information on the most common types of outbreaks reported. This review identified gastrointestinal, influenza-like, and rash-like illnesses as the most commonly reported outbreaks and the OIP was developed to address each outbreak type, broken down by section. Each section includes infection control recommendations, specimen collection information, and line lists customized for each outbreak type. Lastly, the OIP contains a description of the Florida Statute that mandates outbreak reporting and how each facility can utilize DOH-Manatee when experiencing an outbreak.

RESULTS: The OIP has been applied during outbreak responses within Manatee County. The OIP has also been distributed and utilized by a variety of facilities including schools, daycares, ALFs, and nursing homes when an outbreak was reported in these locations. These facilities in Manatee County have used the OIP during their outbreak response activities to monitor the number of ill individuals, enact control measures quickly and effectively, and submit clinical specimens to the Florida Bureau of Public Health Laboratories for testing.

CONCLUSIONS: The OIP was designed as a quick reference packet that emphasizes the importance of prompt response while initially addressing outbreaks. Having the OIP cover general types of outbreaks based on symptoms and not specific diseases allows for broad use of the packet to address multiple outbreak and facility types. Through an inclusion of the most common types of outbreaks, in addition to letters detailing the importance of communicable disease outbreak reporting DOH-Manatee was able to create a resource for use in many different outbreak situations.

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Disease Prevention; Outbreaks; Infection Control
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9664
Abstract Type	Poster
Abstract Title	Using Death Certificate Data to Improve Estimation of Mortality: The New York State Department of Health Active Bacterial Core Surveillance Experience, 2000-2016
Abstract	BACKGROUND: New York State Emerging Infections Program (NYSEIP)'s Active Bacterial Core Surveillance (ABCs) program conducts active, population-based surveillance within 15 NYS counties for laboratory confirmed cases of five invasive pathogens. Although mortality information is critical in reliably estimating the severity and burden of these diseases, surveillance information on vital status is only assessed at hospital discharge with no additional follow-up. The objectives of this analysis were to assess the contribution of death certificate (DC) data to ABCs mortality estimation and to characterize deceased ABCs cases pre- and post-discharge. METHODS: ABCs cases diagnosed between 2000 to 2016 were linked with NYS DC records using date of birth, last name, first name, and gender. Analysis was restricted to hospitalized cases for purposes of comparing patients who died during hospitalization for an ABCs pathogen to those who died within 30 days post-discharge. RESULTS: Of 10,611 ABCs cases reported during 2000-2016, 90.3% (n=9,583) were hospitalized of which 9.7% died during hospitalization and an additional 4.3% died within 30 days post-discharge. Among those deceased within 30 days post-discharge, the majority (> 60%) of deaths occurred within the first 7 days of discharge. In both groups, "other sepsis" was the most commonly stated underlying cause of death (COD) (18.4% of deaths during hospitalization, 9.0% of deaths within 30 days post-discharge). Majority (> 60%) of the underlying and contributing COD under sepsis or pneumonia were unspecified types of the illness. A significantly greater proportion (p<0.05) of those deceased within 30 days post-discharge were 65 years or older, had prior history of diabetes mellitus, and had longer length of hospital stay compared to those deceased during hospitalization. Those deceased during hospitalization were significantly (p<0.05) more likely to have an intensive care unit admission than those deceased within 30 days post-discharge. CONCLUSIONS: Assessing mortality at hospital discharge likely underestimates the overall ABCs mortality, especially in the first week post-discharge. As demonstrated by this analysis, DC can augment ABCs vital status surveillance methodology and improve mortality estimation. However, using DC data to estimate the increased risk of mortality due to ABCs pathogens was limited by the lack of cause-specific mortality documentation on DC files.
Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Surveillance; Emerging Infections
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9905

Abstract Type Poster

Abstract Title Viral Meningitis Outbreak in Washoe County, Nevada, 2017

Abstract

BACKGROUND: Viral meningitis is a reportable condition in Nevada. In July 2017, an increased number of viral meningitis cases were reported. Initially thought to be undiagnosed West Nile Virus, the Washoe County Health District (WCHD) instructed physicians to conduct additional testing on patients with symptoms consistent with viral meningitis. In August and September 2017, a significant increase in cases positive for Enterovirus (EV) was observed. No epidemiological links were identified through medical chart review. On September 28, 2017 Lassen County Public Health in Susanville, California notified the WCHD regarding their community-wide outbreak of viral meningitis. This prompted the WCHD to begin an in-depth outbreak investigation to identify epidemiological links between cases in both counties.

METHODS: Data was collected from medical chart review, case interviews, and lab results on each case. Case interviews were conducted to obtain exposure history. Cerebrospinal fluid (CSF) testing was conducted at the treating hospitals. EV testing was conducted on CSF, serum samples, or throat swab through commercial laboratories. The Centers for Disease Control and Prevention (CDC) performed rRT-PCR testing and sequencing on 22 EV positive specimens.

RESULTS: Fifty-nine cases with illness onset from July 15 to December 3, 2017 were identified. The median age was 10 years (range <1year to 81years), with 43 (73%) under the age of 18. Thirty-seven (63%) were male. Twenty-six (44%) were Hispanic. Predominant symptoms included headache (88%), fever (85%), vomiting (56%), stiff neck (49%), and photophobia (37%). Fifty-five (93%) were hospitalized; no deaths were reported. Forty-five (45%) had two or more exposure settings. An epidemiological link between Lassen County and Washoe County outbreaks was identified, i.e., regular football games hosted in both counties. Three small clusters were identified in three schools with one cluster also associated with an apartment complex. A total of 31 cases were positive for EV. Twenty-three specimens were sent to CDC for further testing; 17- Echovirus 30, 2- Echovirus 9, 1- Coxsackievirus A10, and 1- Coxsackievirus B5 were identified. Two specimens were invalid. A strain was matched to the Lassen County, CA outbreak by genetic sequencing analysis on Echovirus 30 specimens.

CONCLUSIONS: This outbreak was largely due to Echovirus 30 circulating in the community. Football games between Washoe County and Lassen County epidemiologically linked some cases. For other cases, ill school and household contacts were likely the source of infection. The long duration of this outbreak also illustrates the difficulties in controlling a disease spread by person to person contact.

Committee Infectious Disease

Topic Miscellaneous Infectious Diseases

Keywords Local Epidemiology; Outbreaks; Infectious Diseases

Consider for Different Presentation? No

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Submission Type Breakout/Quick/Lightning/Poster

ID 9349

Abstract Type Quick

Abstract Title Antibiotic and Antifungal Treatment Among Patients with Confirmed Coccidioidomycosis — Southern California, 2011

Abstract

BACKGROUND: Coccidioidomycosis, caused by inhaling *Coccidioides* spp. fungi, can cause respiratory symptoms commonly mistaken for bacterial pneumonia and progress to severe disseminated disease. Antibiotics are ineffective in treating coccidioidomycosis, whereas antifungals are essential for treating severe disease. We investigated coccidioidomycosis testing and treatment patterns in an integrated health care delivery system to identify gaps in the diagnosis and treatment of this neglected disease.

METHODS: We identified persons with coccidioidomycosis diagnoses during 2011 using Kaiser Permanente Southern California electronic health records. Cases were confirmed by positive complement fixation or immunodiffusion antibody test, culture, or histological report identifying *Coccidioides*. To analyze complex longitudinal events (antibiotic and antifungal treatments), we used EventFlow to identify sequences and time between events before and after first positive coccidioidomycosis test. We included antifungals given ≤ 1 year and antibiotics given ≤ 3 months of testing.

RESULTS: Among 530 patients with confirmed coccidioidomycosis, 77% received antibiotics ≤ 3 months before or after first positive test; 80% received antifungals during the year before or after first positive test. Among those treated with antibiotics, the majority (70%) received antibiotics before their first positive test; among those with antifungals, 79% received them ≤ 1 year after first positive test. For patients receiving antibiotics before positive tests, median time between the 2 events was 12 days (interquartile range = 2–33 days), and 74% received >1 antibiotics course before positive tests. The most common event sequence (35%) was antibiotic treatment followed by positive test and then antifungal treatment.

CONCLUSIONS: Most patients received antibiotics before their coccidioidomycosis test, with many receiving multiple antibiotics courses and experiencing diagnosis delays. Positive coccidioidomycosis tests led to markedly lower rates of antibiotic treatment and to the initiation of antifungal treatment. Clinicians in coccidioidomycosis endemic regions including California should consider expanding coccidioidomycosis testing to reduce unnecessary antibiotic use and guide correct treatment.

Committee Infectious Disease

Topic Miscellaneous Infectious Diseases

Keywords Infectious Diseases; Electronic Health Records

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9031

Abstract Type Quick

Abstract Title Burden of Clostridium Difficile Infection (CDI) in Massachusetts Emergency Departments (EDs)

Abstract

BACKGROUND: *Clostridium difficile* is a spore-forming gram-positive bacillus; *C. difficile* infection (CDI) is the leading cause of antibiotic-associated nosocomial diarrhea and colitis in the United States. CDI can be acquired in a health care setting or in the community. CDI represents a huge burden in the United States, accounting for over 450,000 cases and nearly 30,000 deaths; however, the burden of CDI in Massachusetts is not well established. We used emergency department (ED) syndromic surveillance to measure the burden of CDI in the state.

METHODS: Massachusetts collects demographic and clinical data from EDs throughout the state as part of the National Syndromic Surveillance Program (NSSP), a CDC-funded program. As of 2016, approximately 85% of statewide ED visits were captured within the system. The number of ED visits in 2016 related to CDI was measured using the ICD-10 code for CDI, A04.7. Demographic characteristics of individuals with CDI related ED visits, as well as hospital admission status and comorbidities were ascertained and compared to all ED visits, and chief complaint terms most frequently associated with CDI were also analyzed.

RESULTS: In 2016, there were 2,389,367 visits to Massachusetts EDs captured by the Massachusetts syndromic surveillance system. Of those visits, 3,182 (0.1%) contained the ICD-10 code for CDI. When comparing CDI-related visits to all ED visits, 86% were hospitalized (vs. 16%), 57% were female (vs. 53%), 60% were ≥60 years of age (vs. 27%), and 88% were white (vs. 71%). The most frequent chief complaint terms captured during CDI-related visits were: pain, diarrhea, abdominal, and fever. The most frequently used phrases were abdominal pain, gastrointestinal disorder, and flank pain. The most frequent co-morbid diagnoses were hypertension, dehydration, hyperlipidemia, and acute kidney failure.

CONCLUSIONS: CDI has been a growing epidemic in the United States, and statewide estimates of CDI are not well established. We found that most CDI visits resulted in a hospital admission suggesting that ED surveillance is likely to capture the most severe consequences of CDI. Continued monitoring to detect real-time changes in the incidence of CDI over time will be helpful for designing prevention efforts and evaluating their impact.

Committee Infectious Disease

Topic Miscellaneous Infectious Diseases

Keywords Syndromic Surveillance; Healthcare Associated Infections (HAI); Antimicrobial Resistance

Consider for Different Presentation? Yes

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Affiliation State Public Health Agency

Submission Type Breakout/Quick/Lightning/Poster

ID 9677

Abstract Type Quick

Abstract Title Ebola Virus Persistence in Semen, a Review of the Literature

Abstract

BACKGROUND: In March 2015, a woman from Liberia contracted Ebola Virus Disease (EVD). A public health investigation revealed one epidemiologic link to Ebola, unprotected sex with a male EVD survivor 199 days after he recovered from Ebola. Genetic analysis of the Ebola viruses (EBOV) recovered from the woman and from the semen of the male survivor closely matched. Subsequent studies of survivors of the 2014 EVD outbreak in West Africa have led to many scientific discoveries on EBOV persistence in semen. We performed a literature review to better understand EBOV persistence in semen and the potential risk of EBOV transmission through sex.

METHODS: PubMed was searched for publications using the terms “Ebola” and “semen”. Search results were limited to case reports and cohort studies stemming from the 2014 West Africa EVD outbreak. Fourteen publications discussing EBOV persistence in semen were selected for review. Information was collected pertaining to study participant demographics, testing platforms utilized, and duration of EBOV persistence in semen.

RESULTS: All reviewed publications reported semen testing results in men >15 years of age; with a range of 15-79. In total 11 publications reported semen-test results performed on EVD survivors in Liberia, Sierra, and Guinea. Three publications described semen-test results performed on EVD survivors repatriated to the United States or India. All used real-time polymerase chain reaction (qRT-PCR) to test for the presence of EBOV RNA. However, qRT-PCR assays varied between publications. Three publications described virus isolation attempts for qRT-PCR positive specimens. All observational cohort studies found that the percentage of men with positive semen results declined with increasing time after illness recovery. One observational cohort study found that EBOV persistence in semen was associated with age, with semen collected from men older than 40 years more likely to test positive. The longest period of detection of EBOV RNA in semen from illness recovery was 565 days. The highest qRT-PCR cycle threshold value at which virus was successfully isolated was 30. The longest period between a male survivor’s EVD onset to transmission of EBOV through semen was 470 days (Ct=23).

CONCLUSIONS: For the vast majority of male EVD survivors, EBOV virus persistence in semen declines over time. However, individual variations do exist. As such, educating male survivors on the risks of sexual transmission and proper condom use plays an important part in mitigating future outbreaks. Further research is needed to understand risk factors for prolonged infectious EBOV persistence in semen.

Committee Infectious Disease

Topic Miscellaneous Infectious Diseases

Keywords Infectious Diseases; Sexually Transmitted Diseases; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10054

Abstract Type Quick

Abstract Title Evaluation of the Coccidioidomycosis Surveillance System in Washington State, 2012-2015

Abstract

BACKGROUND: Coccidioidomycosis is an emerging infection in Washington State (WA), with the first endemically acquired infections identified in 2010. In April 2014, the disease was added to the list of notifiable conditions in WA. We conducted a surveillance evaluation to assess the frequency of *Coccidioides* testing, the prevalence of coccidioidomycosis based on laboratory data, and the completeness of coccidioidomycosis case reporting to the WA Department of Health from 2012 to 2015.

METHODS: Local reference laboratories and hospitals throughout WA were contacted to determine coccidioidomycosis testing availability; nine clinical laboratories offering testing for WA residents were identified. We requested positive and negative results for laboratory tests specific to coccidioidomycosis from these nine laboratories. Six laboratories provided results covering testing from 2012 to 2015, and a seventh laboratory provided results from 2014 to 2015. Two laboratories declined participation. Test results were limited to WA residents based on patient zip code if available, otherwise insurance subscriber zip code if available, otherwise healthcare provider zip code. The frequencies of *Coccidioides* testing and positive results were determined from the clinical laboratory test results. We calculated the percentage of positive results reported by comparing clinical laboratory results from the six laboratories reporting results from 2012 to 2015 with cases of coccidioidomycosis reported to the Washington State Public Health Issue Management System (PHIMS).

RESULTS: From 2012 to 2015, the seven included laboratories tested 4,038 WA residents for coccidioidomycosis. Of these tested individuals, 227 (5.6%) had at least one positive test result. Among these 227 with at least one positive *Coccidioides* test result, 40 (17.6%) were reported to the WA Department of Health. Excluding test results from one clinical laboratory which was missing data before 2014, 130 individuals had at least one positive test result from January 1, 2012 to March 31, 2014; 66 individuals had at least one positive test result from April 1, 2014 to December 31, 2015. Reporting increased from 12 of 130 positive individuals (9.2%) pre-April 2014 to 19 of 66 positive individuals (28.8%) post-April 2014, when the condition became notifiable.

CONCLUSIONS: There are significant gaps in coccidioidomycosis case reporting to the WA Department of Health, with less than a third of positive patients reported since surveillance for this condition began in April 2014. Reporting has increased over time, but significant gaps remain. Complete reporting from laboratories is necessary for better understanding of the epidemiology of this emerging condition in WA.

Committee Infectious Disease

Topic Miscellaneous Infectious Diseases

Keywords Surveillance; Emerging Infections; Evaluation

Consider for Different Presentation? Yes

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Institution Washington State Department of Health

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10353
Abstract Type	Quick
Abstract Title	Invasive Group A <i>Streptococcus</i> Outbreak in People Experiencing Homelessness and Injection Drug Users Salt Lake County, Utah

Abstract

BACKGROUND: In 2016 an increase in invasive group A *Streptococcus* (iGAS) cases in injection drug users (IDU) and those experiencing homelessness was detected through routine surveillance in Salt Lake County (SLCo), Utah. A review of past surveillance data revealed that the increase began at the end of 2014. An outbreak investigation was initiated to identify a source and prevent additional cases.

METHODS: An outbreak case was defined as isolation of group A *Streptococcus* from a normally sterile site in a Salt Lake County resident currently experiencing homelessness, or who had reported IDU within the last month of onset , and reported 1/1/2014 to present. Available samples collected from a sterile site were collected from each case and sent to the Centers for Disease Control and Prevention (CDC) *Streptococcus* lab for further genomic testing. Cases were interviewed with a questionnaire designed to assess where they were currently staying, injection drug practices, and how their drugs were obtained.

RESULTS: From January 2014 to December 2017, 135 cases have been identified. Of these, 66% were homeless, 63% had reported IDU, and 40% were both homeless and IDU. Twelve different T-types of iGAS have been identified by the CDC. Sixteen samples had a common strain, T-type 14 and subtype emm49, which began appearing in 2016.

CONCLUSIONS: This ongoing outbreak has proven challenging to contain due to a lack of resources and the complex population it is occurring in. Information gathered from the Salt Lake City Police Department revealed that a possible mode of transmission for iGas in this population could be mouth-to-mouth drug transactions, which occur frequently near the local homeless shelter. Results from the case interviews corroborate this hypothesis.

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Outbreaks; Infectious Diseases; Social Inequalities
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9258
Abstract Type	Quick
Abstract Title	Knowledge, Attitudes, and Practices Regarding Coccidioidomycosis Among Healthcare Providers in Four Counties in Washington State, 2017
Abstract	BACKGROUND: Coccidioidomycosis is an emerging infection in Washington State (WA) and the epidemiology of the disease in WA is poorly understood at present. Under-recognition and under-reporting of the disease is suspected based on reports of only severe disease. Disease surveillance relies on clinical awareness and reporting to public health. We sought to characterize healthcare provider knowledge, attitudes and practices regarding coccidioidomycosis awareness, diagnosis, and treatment in south-central WA. METHODS: We conducted an online, self-administered cross-sectional knowledge, attitudes, and practices (KAP) survey from February – April 2017. The target population for this survey was healthcare providers currently working in four counties in south-central Washington, specifically Benton, Franklin, Yakima, and Walla Walla counties, representing a region thought to be endemic for the <i>Coccidioides</i> fungus. We assessed awareness of reporting requirements, confidence in ability to diagnose and treat disease, confidence that knowledge is current, calculated knowledge score, and consideration of risk in patient population. RESULTS: We received 86 survey responses, with an estimated response rate of 10-13%. The majority of respondents were unaware of reporting requirements for coccidioidomycosis in WA, and further unaware that the disease had been reported in the state. Less than a third of survey respondents reported confidence in their ability to diagnose coccidioidomycosis and confidence that their knowledge is current. The majority of respondents never or rarely consider a diagnosis of coccidioidomycosis, and <25% of respondents indicated a working knowledge of serologic tests for the infection. The average knowledge score for respondents was 65%. Previous education, training, or practice with coccidioidomycosis was the only identified predictor of confidence and consideration of risk. CONCLUSIONS: Surveillance for coccidioidomycosis in WA relies on healthcare provider knowledge of the disease and timely diagnosis and reporting. Our results indicate that the majority of surveyed healthcare providers in a region known to be endemic for coccidioidomycosis in WA are not confident in their ability to diagnose or treat the disease and not confident that their knowledge of coccidioidomycosis is current. Additionally, more than a third did not know <i>Coccidioides</i> could be found in WA or that coccidioidomycosis is reportable to the local health department. These data indicate the enormous need for education and training among this healthcare provider population, and support the concern that only a small proportion of existing cases of coccidioidomycosis are reported to the health department.
Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Prevention; Zoonotic Diseases; Emerging Infections
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9749
Abstract Type	Quick
Abstract Title	Surveillance for Unexplained Critical Illnesses and Deaths of Possible Infectious Etiologies, Minnesota, 2012-2016

Abstract

BACKGROUND: Since 1995, the Minnesota Department of Health (MDH) has conducted surveillance for unexplained critical illnesses and deaths of possible infectious etiology (UNEX). Priority is given to cases <50 years of age with no significant underlying medical conditions; however, any reported unexplained death or illness with infectious disease hallmarks may be investigated.

METHODS: Cases are reported to MDH primarily by medical examiners and infectious disease physicians. In addition, possible cases are identified by death certificate review for infectious disease syndromes. Information is collected from medical records, scene investigation findings, and autopsy and pathology reports. Further laboratory testing on patients or decedents is conducted by MDH or the Centers for Disease Control and Prevention. Data for cases reported from 2012 - 2016 were analyzed and summarized by syndrome.

RESULTS: 428 cases total cases were identified (358 deaths, 70 critical illnesses). 249 (58%) were reported by medical examiners, 93 (22%) were reported by clinicians or clinical pathologists, 82 (19%) were found by death certificate review, and 4 (1%) were discovered by other methods. 194 (45%) cases had a respiratory syndrome, 102 (24%) sudden unexpected death, 62 (15%) neurologic syndrome, 24 (5%) cardiac syndrome, 20 (5%) gastrointestinal syndrome, 19 (5%) shock/sepsis, 2 (<1%) genitourinary syndrome, and 8 (2%) with multiple systems involved. Median age was 25.5 years (range, newborn to 93 years). 391 (91%) cases had specimens tested, and 197 (50%) of these had pathogens identified as confirmed, probable, or possible causes of illness. Etiologies in fatal cases included *Treponema pallidum* in a newborn, Lyme disease carditis, malaria, enterovirus D68, hantavirus, *Legionella pneumophila*, 3 cases of *Haemophilus influenzae* type f, 2 cases of *Neisseria meningitidis*, 5 cases of influenza B, and 38 cases of influenza A. Etiologies of note in non-fatal cases included *Leptospira* spp. (with Bell's palsy), lymphocytic choriomeningitis virus, *Streptococcus salivarius*, Jamestown Canyon virus, and 3 cases of La Crosse encephalitis virus.

CONCLUSIONS: UNEX surveillance enables case-based investigation to establish potential etiologies for otherwise unexplained cases. Infectious disease cases of public health importance including emerging and novel diseases have been detected through this surveillance effort. Similar programs should be considered elsewhere as resources allow.

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Emerging Infections; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10151

Abstract Type Quick

Abstract Title Viral Meningitis Outbreak — Lassen County, California, 2017

Abstract

BACKGROUND: On September 27, 2017, California Department of Public Health (CDPH) received a report of suspected viral meningitis cases in Lassen County. We investigated to characterize the outbreak and provide control measures.

METHODS: We reviewed medical records of patients reported by the local hospital. A case was a California resident with cerebrospinal fluid (CSF) pleocytosis (WBC>5) and negative bacterial culture, or an emergency department visit with headache, fever, and stiff neck on or after September 1, 2017. CDPH laboratory performed real-time polymerase chain reaction testing of CSF or respiratory specimens for enterovirus (EV) detection and sequencing of EV for molecular typing.

RESULTS: Fifty medical charts were referred by local hospital; 35 patients met the case definition. Samples from 17 patients were tested for EV: 14 were positive for echovirus 30, 2 for coxsackievirus B5, and one was negative. Median age of patients was 16 years (range: 13–43); 60% were male. Common symptoms included headache (100%), nausea (71%), and photophobia (69%). Nineteen (54%) patients were hospitalized; no deaths were reported. Eighteen patients were students at one high school; 7 were on the football team. All affected team members tested positive for echovirus 30. Investigation of team practices revealed players were required to share water bottles. Genetic sequence analysis showed Lassen County echovirus 30 samples were nearly indistinguishable from samples from neighboring Washoe County, Nevada, which also experienced a viral meningitis outbreak (55 patients) during July 15–December 3, 2017.

CONCLUSIONS: This outbreak is probably attributable to echovirus 30, which commonly causes meningitis. Transmission among high school football players might have been enhanced by water bottle sharing. Lassen County established a 24-hour call center to address community concerns and press releases were issued to communicate health messages, including instructions on personal hygiene and recommendation for affected individuals to self-isolate at home.

Committee Infectious Disease

Topic Miscellaneous Infectious Diseases

Keywords Outbreaks; Infectious Diseases; Epidemiology

Consider for Different Presentation? Yes

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Submission Type	Roundtable
ID	10296
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 2018 Annual Conference.

Brief Summary:

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

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Surveillance
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10300
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 2018 Annual Conference.

Brief Summary:

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

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Surveillance; Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	10303
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.

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Surveillance
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9799
Abstract Type	Roundtable
Abstract Title	Underdiagnosed and Underappreciated: Improving Surveillance and Our Understanding of Coccidioidomycosis (Valley Fever) in the United States

Abstract

Key Objectives:

- Describe work examining coccidioidomycosis in endemic states and in states where it is not known to be endemic
- Discuss the current coccidioidomycosis CSTE case definition and surveillance data to better understand the burden of disease and inform improvements
- Discuss gaps in the understanding of the true coccidioidomycosis burden and geographical distribution
- Discuss efforts to improve clinical and public awareness of coccidioidomycosis
- Identify opportunities for collaboration to better understand this underdiagnosed disease
- Discuss new and existing diagnostic tests and their possible impacts on surveillance

Brief Summary:

There is growing recognition of the public health impact of coccidioidomycosis (Valley fever) in the United States. The causative fungus *Coccidioides* is endemic in the southwestern United States, with most cases reported from Arizona and California. However, the geographic range of this disease has changed since skin testing studies were conducted nearly 70 years ago, evidenced by cases acquired outside historically described endemic areas. The disease is also relevant in states outside of endemic areas because interstate travel is common and people may seek healthcare in these states after traveling from endemic areas. Primary pulmonary coccidioidomycosis can mimic symptoms of influenza or bacterial pneumonia; disseminated disease can also occur, which carries significant risk of death. Substantial delays to diagnosis and misdiagnosis are common, and patients often receive several courses of ineffective antibacterial agents. State and local public health departments and the Centers for Disease Control and Prevention (CDC) have worked collaboratively to increase awareness of coccidioidomycosis among healthcare providers and the public. Increasing clinical awareness is key to improving accurate diagnosis of coccidioidomycosis. Coccidioidomycosis first became nationally notifiable in a Council of State and Territorial Epidemiologists (CSTE) position statement in 1995. Although coccidioidomycosis is now reportable in 22 states, and approximately 10,000 cases are reported annually, this number underestimates the true burden of disease. In areas with high incidence, verifying clinical criteria, in addition to laboratory criteria, is challenging due to the high incidence of disease and limited public health resources. Thus, Arizona and several counties in California with high incidence have adopted a coccidioidomycosis case definition that requires laboratory components only. This roundtable will offer an opportunity for states and territories to share experiences of applying the current CSTE case definition, surveillance efforts, and lessons learned. This discussion could lead to improved data collection and new opportunities for collaboration.

Committee	Infectious Disease
Topic	Miscellaneous Infectious Diseases
Keywords	Infectious Diseases; Surveillance; Epidemiology
Consider for Different Presentation?	No
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Submission Type Breakout/Quick/Lightning/Poster

ID 9140

Abstract Type Breakout

Abstract Title Identifying Vaccine-Associated Rash Illness Amidst a Large Measles Outbreak — Minnesota, 2017

Abstract

BACKGROUND: During April–August 2017, Minnesota experienced a large measles outbreak. After a measles vaccination campaign was initiated, including an accelerated 2-dose pediatric schedule, numerous vaccine-associated rash illnesses (VARI) were detected. VARI is non-contagious but difficult to distinguish from measles. Often, decisions about public health control measures, including contact investigation, immunity assessments, and exclusion, need to be implemented before viral genotyping results are available. We compared characteristics of VARI and confirmed measles cases to inform public health decision making.

METHODS: We defined measles cases per the Council of State and Territorial Epidemiologists definition. VARI was defined as a rash occurring within 21 days after measles, mumps, and rubella (MMR) vaccination, and detection of measles vaccine strain (genotype A) in naso/oropharyngeal swab or urine by real-time reverse transcriptase polymerase chain reaction (rRT-PCR) and genotyping. The Minnesota Immunization Information Connection (MIIC), Minnesota’s immunization information system, was used to monitor MMR administrations. We collected clinical and exposure data on all persons with positive measles rRT-PCR testing, including those with measles and those with VARI, through routine case investigation.

RESULTS: Over 51,000 MMR doses above expected were administered during the outbreak. We identified 71 measles cases and 34 VARI. The median age of VARI patients was 1.1 years (range 10 months–48 years) and for measles cases 2.8 years (range 3 months–57 years). VARI detection increased in parallel with rising MMR administration. The presence of fever was similar among VARI and measles cases (94% vs 100%), but differences were seen in the proportion with cough (41% vs 94%; $p<.001$), coryza (47% vs 83%; $p<.001$), and conjunctivitis (24% vs 66%; $p<.001$). Presence of any of the 3C’s (cough, coryza, or conjunctivitis) for VARI was 76% and for measles cases 96% ($p<.005$). Exposure to infectious measles cases varied (VARI 0%; measles cases 96%).

CONCLUSIONS: Surges in MMR administration and heightened community awareness during measles outbreaks can result in increased VARI detection, consuming considerable public health resources. During an outbreak, history of measles exposure and possibly clinical presentation should be considered when assessing the likelihood of VARI among measles rRT-PCR positive persons with history of recent MMR. Ultimately, rapid, non-resource intensive vaccine strain-specific diagnostic assays are needed to most efficiently distinguish between VARI and measles.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Outbreaks; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10235

Abstract Type Breakout

Abstract Title Imported Congenital Rubella Syndrome in Houston, TX

Abstract

BACKGROUND: Congenital rubella syndrome (CRS) is an extremely rare illness in infants resulting from maternal infection with rubella virus during pregnancy. Symptoms associated with CRS include cataracts, heart defects, hearing impairment, and developmental delays. Houston Health Department (HHD) investigated a report of CRS in a 2-month-old male infant diagnosed with congenital heart disease, bilateral cataracts, mild hearing loss, and other issues.

METHODS: On 12/20/17 HHD was informed by the Texas Department of State Health Services (DSHS) of a suspect case of CRS. HHD Bureau of Epidemiology (BOE) initiated the investigation by interviewing the mother of the case to obtain symptoms, verify vaccination history of all close contacts, and travel history. The mother was a recent immigrant from Nigeria who arrived in the US in early September 2017 with two other children. The case patient was born less than 3 weeks after the mother arrived in the US. No close contacts were identified beyond immediate family members; the two siblings were current for MMR. The patient was originally seen on 11/9/2017 at a genetics clinic; the patient was positive for rubella IgG antibodies. Nasal wash, blood, and urine specimens were collected on 12/18/17 for testing at CDC. Serology was positive for rubella IgM antibodies and RT-PCR positive. HHD BOE notified the hospital's infection preventionist (IP) about the disease, requested all patient clinical encounters, and advised the IP to implement prevention control measures for clinical staff and initiate contact tracing. HHD BOE coordinated with HHD Immunizations Bureau to vaccinate, test, and further educate the mother to emphasize the public health importance of contact precautions.

RESULTS: All facilities with in- and out-patient visits were notified by the hospital and HHD BOE of recent exposure to a CRS patient. Serology is pending for the patient's mother. HHD BOE will coordinate with the hospital to track patient throughout disease progression and complete the mother's MMR vaccination.

CONCLUSIONS: Although imported cases of CRS occur more often than domestic cases, instances of CRS are rare and far between. Continued education is needed on the importance of vaccination and the extended infectious period for CRS cases. Infants with CRS shed a large amount of virus for an extended period. With the virus present in saliva and urine CRS patients need to be kept in both contact and droplet isolation for minimum 1 year to avoid unprotected exposures among pregnant and unvaccinated persons.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Maternal and Child Health; Vaccine-Preventable Diseases; Immigration & Migrant / Refugee Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9451

Abstract Type Breakout

Abstract Title Investigation of an Increase in Mumps in New York City, 2016–2017

Abstract

BACKGROUND: The number of suspected mumps reports to the New York City (NYC) Department of Health and Mental Hygiene (DOHMH) increased sharply beginning July 2016. An investigation was conducted to determine factors associated with the increase in mumps reports.

METHODS: Reports of suspected mumps from providers and laboratories were investigated and classified as cases according to the Council of State and Territorial Epidemiologists confirmed and probable case definitions. Changes in the average monthly number of reports and cases were calculated for the period of increase (7/1/2016 through 6/30/2017) compared to a baseline period (1/1/2012 through 6/30/2016). Outbreaks of 20 or more cases were excluded. Facilities visited, demographics, epidemiologic linkages, and geographic distribution of cases were assessed.

RESULTS: Compared to the baseline period, an increase in the average monthly number of reports (from 15 to 68 reports /month) and cases (from 3 to 25 cases/month) occurred from 7/1/2016 through 6/30/2017. No geographic or epidemiologic linkages indicating a large outbreak were identified. During 7/1/2016 through 6/30/2017, a majority of reports (62%) and cases (55%) visited one particular urgent care chain (UCC) that expanded over 6 years to 43 sites throughout NYC. In July 2016, in response to an outbreak of mumps outside of NYC occurring at the time, this UCC implemented check-lists for clinic managers and providers specifying mumps PCR testing requirements for patients with parotitis and notification to DOHMH.

CONCLUSIONS: During the baseline, mumps was underreported. The increase in cases observed in NYC was largely driven by increased testing and reporting, particularly from one large UCC. Our findings suggest that UCCs can dramatically improve case ascertainment by implementing policy changes across many facilities through a centralized structure, and can be valuable partners for disease surveillance.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Surveillance; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9623

Abstract Type Breakout

Abstract Title Rotavirus Outbreak Among Vaccinated Daycare Attendees in Polk County, Florida, April 2017

Abstract

BACKGROUND: Rotavirus is one of the leading global causes of gastrointestinal illnesses among children. Since the introduction of rotavirus vaccines beginning in 2006, morbidity associated with the virus has declined greatly. However, rotavirus continues to circulate, posing a threat to young children and vulnerable populations. An investigation of a rotavirus outbreak among daycare attendees in Polk County, most of whom had been vaccinated, demonstrates the continuing impact of this pathogen in the post-vaccine era.

METHODS: Following notification of the outbreak by the daycare, the Florida Department of Health in Polk County's Epidemiology Program conducted two site visits and collected two stool specimens. A detailed line list of all who were ill, including name, age, gender, classroom, symptoms, onset and recovery dates, and any medical treatment, was maintained throughout the outbreak period. Medical records were requested for 25 individuals, and case surveys were conducted in both Spanish and English with parents or guardians of affected children. Vaccination histories were obtained through the Florida SHOTS database.

RESULTS: A total of 40 children and 8 adults met the case definition of vomiting or diarrhea in a daycare attendee or staff member from April 6 to April 24. The most commonly reported symptoms were diarrhea (94%), vomiting (29%), and fever (23%). Thirteen children met a severe case definition, which included one or more of the following criteria: symptoms lasting six or more days (12), or including six or more diarrhea or vomiting episodes per day (3), or hospitalization (1). Ninety-seven (92%) children received at least one rotavirus vaccine, with 79 (75%) fully vaccinated. Twenty-seven (68%) of the 40 ill children were fully vaccinated, including eight (62%) of those who met a severe illness case definition. Of the 106 daycare attendees, all were age-eligible to receive one or more doses of the rotavirus vaccine. Both stool specimens collected were positive for rotavirus A, G12P[8], an emerging strain implicated in outbreaks worldwide over recent years.

CONCLUSIONS: Rotavirus continues to contribute to morbidity associated with diarrheal illnesses among young children, and as displayed by the large numbers affected during this outbreak. Numerous studies indicate rotavirus vaccine effectiveness between 80 and 87% against severe rotavirus disease. This investigation demonstrates that even within a highly-vaccinated population, rotavirus infection should be considered as a possible cause of diarrheal illness outbreaks, and stool specimens should be tested for the pathogen.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Information Databases; Vaccine-Preventable Diseases; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9880

Abstract Type Breakout

Abstract Title Toxigenic *Corynebacterium diphtheriae* in a Horse with Respiratory Illness, New Hampshire, 2017

Abstract

BACKGROUND: *Corynebacterium diphtheriae* is considered a human-specific pathogenic bacterium. Natural infections of *C. diphtheriae* in horses are infrequently reported, but more recent reports describe toxigenic *C. diphtheriae* wound infections. On November 6, 2017, a suspect *C. diphtheriae* infection in a horse with respiratory illness was reported. We launched an investigation to assess human exposures and prevent additional illnesses.

METHODS: Specimens from the horse were collected and sent to the New Hampshire (NH) Public Health Laboratories (PHL) and the Centers for Disease Control and Prevention (CDC) for 16S rRNA gene sequencing, biochemical testing, Elek testing, and PCR. The NH State Veterinarian inspected the farm to ensure appropriate isolation of the horse while awaiting confirmatory testing. We identified and tested human contacts of the horse. Recommendations for antibiotic prophylaxis were held pending additional laboratory testing but immunization status was assessed and contacts were recommended re-immunization if not current within prior five years. To assess for carriage, nasal and oropharyngeal swabs were obtained for all nine identified NH contacts and two of three NJ contacts.

RESULTS: The horse was purchased at a New Jersey (NJ) livestock auction on October 25th and transported to NH on October 29th. The horse, originally from North Carolina, was brought to NJ in July, spent approximately two weeks in the NJ auction barn, and was ill 2-3 days prior to shipment to NH. Symptoms included copious, thick, bilateral yellow nasal discharge. Isolation had been appropriately instituted for this horse upon arrival at the NH farm. The initial specimen was collected from the horse on October 30th and the NH Veterinary Diagnostic Laboratory identified a species suspicious for *C. diphtheriae* through culture and MALDI-TOF mass spectrophotometry. NH PHL confirmed identification of *C. diphtheriae* using 16S rRNA sequencing. On November 15th, CDC confirmed a genotypic and phenotypic toxigenic strain; no change in public health response was warranted because all contacts had tested negative or had > 10 days lapse since last exposure and were not ill.

CONCLUSIONS: This case provided an opportunity to reconsider *C. diphtheriae* as a zoonotic pathogen. A human source of infection to this horse was not identified, supporting the possibility that horses may act as a reservoir. This case highlights the need for further examination of equine infections to fully understand the implications of *C. diphtheriae* in horses, routes of transmission, and risk to human handlers.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases; Infectious Diseases; Veterinary Public Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9029

Abstract Type Breakout

Abstract Title Validation of Vaccine-Preventable Disease (VPD) Death Reports: July 2012 – September 2017

Abstract

BACKGROUND: Accurate ascertainment of cause of death (COD) is necessary to ensure validity of published data. Two U.S. systems collect death data related to vaccine-preventable diseases (VPD): the National Center for Health Statistics' (NCHS) National Vital Statistics System and the National Notifiable Disease Surveillance System. The Council of State and Territorial Epidemiologists supports validation of VPD-related rare deaths (position statement 01-ID-09).

METHODS: The National Center for Immunization and Respiratory Diseases (NCIRD) and NCHS established protocols in 2012 and 2014 for validation of rare cause VPD death reports. NCHS receives jurisdictions' death records, codes the COD, and reports specified rare VPD deaths to NCIRD for investigation with appropriate jurisdiction epidemiology/immunization offices. Rare VPD identified as underlying or contributing COD are included in the validation protocol, but only underlying COD are used in standard NCHS reports. This summary includes reports of deaths occurring July 15, 2012, through September 30, 2017. Tracking COD recoding began in 2016.

RESULTS: Reports of deaths coded as VPDs were received from 45 jurisdictions. Of 269 reports received (161 with the VPD listed as the underlying COD), 127 (85 underlying COD) were validated by NCIRD and state epidemiology/immunization programs, 121 (59 underlying COD) were identified as having a cause of death other than the VPD, and 21 (17 underlying COD) were lost to follow up (LTF) and could not be investigated. Among 89 varicella reports, 10 were validated, 65 were determined to have another COD, and 14 were LTF. Of 49 meningococcal reports, 34 were validated, 14 were determined to have another COD, and 1 was LTF. Among 35 pertussis reports, 27 were validated, 4 were determined to have another COD, and 4 were LTF. Of 13 mumps reports, 1 was validated, 11 were determined to have another COD, and 1 was LTF. Of 17 measles reports, 1 was validated and 16 were determined to have another COD. Of 3 diphtheria reports, 2 were determined to have another COD and 1 was LTF. The 6 rubella and 3 polio reports were found to have other COD. All 54 CRS reports were validated. Of 84 reports in 2016, 32 were found to have another COD; 16 of those were recoded to another specified COD category.

CONCLUSIONS: Rare-cause validation includes vital records offices, COD certifiers, and NCHS staff. Death report investigation by NCIRD and jurisdiction epidemiology and/or immunization programs is also required to make the data more accurate and usable.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Collaboration; Information Systems; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10130
Abstract Type	Breakout
Abstract Title	Whole Genome Sequencing to Enhance Public Health Investigation of Mumps Outbreaks in Massachusetts

Abstract

BACKGROUND: Massachusetts experienced a surge in reported mumps cases in 2016 and 2017, many associated with outbreaks. A high population density, and the presence of many colleges and universities, with potential for transmission within and between institutions and into the surrounding communities, makes outbreak investigation challenging. We describe the utility of whole genome sequencing (WGS) to assist public health investigations of mumps outbreaks.

METHODS: We collected data on mumps cases reported to the Massachusetts Department of Public Health (MDPH) from January 1, 2014–July 31, 2017 via the Massachusetts Virtual Epidemiologic Network (MAVEN) surveillance system. In collaboration with the Broad Institute, we constructed sequencing libraries from 200 PCR-positive specimens from Massachusetts and 59 PCR-positive specimens from other US jurisdictions (provided by CDC). We performed whole genome nucleotide sequencing using the Illumina HiSeq 2500 platform. Twenty-three mumps whole genome sequences downloaded from GenBank were also included. To look for genetic changes between patient samples, we reconstructed the phylogeny of mumps genomes using Bayesian Evolutionary Analysis by Sampling Trees (BEAST) software. We annotated phylogenies using case data including institutional association and epidemiologic linkage. We reconstructed possible transmission trees within outbreaks using the *outbreaker* software package in R, and analyzed the extent to which genetic results could predict epidemiologic linkage.

RESULTS: Eleven mumps cases were reported in Massachusetts during 2014–2015, and 371 reported from January 1, 2016–July 31, 2017. We obtained 160 high-quality mumps virus genome sequences from Massachusetts specimens, and 43 sequences from other US jurisdictions. We identified two distinct lineages of mumps virus. One of these lineages is more closely related to sequences from 2014–2015, while the other lineage contains almost exclusively 2016–2017 institution and community outbreak-associated sequences. Mumps viruses from states other than Massachusetts were often very genetically similar to the virus detected in local cases. Genetic distance was shown to be a good predictor of epidemiologic linkage.

CONCLUSIONS: Genetic similarity of viral genome sequences from mumps cases in Massachusetts and other jurisdictions suggests mumps virus may be widely circulating in the United States, not confined to sporadic outbreaks. Within Massachusetts, the data suggest transmission occurred both between institutions and into the community. Our observation that genetic distance is a good predictor of epidemiologic linkage indicates that whole-genome data can be used to infer linkage between cases not identified by traditional epidemiological methods, showing the power of WGS to inform public health investigations and interventions.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Genomics; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9871

Abstract Type Lightning

Abstract Title Descriptive Epidemiology of *Haemophilus Influenzae* Strains, Georgia, 2010-2016

Abstract

BACKGROUND: *Haemophilus influenzae* serotype b (Hib) infection was once a leading cause of morbidity and mortality, particularly affecting young children. Hib has largely been controlled by vaccine; however, there is no vaccine for the nontypeable strains of *Haemophilus influenzae* (NTHi). NTHi is a common cause of localized respiratory infections, including sinusitis, otitis media, and pneumonia, and NTHi has now become the leading cause of invasive Hi infections in the U.S. The Georgia Department of Public Health (GDPH) reviewed data from reported invasive NTHi case-patients to ascertain the burden of disease, demographics of cases, and severity of infection among patients with invasive NTHi infection compared to the same information from reports of typeable (a, b, c, d, e, f) strains (THi).

METHODS: GDPH epidemiologists reviewed cases of Hi reported between January 1, 2010 and December 31, 2016. A case was defined as laboratory-confirmed Hi isolated from a sterile site. For this analysis, the bacterial isolate must have been confirmed and serotyped at the Georgia Public Health Laboratory or the Centers for Disease Control and Prevention (CDC). Medical chart abstractions were completed using a form developed by the Active Bacterial Core Surveillance program of the CDC's Emerging Infections Program. Fisher's exact and Student's t-test were used to compare data from THi and NTHi groups.

RESULTS: 617 reports of NTHi and 250 reports of THi infections were received by GDPH from 2010-2016. For both NTHi (54%) and THi (63%) infections, females were more often affected. The mean age was 55 years for NTHi cases, significantly older than the mean age of 46 for THi ($p<0.0001$). The most common clinical manifestations of disease were pneumonia, followed by primary bacteremia, and meningitis, in both groups. One or more underlying medical conditions were documented in 67% and 78% of NTHi and THi cases, respectively. Intensive care unit admission served as a proxy for severity of disease, and was similar among NTHi and THi cases at 45% and 44%, respectively. 17% of NTHi cases died compared to 10% of THi cases, which was statistically significant ($p<0.05$).

CONCLUSIONS: NTHi infections were the most common type of invasive Hi infection reported to GDPH in each of the years from 2010-2016. These data increase awareness about the burden of more severe clinical syndromes (i.e. pneumonia) among adults, particularly those with underlying conditions. Continuing to monitor trends in NTHi infections could have implications for future vaccine development.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Epidemiology; Infectious Diseases; Respiratory Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10089

Abstract Type Lightning

Abstract Title Eliminating Tuberculosis By Researching Barriers for Child Morbidity Missing Source Cases

Abstract

BACKGROUND: Texas has been identified by the Centers for Disease Control and Prevention (CDC) as a state with extensive recent transmission for tuberculosis (TB). Recent transmission is attributed to cases being born from a high tuberculosis incidence country and being exposed prior to arrival in the United States. Texas has the highest rate of child morbidity compared to other high incidence states, Florida, California, and New York. Between 2010 and 2014, Texas' TB rate was 2.91 per 100,000 among children ages 0-4. Identifying and addressing barriers for source case finding in children has the potential to reduce transmission in Texas.

METHODS: The inclusion criteria for the study were children diagnosed between ages 0-4 in 2010-2015 in Texas. TB in this cohort is attributed to recent transmission. Children in this age group haven't began attending school, therefore source cases should be more easily identified. This timeframe was chosen because it reflects the most recent and complete contact investigation data. Phone calls were made to local health departments confirming all missing source case information. All analysis used SAS 9.4 statistical software.

RESULTS: 194 cases were identified for analysis. On a yearly average 73% of child morbidity cases were reported without a source case. When compared to adult morbidity, significant differences were found in county of birth, travel history, and birth country of guardians (p-values here?). In this sample 94% of child morbidity cases were born in the US and 86% did not have travel history reported. The majority of these children (86%) had parents born in a high incidence country. Phone calls to local health jurisdictions revealed that these families may not be identifying all family members the child was exposed to during contact investigations.

CONCLUSIONS: After reviewing Texas data, the high rate of child morbidity does not appear attributable to reactivation for the children or exposure in a high incidence country. The leading barrier to finding the exposure source of child cases is not identifying actively infected people through contact investigations. Next steps to identify additional barriers could include developing a chart abstraction tool to identify supplementary risk factors and providing guidelines to families about exposure locations and time lengths.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases; Epidemiology; Respiratory Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9961

Abstract Type Lightning

Abstract Title Rubella Infection in an Unvaccinated Pregnant Woman - Johnson County, Kansas

Abstract

BACKGROUND: Rubella, which is subclinical in up to half of all infections, was declared eliminated from the US in 2004, although transmission still commonly occurs in many parts of the world. On December 14, 2017, the Johnson County Department of Health and Environment (JCDHE) received a phone call from an elementary school reporting a pregnant mother of one of their students was diagnosed with rubella and was taking her unvaccinated child to the doctor. JCDHE had not received any other notification of this patient and initiated an investigation immediately in conjunction with the Kansas Department of Health and Environment.

METHODS: The patient was interviewed and medical records reviewed. Serum was collected on December 12 and sent to a commercial laboratory for IgM testing; IgG testing was subsequently performed. Specimens were forwarded to the Centers for Disease Control and Prevention for avidity testing. She presented to two emergency rooms, a family care provider, her OB-GYN, and attended work prior to her diagnosis. Healthcare workers and contacts at these locations were followed up with to determine immunization and pregnancy status.

RESULTS: The unvaccinated case-patient was rubella IgG negative during her first trimester prenatal testing. She reported symptom onset on December 6, consisting of a burning, itchy rash, fever, cough, coryza, and congestion; she was 18 weeks pregnant. She had no travel history nor contact with any symptomatic individuals. Her unvaccinated brother stayed in her home during the exposure window after returning from a trip to India; he had a rash at that time and was diagnosed with poison ivy. The patient's laboratory results were IgM and IgG positive with low avidity, indicating a recent infection. One hospital employee was unvaccinated and excluded from work; the patient's unvaccinated daughter was immunized on December 14 and excluded from school. All other contacts of child-bearing age were either immune or advised about the risks of becoming pregnant following a rubella exposure.

CONCLUSIONS: Rubella can have serious consequences when contracted during pregnancy, particularly in the first trimester. This occurrence of rubella was in an unvaccinated pregnant woman in her second trimester with no history of travel. A potential source of infection is her unvaccinated brother who returned from India; serological testing is pending. Notification occurred from an elementary school; additional training needs to occur to ensure healthcare providers, specifically OB-GYNs, are aware of the reporting requirements and resources available at the local health department.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Immunization; Infectious Diseases; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9926

Abstract Type Poster

Abstract Title An Outbreak of Mumps Among Kentucky College Students

Abstract

BACKGROUND: An outbreak of mumps was identified at a Kentucky university in February of 2016, the first outbreak of mumps reported in Kentucky in recent history. An outbreak investigation was initiated by the local health department with assistance from the university health center. The outbreak spanned nearly the entire spring semester and was declared over July 31, 2016.

METHODS: Initial cases were identified through the university health center based on similar symptoms in a short time period. Once identified as a cluster, the local health department was involved and confirmatory lab testing was ordered. The investigation continued with the confirmation of mumps as the outbreak etiology. Case investigations were initiated in an attempt to determine exposure sources as well as vaccination history. Health alerts shared with other healthcare providers allowed for additional case finding and the sharing of appropriate control measures. Summary statistics were utilized to describe the vaccination history of cases, laboratory results, and the predominant illness characteristics.

RESULTS: A total of 90 cases were identified in the outbreak investigation based on the Centers for Disease Control and Prevention (CDC) case definition for suspect, probable, and confirmed cases of mumps. Students at the university accounted for 93% of the cases, with the remaining 7% split between staff and community members. Laboratory confirmation of mumps infection applied to 11% of the cases and nearly 87% reported a positive immunization history of two MMR (measles-mumps-rubella) vaccines.

CONCLUSIONS: This outbreak was a learning experience for healthcare providers, Kentucky universities, and state and local public health agencies. Interventions used such as an additional dose of MMR vaccine for certain groups and isolation of all cases may have possible utility, but their effectiveness was not evaluated in this investigation. The investigation and response strengthened the connection between the university and the local public health system and increased the public health knowledge base of the university health center.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases; Outbreaks; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9549

Abstract Type Poster

Abstract Title Analysis of Positive Rubella IgM Labs Reported in Florida, 2014-2016

Abstract

BACKGROUND: The Florida Department of Health (DOH) adheres to the Council of State and Territorial Epidemiologists case definition for rubella which requires confirmatory laboratory evidence, with or without clinical symptoms, to be considered a case. Confirmatory laboratory evidence includes a positive immunoglobulin M (IgM) lab. Every year, dozens of positive rubella IgM labs are reported in Florida among persons who have no obvious risk factors for acquiring rubella and are determined to not represent an acute infection.

METHODS: Positive rubella IgM labs received by electronic laboratory reporting in Merlin, the DOH disease reporting system, between December 29, 2013 and December 9, 2016 were reviewed. Variables including demographics, type of ordering provider, reported rubella IgG labs, and if documented in the lab notes, the reason for testing, were collected. Measles, mumps, and rubella (MMR) vaccination status and demographics were gathered from Florida Shots, the statewide immunizations database. The data were compiled using Microsoft Excel 2016. Descriptive analysis of the data was performed using Epi Info 7.

RESULTS: Positive rubella IgM lab results were reported for 135 unique individuals. Of those 135, two were determined to be cases while the rest were judged to not be cases by county investigators. The most commonly documented reason for testing was routine prenatal screening (n=55, 41%) and 85% of persons with positive IgM labs were women with a median age of 31 years old.

CONCLUSIONS: These findings demonstrate a limitation of the current rubella case definition that allows for a positive IgM result, with or without clinical symptoms, to be considered confirmatory laboratory evidence of infection. Rubella was eliminated from the United States in 2004 and fewer than 10 imported cases are now reported each year. The positive predictive value of the IgM assay is very low for persons tested in the absence of symptoms or exposure. This analysis does provide opportunities for education of health care providers. Many of the IgM labs were ordered by physicians who were testing for evidence of immunity to rubella and not for active infection. Local health departments may choose to reach out to healthcare providers and encourage appropriate use of rubella IgM testing in accordance with Centers for Disease Control and Prevention guidelines.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10178

Abstract Type Poster

Abstract Title Impact and Utility of Whole Genome Sequencing on a Cluster Investigation in Northeast Texas

Abstract

BACKGROUND: The Texas Tuberculosis (TB) Program was notified that G00617 was identified as a Large Outbreak of TB in the US (LOTUS) cluster in 2016. G00617 was associated with an outbreak in 2012 involving cases with characteristics associated with poor treatment outcomes or recent transmission, including: homelessness, substance abuse, and cases under five-years-old. The cluster investigation was limited by cases outside the jurisdiction and poor historians. Whole Genome Sequencing (WGS) results were explored to refute or confirm links to this outbreak.

METHODS: Between January 2014 and January 2017, 15 genotyped cases were identified. A call was held to collect epidemiological data on cases, where the regional jurisdiction indicated six additional associated cases. Data collected by the program, including infectious periods, known epi-links, and contact investigation findings, were analyzed. After identifying commonalities, cases were re-interviewed to establish missing epi-links and assess for potential sites of transmission. Other jurisdictions with clustered cases were contacted for data on affiliated cases. WGS results for G00617 were provided to the state program and shared with the regional jurisdiction to discuss findings and determine where to focus investigative resources.

RESULTS: Before WGS, the regional jurisdiction confirmed epi-links for 14 of 21 cases. Two additional epi-links were suspected from interviews. Of the five remaining cases, homelessness and substance abuse were identified as risk factors. Two of these cases were outside the regional jurisdiction but indicated family ties in the outbreak jurisdiction. After WGS, links were confirmed for 20 of 21 cases, an increase of 43 percent. The two suspected links were confirmed, linking the current outbreak to the 2012 outbreak, as well. Four unknown cases were nearly identical to other outbreak cases. The last unknown case, who indicated family in the northeast Texas area, was not closely related genetically. The regional health department characterized this outbreak as epidemiologically linked household and family transmission. Continued monitoring was recommended.

CONCLUSIONS: The discriminatory power of WGS in TB control is far greater than traditional methods. As evidenced by G00617, there is potential to focus investigations within a genotyped cluster to save limited resources, especially when dealing with large, cross-jurisdictional outbreaks.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Outbreaks; Respiratory Diseases; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10134

Abstract Type Poster

Abstract Title Mumps Outbreak at a University Athletics Department Summer 2017

Abstract

BACKGROUND: Mumps is an infrequently reported infectious disease in Travis County, but steadily increasing in incidence. In 2014, only 1 case was reported, in 2015 8 cases were reported, and in 2016, approximately 19 cases were reported. To date for 2017, 31 cases of mumps have been reported. In this abstract, we describe an outbreak that occurred at a university athletics department during the summer of 2017. At this university, the MMR vaccines are required only for international students and recommended for all others.

METHODS: Austin Public Health (APH) participated in conducting interviews that collected symptom onset dates, demographics, testing type, travel history, athletic activities, and extracurricular activities. Vaccine history was not easily obtained as the university does not keep or require records, but most reported that they had attended public school in Texas as children. APH provided recommendations on testing and infection control to the athletics department and conducted a follow up meeting regarding disease reporting and infection control measures. The athletics department sent out alerts and provided education to staff and students. The APH nurses assisted in conducting a MMR booster vaccine clinic onsite for student athletes that opted for it.

RESULTS: APH conducted 29 interviews for those that were symptomatic and tested. There were 9 confirmed cases of mumps and 11 that met probable case definition. Of the confirmed and probable cases, all 20 reported parotitis, and 2 of the 22 males reported orchitis. The ages of those that were symptomatic ranged between 18-45 years, 22 males and 7 females. Of those that were tested, there were 13 football players, 7 staff members, 3 soccer players, 2 basketball players, 1 golfer, 1 swimmer, 1 track and field athlete, and 1 that identified as "none." The symptom onset dates ranged from 6/12/17-9/4/17, with the majority of cases reported in July. The initial case by onset of symptoms reported travel history to Haiti at the end of May. The last date of symptom onset was 9/4/17.

CONCLUSIONS: Transmission of mumps was associated with athletic activities and specifically the football department. Low student census during summer session contributed to controlling mumps transmission. In addition, increased awareness of reporting, infection control measures, and booster vaccines controlled transmission and should be sustained to reduce the incidence and severity of future outbreaks in densely populated areas such as university settings.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Collaboration; Outbreaks; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10233
Abstract Type	Poster
Abstract Title	Mumps Outbreak at Trucking Company - Johnson County, Kansas

Abstract

BACKGROUND: Mumps is a contagious disease that can occur at any time of the year, especially in a crowded environment such as a dorm, workspace, sports team or class. In early 2017, Johnson County Department of Health and Environment (JCDHE) began to see an increase in Mumps cases due to outbreaks in neighboring states and counties. A neighboring county health department notified JCDHE of a positive case of mumps that identified 2 coworkers from trucking company who also had symptoms. A hospital notified JCDHE of another case that was connected with this place of business. JCDHE began a workplace investigation into exposures in conjunction with the Kansas Department of Health and Environment on March 27, 2017.

METHODS: Onsite visits were held at the trucking company. All reported symptomatic individuals were interviewed. Several employees had been previously tested and calls were made to collect their test results. Individuals who were asymptomatic were interviewed later. One buccal swab was collected and sent to the state lab for testing. Information was developed to educate the staff about the disease. The building was inspected for potential places of transmission.

RESULTS: There were two confirmed and thirteen probable mumps cases associated with this outbreak. Ill persons ranged from 22 to 46 years of age and fourteen ill were male. Fourteen of the patients had received both MMR vaccinations with one only receiving one dose. Onset dates ranged from February 16 to March 27, 2017. Fourteen ill reported parotitis and one had orchitis as a complication of mumps. Seven sought healthcare, and one person was hospitalized. Duration of illness ranged from 2 to 15 days (median duration: 5.5 days; duration unknown for five persons). Laboratory testing was conducted for seven ill persons; two (13%) were positive for mumps by PCR, two (13%) were positive by IgM, and four (27%) were positive by IgG.

CONCLUSIONS: Timely reporting is crucial for public health interventions. Several initial patients were seen in the ER or urgent cares and were not tested for mumps or diagnosed with another illness. Two initial confirmed cases were out of jurisdiction, causing a delay in reporting of workplace exposures. Proper testing was not utilized, most offices were not aware of collecting buccal swabs during the first 5 days of parotitis or they collected serology during the first 5 days instead. Education for staff at urgent care offices was created to help assist with proper testing and timely reporting.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Occupational Exposure; Vaccine-Preventable Diseases; Essential Public Health Services
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	8999
Abstract Type	Poster
Abstract Title	Perceptions of Immunizations As Health Prevention Among Female Mexican Immigrants in Oklahoma

Abstract

BACKGROUND: Research on health prevention behaviors of Mexican immigrant mothers regarding immunizations has been limited. As of 2014, Hispanics or Latinos comprised 9.6% of the population of the state of Oklahoma and were the largest minority group within Oklahoma. This minority population has continued to grow at a rapid rate in Oklahoma. The purpose of this study was to explore the perceptions of immunizations held by Mexican immigrants who are mothers residing in Oklahoma. The aim of this study was to identify their perceived risk of contracting a vaccine-preventable diseases if not immunized and knowledge of immunizations as a health prevention behaviors.

METHODS: The health belief model and the sociocultural theory provided the theoretical underpinnings for this qualitative study. Semistructured interviews were conducted with a purposeful sample of 12 immigrants living in a rural area of Oklahoma. Data were triangulated and analyzed to identify themes and patterns.

RESULTS: Findings indicated participants perceived susceptibility of contracting a vaccine-preventable disease if not immunized, with the severity of the disease having the potential to cause death. Identified barriers in immunization uptake were language barrier, lack of immunization information in Spanish, and fear of deportation.

CONCLUSIONS: Recommendations include public health outreach providing culturally, linguistic appropriate immunization information to immigrants within communities. Findings provide health psychologists and other health care professionals the ability to formulate interventions targeting immunizations in female Mexican immigrants. These interventions could promote positive social change by decreasing immigrants' and their children's risk of morbidity and mortality related to lack of immunization uptake.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Maternal and Child Health
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 8957

Abstract Type Poster

Abstract Title Vaccination Response Following an Infant Pertussis Death in an Indiana Amish Community 2017

Abstract

BACKGROUND: On March 29, 2017, the Indiana State Department of Health (ISDH) was contacted by the Parke County Health Department regarding the death of a two-week old Amish infant to pertussis. The infant case met the Council for State and Territorial Epidemiologists clinical criteria for pertussis and was later linked to other laboratory-confirmed cases. As a result of this event, the local Amish community requested education through their midwife, and a presentation focused on vaccine-preventable diseases and vaccine safety was held on April 5, 2017.

METHODS: An ISDH Field Epidemiologist led the session. Hand-drawn representations of cocooning, herd immunity, and basic immunological concepts were used in lieu of traditional electronic presentation strategies to demonstrate cultural respect. Identifying a prominent representative from the community (the midwife) assisted in making community members comfortable and women frequently directed questions through her. Questions regarding pertussis raised during the session focused on vaccine safety and duration of vaccine-induced immunity. This supported previous studies suggesting that vaccination safety concerns play a larger role than religious opposition in vaccine uptake in Amish communities.

RESULTS: On April 7, 2017, a pertussis outbreak was declared in this community and two vaccination clinics providing MMR, Tdap, and DTaP were held on April 11th and April 18th. MMR vaccine was offered due to interest displayed during education session. No adverse events were reported, and across both clinics, 46 total patients were vaccinated with 33 MMR (72%), 6 DtaP (13%), and 19 Tdap (41%). Continued community engagement by public health partners, such as the Field Epidemiologist beginning a game of volleyball after the 4/18 clinic, built rapport with this community and strengthened relationships. To date, the Valley Health Professionals mobile medical bus has been able to vaccinate an additional 22 people, giving 19 additional doses of MMR and 9 of DTaP.

CONCLUSIONS: This event provides additional evidence that vaccine safety and child health is of primary importance to Amish families when considering vaccination. Knowledge of pertussis and its potential for severe outcomes in infants was low, but increasing this knowledge through education may be effective in encouraging prioritization of vaccination. Building relationships with nontraditional healthcare providers, such as midwives, and developing strong collaborations among public health entities helps increase the effectiveness of public health responses in Amish communities. Disease complications and outbreaks of pertussis, and other vaccine preventable diseases, provide opportunities to engage with communities normally averse to vaccination and improve prevention of vaccine-preventable disease.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Outbreaks; Underserved Populations; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10258

Abstract Type Quick

Abstract Title Assessing Human Papillomavirus Vaccination Coverage Via School Reporting, Allegheny County, PA

Abstract

BACKGROUND: Approximately 30,000 cases of cancer attributable to human papillomavirus (HPV) are diagnosed in the United States each year. Although safe and effective vaccines against HPV are widely available, national and state survey data indicate that coverage remains low. Monitoring coverage at the local level is challenging, given the limitations of existing data sources. To assess coverage and monitor trends among adolescents in Allegheny County, the Allegheny County Health Department (ACHD) mandated reporting of HPV vaccination status for seventh and twelfth graders at all schools by school officials.

METHODS: Beginning in the 2017-2018 school year, schools in Allegheny County are required to report the number of seventh graders who received at least one HPV vaccine and the number of twelfth graders who received at least two HPV vaccines, even though the vaccine is not required for school entry. Data must be submitted by December 31 to ACHD via a Survey Monkey questionnaire along with total enrollment and the total number of students vaccinated for the required school vaccines.

RESULTS: As of January 2, 2018, ACHD received reports from 143 schools housing seventh grade students and 89 high schools housing twelfth grade students, representing approximately 90% of the expected population for these grades. Of 11,022 seventh grade students, 5,612 (51%) received at least one HPV vaccine. The median percentage of students receiving ≥ 1 HPV vaccine was 48% by school. Of the 143 schools with seventh graders, 22 reported HPV coverage $< 25\%$ and 20 reported coverage $\geq 75\%$. Reports from high schools show that of 11,390 students in twelfth grade, 5,990 (53%) received at least two HPV vaccines. The median percentage of twelfth graders receiving ≥ 2 doses was 54% by school. Of the 89 high schools, 16 reported coverage $< 25\%$ and 15 reported coverage $\geq 75\%$.

CONCLUSIONS: Increasing HPV vaccination coverage is a goal of most pediatrics practices and public health agencies and is one of the Healthy People 2020 national objectives. ACHD has implemented mandatory reporting of HPV vaccination status by schools to monitor coverage. Preliminary data indicate that about half of seventh graders have received at least one HPV vaccine dose and half of twelfth graders have received at least two. School vaccination data can be useful for identifying populations with low coverage.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Infectious Diseases; Vaccine-Preventable Diseases; Cancer

Consider for Different Presentation? Yes

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Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	9986
Abstract Type	Quick
Abstract Title	Collaborating with Key Stakeholders to Prevent Perinatal Hepatitis B Transmission: Summary of Birthing Center Site Visits

Abstract

BACKGROUND: The Vermont Perinatal Hepatitis B Prevention Program (VPHBPP) seeks to reduce the incidence of hepatitis B virus (HBV) in infants born to women with HBV. VPHBPP identifies the HBV status of pregnant women and communicates this information to the birthing hospital, ensures prophylaxis and access to hepatitis B immune globulin and HepB vaccine at birth for all infants born to hepatitis B surface antigen positive mothers, follows infants through the HepB vaccine series, and confirms post-vaccination serology. Prenatal care providers, birthing centers, and pediatric offices all have a key role to eliminate perinatal HBV transmission. Providing awareness of increasing risk of perinatal HBV transmission was motivated by a study identifying an increase in acute HBV among injection drug users in rural areas. Vermont is both rural and amid an opiate epidemic. For this project we sought to collaborate with all Vermont birthing centers by conducting site visits to coordinate efforts to prevent perinatal HBV.

METHODS: Letters to birthing center directors were sent out via USPS highlighting VPHBPP and the plan for site visits in the upcoming year. Algorithms on perinatal HBV prevention were developed and included in this mailing. Site visits were scheduled with the nursing managers of the mother and baby units at each center. Visits were conducted with representatives from the center, the VPHBPP Coordinator, and the Maternal Child Health Coordinators from the respective local health offices.

RESULTS: There are twelve birthing centers; eight site visits have been conducted (67%). Of the eight site visits, zero (0%) were aware of the letter and algorithm sent to the center's director. During the visits current recommendations were reviewed, gaps were identified, and resources were provided. Gaps included the challenges of new electronic medical record systems, communication between labor/delivery and mother/baby units, and a lack of understanding of ACIP/CDC recommended practices to prevent hepatitis B transmission. Improvements in the communication and referral process between hospital staff and the health department were discussed. Of the eight site visits completed, eight had a formal HepB vaccine birth dose protocol (100%) and zero had a formal perinatal HBV procedure (0%).

CONCLUSIONS: Site visits with the birthing centers were conducted to enhance outreach and collaboration. Gaps identified during the visits have informed programmatic changes. Stronger relationships have been built through this collaboration between the health department and birthing centers. Other areas for future collaboration include pediatric care and prenatal care providers, as well as targeting home birth services.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Immunization; Collaboration; Hepatitis
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10335

Abstract Type Quick

Abstract Title Demonstrating How Changes to Human Papillomavirus Vaccination Dosing Recommendations Increased Teen Vaccination Rates, Denver Metropolitan Area, 2015-2017

Abstract

BACKGROUND: An effective vaccine to prevent human papillomavirus (HPV) infection is universally recommended by the Advisory Committee on Immunization Practices (ACIP) for teen aged 11-12 years. In October 2016, the ACIP revised the dosing schedule by reducing the number of required doses from 3 to 2 for teens initiating vaccination between 9 and 15 years of age. Tri-County Health Department (TCHD) sought to measure the impact of the new dosing recommendations on teen HPV vaccination rates in our large, 3-county jurisdiction of the Denver metropolitan area.

METHODS: Data from Colorado's immunization registry for teens aged 11-17 years within TCHD's jurisdiction were used to calculate rates of HPV vaccination initiation (≥ 1 valid vaccine doses) and vaccination series completion (≥ 2 or 3 valid doses based on age of initiation and timing of ACIP dosing recommendations). We examined vaccination rates before ACIP dosing recommendations changed (time points in January and May 2015, January 2016) and after ACIP approved a 2-dose recommendation (December 2016 and October 2017). To evaluate the potential impact of a reduced 2-dose requirement, completion rates were recalculated after October 2016 using the "old" 3-dose regimen.

RESULTS: From January 2015 to October 2017, the proportion of teens aged 11-17 years with ≥ 1 valid HPV vaccine doses steadily increased from 41.3% to 59.1%. Rates for teens with a valid completed HPV vaccination series were lower, but still rose by 92% from January 2015 (17.1%) to October 2017 (32.8%). When applying the "old" 3-dose ACIP recommendation, the completion rate for 11-17 year olds in October 2017 was only 25.1% versus 32.8% using the updated 2-dose schedule. The impact on rates related to the 2-dose requirement was most significant for 13-14 year olds as completion rates increased sharply from 24.6% in January 2016 to 37.6% in December 2016 and 41.1% in October 2017. Completion rates under the 3-dose recommendation would have been considerably different with minimal change for this age group (24.6% in January 2016; 27.1% in December 2016; 25.0% in October 2017).

CONCLUSIONS: The potential impact of the 2-dose HPV vaccination recommendation was significant for 11-17 year old teens who initiated vaccination before age 15 years. Completion rates were 31% higher (32.8% versus 25.1%) if compared to the "old" 3-dose recommendation. Higher vaccination rates better protects persons against HPV infection and reduces disease spread. Public health agencies should monitor trends in HPV vaccination completion rates after implementation of the updated ACIP 2-dose recommendation.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Epidemiologic Methods; Immunization; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9707

Abstract Type Quick

Abstract Title Differences in Pertussis Incidence By Race and Ethnicity in the United States, 2010–2015

Abstract

BACKGROUND: Pertussis, or whooping cough, caused by *Bordetella pertussis*, is a highly contagious vaccine-preventable disease. Despite high childhood vaccination coverage, reported pertussis incidence in the United States has increased since the 1980's. Currently, US data on racial and ethnic disparities in pertussis incidence are limited.

METHODS: To assess differences in pertussis incidence by race and ethnicity, we analyzed pertussis cases reported to the Enhanced Pertussis Surveillance (EPS) system from 2010 through 2015, using the CSTE case definition for confirmed and probable cases. Pertussis incidence by race (white, black, American Indian or Alaska Native [AIAN], and Asian or Pacific Islander [API]), ethnicity (Hispanic), and age (<1yr, 1–6yrs, 7–10yrs, 11–19yrs, 20+yrs) was calculated using US census data as denominators. Incidence rate ratios (IRRs) and 95% confidence intervals (CI) were calculated using white race and non-Hispanic ethnicity as the reference categories.

RESULTS: During 2010–2015, 17,181 pertussis cases were reported to EPS; 89% were confirmed. The annual incidence was 16.7 cases per 100,000 population. Overall, pertussis incidence was higher among Hispanic (IRR: 1.56, 95% CI: 1.50–1.63) than non-Hispanic persons. When stratifying by age, Hispanic infants (IRR: 1.58, 95% CI: 1.39–1.78) and adults (IRR: 1.59, 95% CI: 1.46–1.74), experienced higher incidence than non-Hispanic infants and adults, whereas incidence in children aged 1–19 was similar to or lower than that in non-Hispanic children. Overall, pertussis incidence was lower among black (IRR: 0.40, 95% CI: 0.37–0.43), AIAN (IRR: 0.85, 95% CI: 0.76–0.95), and API (IRR: 0.37, 95% CI: 0.33–0.42) persons than white persons. However, after stratifying by age, incidence among black and AIAN infants was similar to or slightly higher than that among white infants (black: IRR: 0.93, 95% CI: 0.78–1.12; AIAN: IRR: 1.19, 95% CI: 0.87–1.64), and incidence was higher in AIAN adults compared to white adults (IRR: 1.25, 95% CI: 1.00–1.56).

CONCLUSIONS: Overall pertussis rates differed by race and ethnicity; however, differences were not consistent across age groups. This finding could indicate true differences in pertussis incidence, or differences in diagnosis or reporting by race and ethnicity. Further investigation into the characteristics and severity of reported pertussis cases by race and ethnicity is warranted to better understand factors that underlie these differences and to inform interventions.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Health Disparities; Infectious Diseases; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9802
Abstract Type	Quick
Abstract Title	Effectiveness of Vaccine Versus Immune Globulin As Protection Against Hepatitis A Infection Among Close Contacts of Hepatitis A Cases — New York City, 2008–2017
Abstract	BACKGROUND: Post-exposure prophylaxis (PEP) is recommended for close contacts of patients with hepatitis A virus (HAV) infection within 14 days of last exposure. Hepatitis A vaccine is recommended for contacts 1–40 years old, and immune globulin (IG) for those <1 or >40 years old, immunocompromised persons, and those with chronic liver disease. We characterized vaccine and IG PEP effectiveness among contacts of HAV cases in New York City (NYC). METHODS: Contacts were identified during case investigations of NYC residents diagnosed with HAV during 2008–2017, including individuals reported to the NYC Health Department as close contacts by HAV patients (anti-HAV IgM and jaundice or serum alanine aminotransferase levels ≥ 100 units/liter) or cases epidemiologically linked to previous HAV cases. PEP effectiveness by type, overall and among contacts >40 years, was calculated as [(1-relative risk of developing HAV infection among those receiving versus not receiving PEP)*100%]. We calculated the sample size necessary for sufficient power to detect non-inferiority of vaccine to IG PEP among contacts >40 years, defined as <5% of vaccine recipients developing HAV infection, using a one-sided binomial test ($\alpha=0.025$). RESULTS: We identified 3,440 contacts, 966 (28%) of whom were PEP-eligible (had close contact with HAV patients, were identified within the PEP window, and were without documented prior vaccination or immunity), and had known PEP receipt status. Of these, 552 received vaccine and 194 received IG. Thirty-seven contacts receiving vaccine and IG simultaneously were excluded from analysis. Of the remaining contacts, 74 developed HAV infection, 16 (22%) of whom received PEP. Vaccine effectiveness was 88% (95% confidence interval [CI]: 80%, 93%), and IG effectiveness was 97% (95% CI: 81%, 99.6%). Among 198 contacts >40 years (range: 41–95 years), vaccine effectiveness for 75 vaccine recipients was 83% (95% CI: 22%, 96%), and IG effectiveness was 100% (approximated lower 95% confidence bound: 27%). Assuming infection risk among vaccine recipients >40 years is 2.7% (what we observed), then ≥ 756 vaccine recipients would be required to achieve 90% power to detect non-inferiority to IG. CONCLUSIONS: Results were inconclusive in determining whether IG is more effective than vaccine in preventing HAV and sample size was insufficient to assess vaccine non-inferiority. Limitations include inability to determine if contacts without documentation might have been immune and to account for immunocompromised status, chronic liver disease, duration or intensity of HAV exposure, and unreported HAV infections. Health departments should pool PEP data to assess vaccine non-inferiority among contacts >40 years old.
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Hepatitis; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9363

Abstract Type Quick

Abstract Title Epidemiology and Surveillance of Meningococcal Disease Among Men Who Have Sex with Men — United States, 2015–2016

Abstract

BACKGROUND: Men who have sex with men (MSM) may be at greater risk for meningococcal disease compared to other men. In the United States, epidemiology of and risk factors for meningococcal disease among MSM are not well described, in part because surveillance systems do not capture sex of sex partners. Since 2015, enhanced surveillance activities collected supplemental data on meningococcal disease cases, including sex of sex partners among adult men, and risk factors among MSM. We assessed the completeness of risk factor variables and described the epidemiology of meningococcal disease cases among MSM from 2015–2016.

METHODS: Meningococcal disease cases among men aged 18–64 years reported to the National Notifiable Diseases Surveillance System from January 2015 through December 2016 by 45 states participating in enhanced surveillance activities were reviewed. States classified cases as occurring in either MSM or men not known to be MSM, which included those with missing information regarding sex partners. We estimated proportions of characteristics among MSM cases with known responses, and compared completeness of risk factor variables between years. Serogroup was determined by PCR or slide agglutination. Available isolates were characterized using whole genome sequencing.

RESULTS: Among 240 cases in adult men, 45.8% had information on sex of sex partner. Completeness of this variable increased from 33.6% in 2015 to 57.3% in 2016. Forty-five (18.8%) cases were in MSM; among these, completeness of HIV status was stable (92.9% to 90.3%) from 2015–2016, whereas completeness of intravenous drug use and travel history decreased [(100.0% to 87.1%) and (100.0% to 48.4%), respectively]. The median age among MSM was 33 years, 45.7% were non-white, 69.7% were associated with an outbreak, 41.5% were HIV-positive, and 13.3% died. Serogroup C accounted for 83.7% of MSM cases, of which 100.0% were sequence type (ST) 11. In contrast, 16.8% of 195 cases in men not known to be MSM were due to serogroup C, of which 76.4% were ST 11.

CONCLUSIONS: Despite improvements in surveillance, missing information on sex of sex partners may result in underreporting of meningococcal disease cases among MSM. High prevalence of HIV and of serogroup C, ST 11 among MSM with meningococcal disease might provide insight into meningococcal disease transmission in this population. Improved surveillance data, including collection of variables to assess sexual and social behaviors, are critical to understand the burden and risk factors for meningococcal disease among MSM and inform policy and prevention strategies.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Surveillance; Epidemiology; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10196
Abstract Type	Quick
Abstract Title	Evolution of Extensive Tuberculosis (TB) Transmission within Congregate Settings in Texas: Implications and Interventions

Abstract

BACKGROUND: In 2008, the Centers for Disease Control and Prevention (CDC) detected a genetic strain of tuberculosis (TB) in Texas, G03270. Though cases detected in this cluster were initially linked to homeless shelters, it began to present in correctional facilities. A cluster investigation (CLI) was initiated to better understand the cause of ongoing transmission and assess for additional interventions, as this genotype was identified as one of the largest clonal TB outbreaks in the nation.

METHODS: The relatedness of cases was assessed using Reported Verified Case of Tuberculosis (RVCT) variables, genotyping data, and epidemiological field data. Specialized transmission tables and phylogenetic tree overlays were developed for data visualization. Newly identified epi-links were also noted, based upon the strength of evidence. Though this outbreak spans nine years, with 56 cases reported May 2008-July 2017, more robust information was available after 2014.

RESULTS: Initially, 14.3% (8 cases) reported a history of homelessness and 55.4% (31 cases) were identified in correctional facilities. The CLI, however, revealed three new cases reporting a history of homelessness, and nine additional cases with correctional involvement. Further analysis suggests that transmission could be attributed to a small number of facilities. Whole Genome Sequencing (WGS) data further supports this finding. Ongoing transmission has been attributed to: (1) Clinical characteristics suggesting late/missed diagnoses; (2) anecdotal interview barriers (e.g., poor historians and patient refusal); (3) contact investigation gaps (e.g., missing contacts, incomplete reporting); and (4) treatment non-adherence. Limitations include a paucity of case/contact investigation information, heterogeneity of environmental design among suspected transmission sites, reporting and diagnostic errors, and difficulties assessing TB education practices and infection control measures.

CONCLUSIONS: Although extensive efforts were made by federal, state, and local stakeholders, and transmission was interrupted in some geographic locations, ongoing transmission continues within correctional facilities. Epidemiological and molecular data suggests specific locations of concern where further intervention is warranted. Future considerations include: ensuring routine TB screenings, providing complete evaluations and follow-up, performing environmental assessments of concerning settings, assessing training needs for homeless shelter and correctional staff, ensuring seamless communication between all stakeholders, and reexamining infection control measures at implicated sites.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Outbreaks; Epidemiology; Respiratory Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10330

Abstract Type Quick

Abstract Title Fetal Outcomes of Mumps during Pregnancy

Abstract

BACKGROUND: Limited studies exist to describe the outcome of mumps in pregnancy. One from the pre-measles/mumps/rubella (MMR) vaccine era reported potential fetal loss associated with infection early in pregnancy. Others have found no increase in the rate of major congenital anomalies among infants of women with mumps in pregnancy. Understanding of potential adverse outcomes among pregnant women with mumps infection remains limited. An ongoing mumps outbreak, beginning March 2017, in Hawaii has allowed us to assess outcomes among infected pregnant women.

METHODS: Information on epidemiological characteristics was collected from all pregnant cases with onset of laboratory confirmed mumps infection between March 1 and December 11, 2017. Case investigations were conducted to collect information about clinical presentation, vaccination status, laboratory testing, and demographic information. Chart abstraction was completed to gather medical information on patients from time of diagnosis to delivery.

RESULTS: As of January 2, 2018, eight (1%) pregnant cases of 770 total mumps confirmed cases were identified. Median age was 27 years (range: 16–31). Three (38%) cases had documented age appropriate MMR immunization; four (50%) had unknown vaccination history. All were on the island of Oahu, with seven (88%) identifying as Pacific Islander (PI). Half (50%) lived in public housing, half (50%) reported employment at time of diagnosis, and all were Medicaid beneficiaries. Over half (63%) were obese (BMI >30). Median gestational age at time of diagnosis was 30 weeks, with six (75%) cases in the third trimester. Although three (38%) cases had scant or late prenatal care, all carried to term. One woman was symptomatic with mumps at the time of delivery and required emergency cesarean. However, all cases delivered with no adverse outcomes other than one with shoulder dystocia and initial low APGARs. Median birthweight was 3419g, with one (13%) low birthweight (<2500g) and three (38%) large for gestational age (>4000g). No additional complications were noted.

CONCLUSIONS: Although there were very few pregnant women among our cohort, similar to previous reports, we observed no fetal loss or congenital malformations. While further comparison of our data with Hawaii's population pregnancy data may help discern concerning issues, outcomes of mumps during pregnancy remain challenging to describe considering the apparently limited cases. States may benefit from discussions regarding data collection methodology for pregnant women and other medically vulnerable populations upon onset of similar outbreaks. Further follow-up and documentation from other outbreaks including ours may help enhance understanding.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Outbreaks; Maternal and Child Health

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9500
Abstract Type	Quick
Abstract Title	Health Department Experience with Mumps Outbreak Response and Use of a Third Dose of MMR Vaccine

Abstract

BACKGROUND: From January 2016–June 2017, US health departments (HDs) reported 150 mumps outbreaks. Most outbreaks occurred among populations with close contact and high 2-dose MMR vaccine coverage and despite implementation of standard control measures. This prompted the Advisory Committee on Immunization Practices (ACIP) to examine the evidence on use of a third dose of MMR vaccine. We surveyed HDs on their mumps outbreak control experiences to inform ACIP deliberations on third dose use.

METHODS: We developed a survey of multiple choice and open-ended questions on mumps outbreak characteristics, outbreak response measures used, and challenges and lessons learned from previous responses. The online survey was distributed by email to state, territorial and city/large urban health department epidemiologists through Council of State and Territorial Epidemiologists (CSTE) and vaccine preventable disease (VPD) coordinators through CDC’s VPD Epidemiology and Laboratory Capacity grantee listserv during August 15–30, 2017.

RESULTS: Of the 81 HD jurisdictions contacted, 61 (75%) responded. Of these, at the time of the survey, 46 (75%) reported having ≥ 1 mumps outbreak(s) since January 1, 2016 and 20 (43%) recommended an outbreak/third dose of MMR vaccine. On a scale from least (0) to most (10), 40% (8/19) of HDs that used an outbreak/third dose and responded to the question gave the intervention an effectiveness score higher than “somewhat effective” (median=5, IQR=3–7), and 53% (8/15) gave a cost benefit score higher than “somewhat cost beneficial” (median=7, IQR=4–7). HDs that used an outbreak/third dose suggested implementing the recommendation early and to a targeted group. Forty-three (73%) HDs reported having a policy for excluding persons without presumptive immunity from outbreak settings; 37 (86%) have some degree of legal authority to implement this policy. Exclusion compliance improved with the use of personalized notification letters, focus groups of excluded persons/community, and standardized messaging. Other control measures included cohorting of exposed or susceptible persons, mobile vaccination clinics and home visits, contact monitoring via text messaging, and facilitating student isolation with meal delivery and excused class absences.

CONCLUSIONS: Survey responses revealed heterogeneity across HDs’ outbreak responses, but also identified common challenges that informed CDC mumps outbreak guidance for HDs. Results on HDs’ values, acceptability, and implementation of a third MMR dose helped support the October 2017 ACIP recommendation for use of a third dose of mumps-containing vaccine for persons at increased risk for mumps because of an outbreak.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Vaccine-Preventable Diseases; Outbreaks
Consider for Different Presentation?	No
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10277
Abstract Type	Quick
Abstract Title	Hepatitis A Mass Vaccination, Dose-Saving Measures, and Factors Associated with Inmate Vaccine Acceptance in a County Jail — Santa Clara County, California, September 2017
Abstract	BACKGROUND: In response to an outbreak of hepatitis A in the county jail, the Santa Clara County Public Health Department launched a seven-day mass vaccination campaign on September 12, 2017 for the 3590 inmates at Jail A and Jail B. Our study objectives were to calculate the proportion of vaccine doses saved by reviewing electronic records of vaccination or immunity prior to vaccine administration and to understand factors associated with vaccine acceptance. METHODS: Each inmate encounter with a vaccinator included evaluation for contraindications and review of medical records for hepatitis A immunity or prior vaccination in both the California Immunization Registry (CAIR) and the county electronic medical records system. We calculated doses saved as the proportion of encounters where vaccine would have been administered but was not due to the inmate's records in either system. At Jail A, inmates either encountered a vaccinator or signed a form declining vaccination; at Jail B, inmates did not sign declination forms. To study factors associated with vaccine acceptance among inmates at Jail A, logistic regression modeling produced adjusted odds ratios for vaccine acceptance by gender, age, race, and encounter date. RESULTS: At Jail A, 1506 (55%) of 2736 inmates had encounters with vaccinators, of which 1088 (72%) resulted in vaccination and 418 (28%) in doses saved due to vaccination/immunity records. At Jail B, 262 (31%) of the 854 inmates had vaccine encounters, of which 172 (66%) resulted in vaccinations and 90 (34%) in doses saved. Modeling of 1482 Jail A encounters with complete demographic data showed strong evidence for an association between increased vaccine acceptance and Asian race (aOR 1.97; 95% CI 1.23–3.20; p-value <0.01). There was strong evidence for an association between vaccine refusal and age 30–39 years as compared to under 30 years (aOR 0.44; 95% CI 0.34–0.58; p-value <0.01). The encounter date was strongly associated with vaccine acceptance (overall Chi-square p-value <0.01). CONCLUSIONS: Reviewing immunization and vaccination registry databases during our mass vaccination campaign resulted in dose-saving of 28% in Jail A and 34% in Jail B. Inmate acceptance of vaccine was associated with race, age, and encounter date. While reviewing medical records in a mass vaccination setting can pose logistical challenges and slow operations, it is worthwhile to conserve limited vaccine supply and prevent unnecessary vaccination. Additional investigation is needed to understand why race, age, and encounter date are associated with vaccine acceptance among inmates.
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Hepatitis; Special/Vulnerable Populations; Immunization
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9421

Abstract Type Quick

Abstract Title Hepatitis B Vaccination in Newborns, Florida 2017

Abstract

BACKGROUND: Effective February 1, 2017, the Advisory Committee on Immunization Practices (ACIP) changed its recommendation for infants born to hepatitis B surface antigen-negative mothers to receive their first dose of hepatitis B vaccine from before hospital discharge to within 24 hours of birth. In recent years, Florida has had low rates of hepatitis B vaccination within the first three days of birth; in 2016 the National Immunization Survey estimated coverage in Florida for infants age 0-3 days at 59%, compared to 71% nationally. Given the new ACIP recommendations, the Florida Department of Health (FDOH) conducted an analysis of hepatitis B vaccination of newborns at hospitals to establish facility-specific rates and identify areas for improvement. All hospitals in Florida are required to send inpatient hospitalization data to the Florida Agency for Health Care Administration (AHCA).

METHODS: FDOH used the AHCA inpatient hospitalization dataset to calculate hepatitis B vaccination coverage of newborns in Florida hospitals in 2017. A birth was defined as any patient whose admission was designated as birth inside this hospital, a required entry, and whose age was equal to 0 days at admission. Vaccination was defined as having an ICD-10-CM code for encounter for immunization listed as a diagnosis or an ICD-10-PCS code for introduction of serum, toxoid, and vaccine listed as a procedure. Since the dataset did not contain dates for diagnoses, timing of vaccine administration could only be calculated for patients with vaccination entered as a procedure.

RESULTS: FDOH identified 52,268 births among 118 Florida hospitals in 2017. Overall, 32,254 (62%) newborns were vaccinated before discharge. Of the 15,818 newborns with a date of vaccine administration, 6,491 (41%) were vaccinated within 24 hours of birth. Individual hospitals had a median of 352 births (range 4-3,389) and 76% vaccination coverage (range 0%-100%). In general, hospitals with fewer than 300 births had higher vaccination coverages (median 81%) than hospitals with 300 births or more (median 71%). Hospitals that primarily recorded vaccination using procedure codes had higher vaccination coverages (median 84%) than hospitals that primarily used diagnosis codes (median 55%).

CONCLUSIONS: Hepatitis B vaccination of newborns in Florida hospitals remained low in 2017, both for vaccination before discharge and for vaccination within 24 hours of birth. FDOH plans to focus outreach efforts on individual hospitals with low vaccination coverages and to use Medicaid data to highlight the financial advantages for hospitals to increase their vaccination of newborns.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Hepatitis; Hospital Data; Immunization

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9454

Abstract Type Quick

Abstract Title Laboratory Testing Algorithm for Asymptomatic Rubella Contacts

Abstract

BACKGROUND: Up to 50% of rubella cases are asymptomatic. Rubella-specific Immunoglobulin G (IgG) titers alone cannot distinguish between evidence of immunity or recent infection. Sole reliance on IgG titers for determining rubella immunity status has led to missed cases of recent asymptomatic rubella infection resulting in cases of congenital rubella syndrome (CRS). An algorithm was developed to guide the management of asymptomatic rubella contacts taking into account the limitations of IgG titers and the potential for asymptomatic reinfection.

METHODS: The pregnancy and immunity status of contacts were used to determine whether additional laboratory testing was warranted. Evidence of immunity was defined as IgG positive titers or receipt of one dose of rubella-containing vaccine prior to exposure, or birth before 1957. In addition to rubella IgG, recommended testing for asymptomatic contacts included IgM to identify recent infection and IgG avidity to distinguish between recent infection and prior immunity or infection.

RESULTS: In the algorithm, no testing was recommended for non-pregnant contacts with evidence of immunity prior to exposure. Non-pregnant contacts with unknown immunity status were recommended for IgM and IgG testing to detect infection and determine their immunity status. Once the immunity status was known, these contacts could be managed accordingly. For non-immune, non-pregnant contacts and all pregnant contacts regardless of immunity status, IgM testing after the incubation period was recommended to detect asymptomatic infection. Because of the potential for false-positive IgM results, IgG avidity testing was recommended for all IgM positive results.

CONCLUSIONS: Asymptomatic infection should be considered in the management of rubella contacts based on pregnancy and immunity status. The algorithm developed can be used to triage testing of asymptomatic contacts to prevent transmission of rubella virus and ultimately cases of CRS.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9847
Abstract Type	Quick
Abstract Title	Multistate Mumps Outbreak Associated with Multiple Social Events during a Holiday Weekend — Washington DC, 2017

Abstract

BACKGROUND: In recent years, mumps outbreaks have increased in the United States, occurring mostly in vaccinated populations. The District of Columbia Department of Health (DC DOH) investigated a mumps outbreak among university students in October 2017. We aimed to identify exposures associated with the outbreak and prevent new cases by identifying persons who should receive a dose of MMR vaccine according to the Advisory Committee on Immunization Practices (ACIP) recommendations.

METHODS: We defined an outbreak case using the Council of State and Territorial Epidemiologists confirmed and probable case definitions for mumps with onset on or after September 27, 2017. Cases were confirmed by reverse transcription-polymerase chain reaction (RT-PCR). Patient isolates that were RT-PCR positive were genotyped. The investigation included patient interviews and vaccination records review.

RESULTS: As of December 22, 2017, 36 confirmed and 10 probable mumps cases were reported from the District of Columbia (35), Massachusetts (9), Georgia (1), and Rhode Island (1). Case-patients involved students from four universities in DC and seven from other states; 17 of DC case-patients attended one university. Of DC case-patients, median age was 19 years, 62.9% (22) were male, 54.3% (19) were Hispanic; and 80% (28) had received two doses of MMR vaccine before the outbreak, 17% (6) had unknown vaccination status, and 3% (1) were unvaccinated due to religious exemption. All 14 case-patient isolates genotyped were genotype G. Eleven DC case-patients attended social events at two bars and a house party in DC that occurred during Columbus Day weekend. DC DOH issued targeted risk reduction messages such as avoiding close personal contact and sharing of drinks and utensils to the universities. Five case-patients were athletes from different sports teams that shared athletic facilities at a university. A third dose of MMR vaccine was recommended for persons accessing a shared locker room visited by one athlete during his infectious period; 41 athletes received an additional dose.

CONCLUSIONS: Participation in events held during a holiday weekend resulted in mumps cases among students from multiple states and universities. By identifying the exposure events, DC DOH was able to identify specific groups at increased risk for mumps, that included athletes sharing a locker room, and recommend a targeted third dose intervention. This outbreak demonstrates the importance of investigating social networks to identify these groups when employing the ACIP recommendation for use of third dose during an outbreak.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Outbreaks; Vaccine-Preventable Diseases; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10034
Abstract Type	Quick
Abstract Title	Mumps Outbreak in a High School: Uptake and Parental Perceptions of 3rd Dose MMR Recommendations, Dallas County, Texas, 2017

Abstract

BACKGROUND: Mumps outbreaks have been widely reported in recent years among highly vaccinated populations, particularly in close-contact settings such as colleges. In February 2017, a mumps outbreak was identified in a large Dallas high school among students who had previously completed the 2-dose MMR vaccination series. Early notification of recommendations for third dose MMR and free vaccination clinics provided an opportunity to assess vaccine uptake, efficacy, and parental perceptions of third dose MMR recommendations.

METHODS: Mumps illnesses were classified as probable or confirmed cases using 2012 CSTE case definitions. Cases were interviewed and medical records were reviewed to collect information about vaccination status, exposure history, and illness characteristics. A 3rd MMR vaccine was recommended to all non-case students, and was offered without charge through school-based vaccination clinics. Supplemental questionnaires assessing parental knowledge and attitudes regarding this third MMR recommendation were administered to guardians of a randomly selected sample of 20 students who received third dose MMR and 50 students who did not receive the vaccine, and frequency-matched on grade and gender. Fishers exact tests and chi-square were used to compare responses. Data analysis was performed using SAS 9.4.

RESULTS: From February to May 2017, 28 PCR-confirmed and 12 probable mumps cases were identified in students attending one high school campus (24.3 cases per 1,000 students). Of the 1,646 enrolled students, 99.8% had documentation of at least 2 doses of MMR prior to the outbreak, including all mumps cases. Three undervaccinated students who declined to receive 1 dose of MMR were excluded from school until the 26th day after the last outbreak case. Following public health recommendations for a voluntary third MMR dose, 291 students (17.6%) elected to receive a third MMR. Since no mumps cases occurred in students who received a third vaccine dose, effectiveness of third MMR could not be calculated for this outbreak. Parental perception of protective benefit of an additional 3rd dose of MMR, was significantly associated with decisions to receive third dose MMR (OR: 4.9; 95% CI=1.6-15.3). **CONCLUSIONS:** Responsiveness to health department recommendations for third MMR vaccination in this outbreak setting was limited, even with broad educational communications and free school-based vaccine clinics. The challenges in achieving robust voluntary uptake of a third MMR dose may not improve substantially despite recent ACIP recommendations, in the absence of school mandates requiring third dose of MMR during outbreaks.

Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Infectious Diseases; Vaccine-Preventable Diseases; School Health
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9957

Abstract Type Quick

Abstract Title Mumps! There It Is! Analyzing National Mumps Case Data for 2016-2017 in the United States

Abstract

BACKGROUND: Since the two-dose measles, mumps, rubella (MMR) vaccination program was introduced in the US in 1989, reported mumps cases have ranged from several hundred to several thousand per year. However, in recent years, there has been a steady increase in the number of reported cases and outbreaks, primarily affecting young, two-dose vaccinated adults (18-22 yrs.) in close contact settings. Beginning in 2016, mumps cases and outbreaks increased significantly and continued through 2017.

METHODS: The Centers for Disease Control and Prevention (CDC) assessed reports of confirmed and probable mumps cases transmitted from 52 jurisdictions who report to the Nationally Notifiable Disease Surveillance System (NNDSS). We calculated overall and age-specific incidence rates (IR) by dividing the annual number of mumps cases by the corresponding U.S. Census Bureau's Bridged Race population estimates. Aggregate outbreak data from January 1, 2016 through June 30, 2017 was voluntarily sent to the CDC by the NNDSS jurisdictions.

RESULTS: From January 1, 2016 – December 2017, 11,715 mumps cases (n= 6,369 in 2016, 49 jurisdictions and n=5,346 in 2017, 50 jurisdictions) were sent to NNDSS. Annual IRs were 20/million and 17/million, respectively. Young adults had the highest IR both years, 87/million in 2016 and 67/million in 2017. Thirty-nine jurisdictions reported 150 outbreaks during this period, resulting in 9,200 outbreak-related cases. Case counts ranged from 3 to 2,952 (median 10 cases per outbreak), with outbreaks lasting from 19-414 days. Smaller clusters consisting of 3-9 cases comprised 50% of all outbreaks; however, 20 (13%) outbreaks had ≥50 cases and accounted for 83% of all reported outbreak-related cases. Most of the outbreaks occurred in close-contact settings (n=134, 89%); universities (n=75/150) were the most common setting. Seventy-five percent of case-patients were vaccinated with two-doses of MMR vaccine. An outbreak or 3rd dose of MMR vaccine was implemented in 35 (23%) outbreaks. Orchitis was the most common complication reported at 4.3%; all other complications occurred in less than 1% of case-patients and only 0.08% of all case-patients were hospitalized.

CONCLUSIONS: Outbreaks in close-contact settings led to the dramatic increase in the incidence of mumps in 2016-2017. The high proportion of vaccinated case-patients suggests waning immunity is a factor; however, low complication and hospitalization rates demonstrate protection against severe disease. Results will help improve CDC outbreak guidance for health departments and highlight the importance of mumps disease and outbreak surveillance in understanding the current epidemic and preventing future mumps resurgences.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases; Epidemiology; NNDSS

Consider for Different Presentation? Yes

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Institution Affiliation Centers for Disease Control and Prevention
CDC

Submission Type Breakout/Quick/Lightning/Poster

ID 9489

Abstract Type Quick

Abstract Title Ongoing Mumps Outbreak Results in Recommendations for a Third Dose of Vaccine — Alaska, 2017

Abstract

BACKGROUND: Mumps is a vaccine-preventable, viral illness characterized by a febrile prodrome and parotitis. The most effective prevention is vaccination with measles-mumps-rubella (MMR) vaccine. In May 2017, the Alaska Section of Epidemiology (SOE) was informed of a mumps case in an Alaska resident. Subsequent cases were identified during July and August. We investigated to determine outbreak scope and prevent further illnesses.

METHODS: Medical records were reviewed; patients with suspected mumps illness were interviewed in-person or by telephone using a standardized questionnaire. We used the Council of State and Territorial Epidemiologists' mumps case definition for classification. Immunization status was verified using Alaska's immunization information system. Buccal swabs were obtained and submitted for confirmatory testing.

RESULTS: By December 22, 2017, a total of 104 confirmed and 18 probable mumps cases were reported to SOE. Among patients with confirmed status, median age was 25 years (range: 3–68 years); 28 (27%) were aged ≤ 18 years; 49 (47%) were female, and 74 (71%) self-identified as Native Hawaiian/Pacific Islander (NH/PI). Immunization status was verified for 54/104 patients with confirmed status; 1 had received 4 MMR doses, 1 had 3 doses, 37 had 2 doses, and 13 had 1 dose. Immunization status was unverifiable for 50 patients. Among patients with ≥ 2 doses of MMR, median time from most recent dose to illness was 11 years (range: 2–20 years).

CONCLUSIONS: This represents the largest mumps outbreak in Alaska since the 1970s, and is disproportionately affecting NH/PI population. In November 2017, the Alaska Division of Public Health recommended a third dose of MMR for NH/PI persons if their second dose was administered ≥ 5 years ago. Children and most adults who meet recommendations for a third dose are eligible to receive state-supplied vaccine through Alaska's Vaccine Assessment Program. The effect of this recommendation will be monitored.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Outbreaks; Epidemiology; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9405
Abstract Type	Quick
Abstract Title	Parotitis Due to Influenza, Other Respiratory Viruses, and Mumps Coinfections Observed during a Statewide Mumps Outbreak, Kansas, 2016-2017
Abstract	BACKGROUND: Between December 2016 and July 2017, the Kansas Department of Health and Environment (KDHE), in collaboration with local health departments, investigated 11 mumps outbreaks in multiple counties. Mumps routinely causes parotitis. While influenza is not usually included in the differential among persons with parotitis, recent studies observed that influenza A and other acute respiratory viruses (ARV) have caused swollen parotids. KDHE encouraged physicians to test for other respiratory viruses in addition to mumps to identify non-mumps parotitis etiologies. This study examined factors associated with non-mumps etiology. METHODS: A cross-sectional study was performed among Kansas residents reported to KDHE between 12/01/2016 and 07/31/2017 that were tested for mumps and ARV. Positive for mumps was defined as PCR or IgM positive; positive for ARV was defined as PCR positive for any disease target on the respiratory viral panel (RVP). Demographic factors (race, ethnicity, age, gender), vaccination status, and mumps symptoms (parotitis, fever) were examined. Frequency, chi-square analysis, and odds ratios were performed using SAS® 9.4. RESULTS: One-hundred fifty-five persons reported to KDHE were tested for mumps and ARV. This study population was median aged 22.7 years (range: 1-77); majority male, non-Hispanic, White; had parotitis, afebrile; and vaccinated. Thirty-nine tested positive for mumps, while 25% (n=39) tested negative for mumps but positive for an ARV and 77 were negative for all etiologies. Observed infections included influenza A (n=20), rhinovirus/enterovirus (n=12), coronavirus (n=6), and influenza B (n=1). This subpopulation was median aged 21 years (range 1 – 55 years). Analysis revealed that children under five years compared to adults over 18 had increased odds of having non-mumps-associated parotitis (OR 9.7, CI: 2.0-71.7). Three percent (n=4) of the study population was coinfecting with ARV (coronavirus, influenza A, rhinovirus/enterovirus) and mumps. This niche subpopulation was median aged 29 years (range: 18-41) and was 100% female. CONCLUSIONS: During Kansas’ mumps outbreaks, 25% of persons that were tested for mumps and RVP tested negative for mumps but positive for an ARV. Children under five years were more likely to experience parotitis due to an ARV, likely due to protection from recent MMR vaccination and this age being more susceptible to ARV complications. Also, in contrast to previous studies, coinfections of mumps and ARV were observed. ARVs should be included in differentials for persons presenting with parotitis; testing mumps and the RVP is recommended to identify non-mumps etiologies causing parotitis preventing unnecessary isolation and contact tracing.
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Outbreaks; Vaccine-Preventable Diseases; Influenza / Pandemic Influenza
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9629

Abstract Type Quick

Abstract Title Prevalence and Characteristics of Recurrent Pertussis Infections Identified through Enhanced Pertussis Surveillance, 2015-2017

Abstract

BACKGROUND: In contrast to relatively stable pertussis rates observed in the United States during the 1970s-1990s, reported cases of pertussis increased significantly in the mid-2000s. Since then, many states have experienced repeated statewide epidemics, increasing opportunities for multiple pertussis exposures. Natural infection is thought to confer longer-lasting immunity than that afforded by vaccines; however, reinfection has been reported in persons recently infected with pertussis. Here we describe the prevalence and characteristics of recurrent pertussis infections identified through Enhanced Pertussis Surveillance (EPS).

METHODS: EPS sites (CO, CT, GA, MN, NM, NY, OR) assessed pertussis cases with onset during 2015-2017 for prior infections. Prior infections were verified through patient interview and retrospective review of surveillance data; years of available data varied by site, the earliest years ranging from 1999 to 2006. Prior infections documented in the surveillance database and meeting the CSTE pertussis case definition for reporting were included in the analysis. For patients with prior infections, differences in clinical characteristics between their first and second infections were assessed using Fisher's exact test.

RESULTS: EPS sites identified 4,681 pertussis cases with onset during 2015-2017. Of these, 47 (1%) patients reported a prior infection, but documentation was available for only 16 (0.3%). Prior infections occurred during 2009-2016 among patients of all ages: < 1 yr (n=3; 19%); 1-10 yrs (n=5; 31%); 11-19 yrs (n=3; 19%), and ≥20 yrs (n=5; 31%). Time between infections ranged from eight months to seven years (median: 3 yrs). All patients with recurrent infection reported clinically significant illness with post-tussive vomiting during the initial infection, and 12/16 (81%) reported these symptoms during reinfection ($p < 0.05$); one patient reported severe disease with pneumonia during reinfection. Among patients with recurrent infection, complete vaccination information was available for 10 (63%) and 15 (94%) at the time of first and second infection, respectively. Of these, pertussis vaccination was up-to-date for age for 80% (8/10) at the time of the first infection and 87% (13/15) at the time of the second infection. A minority of first and second infections were outbreak associated (1st: 9%, 2nd: 14%) or epi-linked (1st: 8%, 2nd: 9%).

CONCLUSIONS: Reports of prior pertussis infection among current pertussis patients are infrequent, but can occur across all ages. Clinically significant disease upon reinfection occurred, despite prior pertussis infection and vaccination. Further data are needed to better characterize pertussis reinfection.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases; Respiratory Diseases; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9859

Abstract Type Quick

Abstract Title Recurrent Parotitis Identified Among Four Patients during Mumps Outbreaks—Kansas, 2016-2017

Abstract

BACKGROUND: Common clinical presentation of mumps is parotitis. Descriptions of recurrent parotitis date back as early as 1919 and have resurfaced with recent mumps outbreaks in the United States. In 2008, national recommendations regarding isolation of persons with mumps changed from nine to five days following parotitis onset. Between December 2016 and July 2017, Kansas Department of Health and Environment (KDHE), in collaboration with local health departments (LHD), investigated 11 mumps outbreaks in multiple counties.

METHODS: Ill persons suspected to have mumps were interviewed with a disease-specific questionnaire for collection of symptoms, complications, and vaccination history. Buccal swabs and blood were collected for mumps testing by polymerase chain reaction (PCR), and immunoglobulin M (IgM) and immunoglobulin G (IgG). Specimens were tested privately, at Kansas Health and Environmental Laboratories (KHEL), and CDC. In accordance with Kansas Administrative Regulation 28-1-6, all persons with mumps were isolated for five days from onset of parotitis.

RESULTS: Total of 167 persons with cases of mumps were reported to KDHE. Four persons reported recurrent parotitis. Median age of four persons was 25.5 years (range: 15-46 years). Parotitis development was documented for three persons; initial parotid swelling occurred on one side with subsequent swelling on the opposite side. Initial swelling had completely resolved before development of new parotitis for three persons and one person still had residual swelling on the initial side when parotid swelling developed on the other side. Time frame between recurring episodes ranged from seven to ten days. All had received two doses of MMR prior to illness onset. Buccal swabs were collected from all upon development of initial parotitis and tested positive for mumps by PCR at KHEL. Additional specimens (buccal and blood) were collected from two persons following recurring parotitis. Specimens tested positive by PCR at KHEL and CDC and by IgM and IgG at CDC. All were isolated for five days for initial and subsequent parotitis occurrences, but were released from isolation in between for two to five days while potentially still infectious.

CONCLUSIONS: Four persons experienced recurring parotitis during Kansas' most recent mumps outbreaks. This could be an underestimation of the true number of persons with recurrent parotitis because all were self-reported. Laboratory evidence confirmed that persons were shedding mumps virus past the five day isolation period potentially exposing others. Increasing the isolation period to ten days could be considered for persons with mumps who have a high risk of exposing other persons.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Vaccine-Preventable Diseases; Outbreaks

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9558

Abstract Type Quick

Abstract Title Varicella Outbreak Response in a Federally Operated Asylum Detention Facility

Abstract

BACKGROUND: Varicella in adults can be severe with complications such as viral pneumonia, secondary bacterial infections of skin lesions, and central nervous system manifestations. We investigated an outbreak of varicella in a population of foreign-born detainees at a detention center that is owned and operated by a private company with federal oversight and contracted medical services.

METHODS: The New Mexico Department of Health (NMDOH) responded to a varicella outbreak at the detention facility in April 2017. Census at the facility was around 600 detainees with a capacity of 1,116 beds and >300 employees. Average stay of detainees was 32 days. A case was defined as a detainee or employee with a generalized maculo-papulovesicular rash and either a PCR positive clinical sample or an epidemiologic link to a confirmed case. NMDOH provided outbreak control recommendations that included vaccinating exposed individuals without evidence of immunity.

RESULTS: A total of 29 varicella cases were identified during the outbreak that lasted 11 weeks; rash onsets ranged from 2/18/2017 to 5/05/2017. All 29 (100%) cases were detainees and male, median age was 22 (range 18-32) years. The index cases were two detainees that had been transferred to the facility from an out of state facility. Of the confirmed cases, country of birth included: India (24; 82.8%), Honduras (2; 6.9%), Ecuador (1; 3.4%), Nepal (1; 3.4%) and Mexico (1; 3.4%). One case was laboratory confirmed for VZV by PCR and 28 cases were epi-linked. No complications, hospitalizations, or immunocompromised conditions were reported among cases. Control measures implemented by the facility included quarantine of detainees exposed to varicella and isolation of patients who developed disease. Vaccination was not offered. High-risk employees, including women of child-bearing age, were excluded from working in affected units.

CONCLUSIONS: Control measures instituted by the facility likely reduced continued spread of varicella. However, regular business operations were disrupted due quarantine of detainees and lengthy duration of outbreak. Due to the dynamic complexity of ownership and operations of the facility, NMDOH was unable to convince the facility to vaccinate detainees that did not exhibit immunity and exposed to a case. Vaccination of detainees that were exposed to varicella might have helped reduce the number of cases, shortened the duration of the outbreak and protected against future exposure. This outbreak highlights the need to foster collaboration with federal facilities around developing a standard outbreak response approach to minimize disruption and control spread.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Outbreaks; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10071

Abstract Type Quick

Abstract Title Varicella-Related Hospitalizations By Varicella Vaccination Status in the United States, 2015-2016

Abstract

BACKGROUND: Evaluation of national hospital discharge data has demonstrated significant declines in varicella-related hospitalizations since introduction of the varicella vaccination program in the United States in 1996. However, detailed medical information and vaccination histories of hospitalized patients are not available through national hospital discharge data to assess characteristics of varicella-related hospitalizations that are still occurring.

METHODS: Starting in August 2015, through CDC's Epidemiology Laboratory Capacity project, jurisdictions can send varicella-related hospitalization data to CDC. Data collected include, demographics, clinical characteristics (e.g., lesion count, complications), vaccination status, reason for hospitalization, and laboratory testing results. Descriptive analyses of hospitalization data during 2015-2016 were conducted to evaluate characteristics of varicella-related hospitalizations.

RESULTS: From 2015 to 2016, 21 jurisdictions reported 303 varicella-related hospitalizations. Overall, median age of hospitalized case-patients was 30 years (n=302; interquartile range: 12-47 years); median length of stay (LOS) in hospital was 4 days (n=276; range, 1-68 days); 58.4% (177/303) were male; 74.0% (91/123) were US-born; 65.6% (105/160) were unvaccinated (and no disease history), and 91.6% (230/251) of case-patients tested for varicella were positive. Median age of vaccinated and unvaccinated hospitalized case-patients was 12.5 years and 31.8 years, respectively (p<0.001); median LOS did not differ by vaccination status (5 days versus 4 days, respectively; p=0.06). Unvaccinated hospitalized varicella case-patients were 3.3 times more likely to have ≥50 lesions compared with vaccinated case patients (p=0.02) but the presence of complications did not differ by vaccination status (p=0.69). Reason for hospitalization by vaccination status was known for 103 case-patients of whom 33 (32.0%) were vaccinated. The main reasons for hospitalization among vaccinated and unvaccinated case-patients were complications (36.4% and 27.1%, respectively), observation (21.2% and 25.7%, respectively), and administration of intravenous antivirals (18.2% and 14.3%, respectively); additionally, 9.1% and 12.8%, respectively, reported "severe varicella" with no further details on presentation. Of 252 case-patients with known immune status, 89 (35.3%) were immunocompromised. Three case-patients, aged 29, 51, and 77 years, died (1 unvaccinated, 2 unknown; immune status unknown for all 3); 2 were diagnosed with pneumonia and 1 with hepatitis and sepsis.

CONCLUSIONS: Varicella continues to cause hospitalizations and in rare occasions, death. A majority of hospitalizations occurred in unvaccinated persons who were more likely to have ≥50 lesions, and who were adults. Catch-up varicella vaccination of adults, and high varicella vaccination coverage among children to reduce virus circulation and protect those ineligible for vaccination remain important to help decrease the burden of varicella hospitalizations.

Committee Infectious Disease

Topic Vaccine-Preventable Diseases

Keywords Surveillance; Vaccine-Preventable Diseases

Consider for Different Presentation? Yes

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Submission Type	Roundtable
ID	9027
Abstract Type	Roundtable
Abstract Title	Enhancing Vaccine Preventable Disease (VPD) Surveillance through the R1 Component of the Epidemiology and Laboratory Capacity for Infectious Diseases (ELC) Cooperative Agreement (CoAg)
Abstract	Key Objectives: Jurisdictions will share experiences, lessons learned, and opportunities for enhanced VPD surveillance activities supported by the VPD (R1) component of the ELC CoAg. Brief Summary: Fifty-two jurisdictions participate in the Enhanced VPD Surveillance (R1) component of the ELC CoAg and have designated a VPD Surveillance Coordinator to ensure linkages and communication between epidemiology, immunization, laboratory, and informatics partners to support VPD-related surveillance activities. Through the second project year, notable outcomes include: improved vaccine history data completeness with at least 38 jurisdictions integrating their immunization registry with surveillance data; enhanced surveillance for meningococcal disease, varicella, and acute flaccid myelitis, with 52 jurisdictions submitting reports that provide enhanced case-based surveillance data for varicella outbreaks as well as supplemental meningococcal data/isolates; projects addressing mumps outbreaks, varicella second dose assessments, and MMR vaccine coverage evaluations, with 10 jurisdictions submitting mumps case-based outbreak reports that include extended epidemiologic data that would otherwise not have been available. During the session, jurisdictions will share their experiences conducting enhanced surveillance and discuss outcomes of their enhanced surveillance projects. Specifically, Minnesota will share how the VPD Surveillance Coordinator position has increased collaboration and communication by creating a defined role that coordinates between epidemiology and immunization programs within the state. This coordination helps align priorities and facilitates data sharing between programs, improving surveillance outreach and follow up efforts. Nevada will discuss how they have leveraged the enhanced surveillance activities to improve data quality and completeness within their state. The state is in the process of implementing in-house indicators to measure data quality in surveillance systems, and the VPD Surveillance Coordinator has specifically made efforts to ensure that data entered into the systems are as complete as possible while also working to improve the systems themselves. New York will describe their experiences building connections between epidemiology and nursing, with additional focus on data provisioning within their state health department, leading to enhanced case data collection and review. The state will also share their recent experiences building infrastructure for mumps outbreaks with support from the CoAg. Other attendees will also share their experiences enhancing VPD surveillance, including challenges, successes and lessons learned.
Committee	Infectious Disease
Topic	Vaccine-Preventable Diseases
Keywords	Epi / Lab Capacity (ELC); Vaccine-Preventable Diseases; Surveillance
Consider for Different Presentation?	No
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9975
Abstract Type	Breakout
Abstract Title	A Case of Mistaken Identity: HSV Encephalitis Confirmed in a Patient Highly Suspect for Rabies Infection

Abstract

BACKGROUND: On Friday morning, March 10, 2017, the Georgia Department of Public Health (DPH) was notified about a suspect human rabies case. The patient, an 85-year-old female, presented to an emergency department on March 6 after she was found in her home unwell and exhibiting “strange” behavior. She was admitted and continued to exhibit unusual behavior such as chewing on blankets and medical equipment, and even bit a personal visitor. On Tuesday, March 7, she began spitting out water and refusing oral fluids. The patient was assessed for seizure disorders, meningitis, and other common neurologic diseases. She continued to deteriorate with a rapidly progressing, unexplained encephalopathy. Rabies infection was suspected due to the patient’s clinical picture, potential for exposure as a resident of a rabies endemic area, and lack of a more likely diagnosis. The patient expired in the evening of March 10, 2017.

METHODS: A rabies risk assessment and consultation with the Centers for Disease Control and Prevention (CDC) Rabies staff was conducted on March 10, 2017. DPH had no documentation of an animal bite report on this patient. Antemortem rabies specimens were collected the same day. Although lower on the list of differential diagnoses, prion disease and herpes simplex encephalitis (HSE) were considered. After the patient expired, DPH collaborated with CDC to deploy a team to procure clinical specimens for rabies and herpes simplex virus (HSV) testing.

RESULTS: On March 11 antemortem serum and cerebral spinal fluid were negative for rabies IgG and IgM antibodies by indirect fluorescent antibody testing (IFA) at CDC, and saliva and tissue biopsy were negative by RT-PCR. On March 17, rabies rapid fluorescent focus inhibition tests (RFFIT) were negative on all antemortem samples. Postmortem brain samples were negative for rabies by direct fluorescent antibody (DFA) test and RT-PCR. Postmortem tissue biopsy was positive by RT-PCR for HSV-1 and negative for HSV-2.

CONCLUSIONS: Given the patient’s clinical presentation, the medical team’s thorough rule out of other causes, and her potential for exposure, rabies was at the top of the list of differential diagnoses. Results of ante- and postmortem testing confirmed HSV-1 infection and ruled out rabies infection. Despite a somewhat classic clinical picture for human rabies infection, it is important to always consider other agents in patients with a progressive infectious encephalitis.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Epidemiology; Collaboration; Veterinary Public Health
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9077

Abstract Type Breakout

Abstract Title A Summary of Zika Cases and Surveillance Activities in 2016, Los Angeles County, California

Abstract

BACKGROUND: In 2014, an outbreak of Zika virus occurred in Brazil and rapidly spread to neighboring countries. The first Los Angeles County (LAC) resident became ill with Zika after returning from El Salvador in late 2015. LAC also has the mosquito species capable of carrying the Zika virus, raising concern for the possibility of local vector-borne transmission in our community.

METHODS: The Acute Communicable Disease Control Program (ACDC) of the LAC Department of Public Health (DPH) performed enhanced surveillance for Zika virus cases, interviewed patients for exposure, engaged in a number of activities to rule out local transmission and tracked the health of infants born to Zika cases.

RESULTS: In 2016, 101 Zika cases were investigated by LAC DPH ACDC. Cases were identified with either Zika virus RNA (52%) or Zika acute phase antibodies (48%). Cases were primarily female (76%), Latino (71%), with an average age of 36.9 years (range: 9-66 years) and residing throughout the county. None were hospitalized. The annual disease rate was 1.1 per 100,000 populations and was highest among Latinos (12.1 per 100,000), followed by whites (5.6 per 100,000), and was higher in females than males (1.6 vs. 0.6 per 100,000). All cases traveled to an Zika endemic region prior to their illness (Central American: 50%, Mexico: 27%) and most became ill in the summer months of July and August (54%). No instances of local transmission of Zika virus, either by vector or sexual, were identified. Eleven infants were born to an LAC Zika case; all eleven appear healthy to date.

CONCLUSIONS: Although the number of Zika cases in LAC were relatively small, creating a surveillance system for any new emerging diseases is challenging, requiring the development of a disease case definition, testing methods, disease procedures and protocols, and enhancing communication between multiple governmental agencies. Through these experiences we have gained much knowledge, making our health agency more adept at managing future emerging diseases affecting our community.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Reproductive Health; Vectorborne Disease; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9127

Abstract Type Breakout

Abstract Title Assessing Rabies Risk Following a Mass Bat Exposure in a National Park Wyoming, 2017

Abstract

BACKGROUND: In August 2017, the Wyoming Department of Health (WDH) was notified that multiple persons had slept overnight in 2 bat-colonized buildings at a national park research facility. Bats are the most common rabies source in the United States; ~1–3 persons die from bat-associated rabies virus yearly. WDH, CDC, and the National Park Service performed rabies exposure risk assessments to guide postexposure prophylaxis (PEP) recommendations.

METHODS: We interviewed persons who slept at the facility since it opened on May 19, 2017 using a standardized risk assessment tool. Their risk level was categorized as follows: no risk (no direct bat contact, no bats observed in the room, and kept room door closed while sleeping); low risk (no direct bat contact or bats observed in the room, but slept with the door open); or high risk (direct bat contact or slept in a room with bats while unaware of direct contact because of medications, deep sleep, or alcohol consumption). Risk categories were used to counsel and encourage consultation with a health care provider; persons at high risk were encouraged to seek PEP. Follow-up assessments were conducted to determine PEP receipt.

RESULTS: Of 171 persons who slept at the facility, 163 (95.3%) were interviewed and categorized as follows: no risk (122, 74.8%), low risk (20, 12.3%), and high risk (21, 12.9%). Eighty persons completed follow-up interviews; 29 persons received PEP, including 6 categorized as no risk, 9 low risk, and 14 high risk.

CONCLUSIONS: Our investigation resulted in identifying persons at risk for rabies exposure. Follow-up interviews identified 14 persons at high risk who were successfully administered PEP following risk assessment recommendations. Standardization of risk categories allowed for consistency in determining exposure risk and facilitated targeted PEP counseling, which can be useful in other mass bat exposure investigations.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; Disease Prevention; Risk Assessment

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10104

Abstract Type Breakout

Abstract Title Assessing Zika Virus Testing Rates Based on Travel Location – Chicago Department of Public Health, 2016

Abstract

BACKGROUND: The Chicago Department of Public Health’s (CDPH) 2016 Zika information campaign targeted travelers and immigrants from areas with active Zika virus transmission. CDPH collected information about individuals approved for laboratory testing following suspected Zika travel-related exposures. This analysis aims to assess whether Zika testing rates in Chicago differ by travel location in order to identify at-risk groups for outreach.

METHODS: The International Air Transport Association provided aggregate data for passengers originating from Zika-affected countries or territories in the Americas arriving in Chicago’s O’Hare and Midway airports. CDPH compiled data on location of possible travel Zika exposure for all Chicago residents authorized for Zika public health testing. Testing rates (TR) were obtained from the number of individuals tested who traveled to Zika-affected locations in the Americas compared to the number of total airport arrivals from these areas. Rate ratios (RR) compared the testing rate for Mexico relative to all other locations in the Americas combined. RRs and 95% confidence intervals (CI) were estimated using Poisson regression analysis.

RESULTS: During 2016, O’Hare and Midway received a total of 1,725,467 passenger arrivals originating from locations in the Americas. Mexico [934,977; 54.2%] contributed the highest percentage of arrivals, followed by the Caribbean [318,513; 18.5%], South America [167,842; 9.7%], Central America [149,955; 8.7%], and Puerto Rico [154,180; 8.9%]. In 2016, CDPH authorized 1,088 test requests for Chicago residents with travel exposure to locations in the Americas. Most authorized test requests indicated travel to Mexico [576; TR=.98], while fewer requests indicated travel to the Caribbean [220; TR=1.10], South America [114; TR=1.08], Central America [123; TR=1.30], and Puerto Rico [108; TR=1.11]. Location of travel exposure was not mutually exclusive, as CDPH authorized some testing based on travel to multiple locations. The estimated rate of testing for those who traveled to Mexico was significantly lower than for those traveling to all other locations combined (RR=0.86, 95% CI=0.77-0.97).

CONCLUSIONS: This analysis shows the rate of testing in Chicago due to a travel exposure in Mexico is significantly lower compared to other locations in the Americas. This analysis assumes: 1) a proportionate number of arrivals from each location are indicated for testing and 2) arrivals to Chicago airports proportionately represent Chicago residents’ travel patterns. Additional outreach targeted toward populations likely to travel to Mexico may help identify at-risk individuals for Zika virus testing.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease; Emerging Infections; Underserved Populations

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9267
Abstract Type	Breakout
Abstract Title	Assessment of Rabies Exposure Risk in Residents of a University Sorority House—Indiana, February 2017

Abstract

BACKGROUND: Bats are the most common source of human rabies infections in the United States; therefore, bat colonization of human dwellings is a public health concern. In February 2017, the Indiana State Department of Health (ISDH) was notified of bat sightings in communal areas of a university sorority house. The initial complainant cited food safety concerns. We investigated to assess rabies exposure risk and identify potential access bat routes.

METHODS: We administered a web-based survey to assess bat exposure risk of 148 persons who resided or worked in the sorority house since February 2016. Respondent risk was categorized as low (no bat exposure), moderate (waking and finding a bat in the same room), or high (bite or other direct contact). Interviews with respondents classified as moderate or high risk were conducted in person or by telephone. An environmental health specialist (EHS) inspected the house for evidence of bat colonization.

RESULTS: Of 100/148 (68%) survey respondents, 94 (94%) reported seeing a bat in the house; 34/94 (36%) reported seeing a bat ≥ 1 /month. Initially, 13 (14%) were classified as having a moderate or high risk for rabies exposures. However, 9 (64%) were reclassified as having a low risk after follow-up interviews. The remaining 4 persons (3 moderate risk and 1 high risk) were recommended for postexposure prophylaxis (PEP). The EHS identified multiple openings that can serve as access points for bats.

CONCLUSIONS: The initial concern was not for rabies, which might indicate limited disease and risk knowledge among this population. ISDH communicated the risk for rabies at meetings with students and university personnel. Building remediation by the EHS removed the bats' access points. Bat exposures should be reported immediately to public health officials, who can conduct rabies risk assessments and make PEP recommendations.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9279

Abstract Type Breakout

Abstract Title Canine Leptospirosis Outbreak without Identifiable Zoonotic Transmission — Maricopa County, Arizona, 2016–2017

Abstract

BACKGROUND: Leptospirosis is a potentially fatal illness caused by exposure to animal urine containing *Leptospira* bacteria; mammalian reservoirs maintain >250 serovars. Infected dogs can transmit leptospires to humans, but transmission frequency and risks are poorly understood. In Arizona, canine leptospirosis is reportable to the state veterinarian (baseline: ≤5 cases annually). During 2016, in Maricopa County, two clusters (nine cases from one household and 18 cases from one boarding facility) of canine leptospirosis were reported; two potential sub-clusters of canine leptospirosis at different boarding facilities were reported in January 2017. We characterized the outbreak, examined risk factors for canine and human infection, and investigated zoonotic potential.

METHODS: During February 2017, we contacted 18 veterinary and four boarding facilities associated with reported cases of canine leptospirosis. Canine blood and urine specimens were tested by polymerase chain reaction (PCR); serum was tested for anti-*Leptospira* antibodies by microscopic agglutination test (MAT) using a *Leptospira* serovar-panel, enzyme-linked immunosorbent assay (ELISA), or rapid diagnostic test (RDT). Laboratory testing was performed at veterinary clinics, commercial laboratories, or the Centers for Disease Control and Prevention. We reviewed canine medical records, interviewed owners regarding owner symptoms and canine exposures, and classified canine cases as confirmed (positive PCR or MAT) or probable (≥2 of the following: clinical signs compatible with leptospirosis, epidemiologic link, or positive ELISA or RDT). We conducted a serosurvey and interviews of exposed persons; those with acute onset of symptoms compatible with leptospirosis were tested by PCR (blood and/or urine) and MAT (serum).

RESULTS: During January 2016–June 2017, we identified 71 canine cases (55 confirmed). We interviewed 39 owners of 43 dogs (confirmed or probable cases); 31 dogs (72%) boarded at one of the four contacted facilities. MAT titers were available for 19 (30%) of 63 dogs with onset after September 30, 2016; *L. interrogans* serovar Canicola (dogs are the reservoir species) was the highest reacting serovar in 16/19 (84%) dogs. All 118 serosurvey participants (nine owners and 109 staff from 17 veterinary clinics and boarding facilities) were seronegative despite canine urine exposure reported by 56/109 (51%) staff, including skin (n=25) and face (n=3) exposure. Six of seven exposed persons with acute illness were tested; all results were negative.

CONCLUSIONS: Boarding facilities likely facilitated canine infection. No exposed humans showed evidence of infection, indicating that canine-to-human transmission is infrequent, even among veterinary and boarding staff that report urine exposure; whether this is serovar-dependent requires further investigation.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords One Health; Infectious Diseases; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9801

Abstract Type Breakout

Abstract Title Dengue Infections Among Miami-Dade Elderly Residents: Differences in Symptomology, Serotypes, and Lengths of Hospitalization, 2010 - 2014

Abstract

BACKGROUND: Dengue is an acute febrile disease and its symptoms can range from mild to severe dengue hemorrhagic fever. Current research has suggested that elderly populations present atypically and are associated with longer hospitalizations. This study aimed to observe differences in symptomology, lengths of hospitalizations, and serotypes among elderly and non-elderly residents of Miami-Dade County.

METHODS: Confirmed dengue cases that were reported between January 1, 2010 through December 31, 2014 were extracted from Merlin, the Florida Department of Health surveillance system. Variables of interest included: age, sex, race, ethnicity, origin of infection, symptomology, serotype, and length of hospitalization (if available). Data were analyzed using SAS v9.4.

RESULTS: During the 4-year span, Miami-Dade County had 124 confirmed dengue cases, with 78% of cases being travel associated. Eighty-seven percent of cases identified as Hispanic and nearly half of the cases were female. Of the cases that were travel associated, 30.4% of cases were acquired from Cuba, 18.8% from Puerto Rico, and 11.6% from the Dominican Republic. The median age among the confirmed cases was 45.0, with 18 (14.5%) being 65 years old or older. The most commonly reported symptoms, aside from fever which was required to meet case definition, included myalgia (71.8%), headache (62.1%), and rash (38.7%). When comparing the rates of individual symptoms among the elderly (65 years old or older) and non-elderly (64 years old or younger), no significant differences were observed. Overall, the median length of stay was 3.5 days (0 – 11). The elderly reported a median of 4 days while the non-elderly reported a median of 3 days ($p = 0.064$). In total, 42 (37.8%) cases had DEN-1, 23 (20.7%) had DEN-2, 10 (9.0%) had DEN-3, 32 (28.8%) had DEN-4, and 4 (3.6%) had two concurrent dengue serotypes. No significant differences were found when observing serotype frequencies by age group.

CONCLUSIONS: Previous literature has indicated that the elderly present with atypical symptoms of dengue virus; however, this study found that there were no significant differences in symptomology based on age. This could be due to the differences in the studies' samples. Current research observes symptoms among those being hospitalized whereas this sample observes all cases in Miami-Dade, regardless of hospitalizations. Average lengths of hospitalizations were higher among the elderly populations; however, significant differences were not noted among the elderly and non-elderly.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9827

Abstract Type Breakout

Abstract Title Detection of Zika Virus IgM Antibodies – Miami Dade County, Florida, 2016

Abstract

BACKGROUND: Zika virus (ZIKV) is a flavivirus spread primarily through the bite of an *Aedes aegypti* mosquito. Clinical symptoms of ZIKV consist of fever, arthralgia, conjunctivitis, and a maculopapular rash. ZIKV IgM levels in clinical specimens are variable but are typically positive four days after symptom onset and up to 12 weeks. The Florida Department of Health in Miami-Dade County conducted a review of laboratory confirmed ZIKV cases to examine characteristics associated with IgM antibody detection.

METHODS: All laboratory confirmed ZIKV cases from 2016 were obtained from Merlin, the Florida Department of Health Surveillance System. Inclusion criteria required meeting the “confirmed” case definition for a ZIKV case (confirmatory testing of RT-PCR in serum and/or urine or IgM with confirmatory PRNT) and provision of both a urine and serum specimen. Variables of interest included demographics (age, gender, race/ethnicity), clinical presentation (symptomatic vs. asymptomatic), origin of infection (locally-acquired vs. travel-associated), previous arboviral infection, and timeframe of IgM detection. The main outcome of interest was the detection of the ZIKV IgM antibody. Descriptive statistics were calculated to summarize the study population. Chi-squared and Fisher Exact tests were used to measure the significance between characteristics and detection of ZIKV IgM antibody.

RESULTS: A total of 468 ZIKV cases met the inclusion criteria. There were no significant differences in IgM detection by age, gender, or race/ethnicity. The four main ZIKV symptoms were not associated with testing IgM positive; however, 282 (66.82%) of the symptomatic ZIKV cases were IgM negative and 25 (54.35%) of the asymptomatic ZIKV cases were IgM negative. Stratification by origin of infection found no association between being symptomatic and IgM results among locally-acquired cases; however, among the 266 travel-associated ZIKV cases, those who were symptomatic were more likely to be IgM negative ($p=0.0042$). There were no significant differences in IgM detection among cases that tested PCR positive in serum, urine, and/or both serum and urine. Pregnant ZIKV cases were 12.85 times more likely to test positive by IgM compared to non-pregnant ZIKV women of child bearing age (15 – 44) (95% CI 4.05 – 40.72, $p<0.0001$).

CONCLUSIONS: The finding that symptomatic travel-associated ZIKV cases were more likely to be IgM negative was likely due to an inherent testing bias during the outbreak. The crucial finding was that pregnant women were more likely to test positive by IgM; however, due to the cross-sectional nature of epidemiologic investigations, we were unable to analyze the temporality of IgM detection.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Local Epidemiology; Epi / Lab Capacity (ELC); Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10215

Abstract Type Breakout

Abstract Title Development of West Nile Virus Risk Levels in a State with Limited Mosquito Surveillance

Abstract

BACKGROUND: West Nile virus (WNV) is the leading cause of domestically acquired arboviral disease in the United States and Kansas. Mosquito-based surveillance is the primary tool for quantifying WNV transmission and human risk. Kansas does not have mosquito control districts; limited mosquito surveillance is conducted by the Kansas Department of Health and Environment (KDHE). From 2013-2016 mosquito surveillance was conducted only in Sedgwick County (SGCO) which historically had the most WNV neuroinvasive disease (WNVND) cases. Mosquito control and public health alert thresholds were successfully developed for SGCO; WNVND cases decreased from 1.98/100,000 (2012) to 0.78/100,000 (2016) statewide. Previously limited mosquito surveillance made it difficult to define statewide WNV transmission risk.

METHODS: Mosquito surveillance was conducted weekly with 23 Encephalitis Vector Survey traps in 4/105 counties from May 17-October 25, 2017. Three regions were represented; west, central, and east. Central region mosquito data was used as a proxy for the west. Threshold measures for risk levels (RL) were developed based on presence of *Culex spp.* mosquitoes (low risk), two-week mean *Culex spp.* mosquitoes ≥ 40 per county (moderate risk), and either human case counts that exceeded the WNV five year (2012-2016) median (east and central regions) or mean (west region) case counts or WNV positive mosquito pools (high risk). RL of minimal, low, moderate, and high had coordinating prevention measures. RL were updated weekly from June 16-November 3, 2017 and posted on the KDHE Arboviral Disease webpage. We compared WNVND case counts and incidence from 2016-2017.

RESULTS: KDHE published the first WNV press release of the year on June 10, 2016 and June 9, 2017 respectively. Arboviral webpage views increased 471% when June 2016 (n=134) and June 2017 (n=2,188) were compared. Views from June-November increased 107% from 2016 (n=2,245) to 2017 (n=4,645). WNVND case counts decreased from 2016 (n=17) to 2017 (n=9); this was the lowest number of WNVND in six years (2012-2016, five year median=18, range 12-34). Kansas WNVND incidence decreased from 0.78/100,000 (2016) to 0.41/100,000 (2017) while U.S WNVND incidence remained the same (0.41/100,000).

CONCLUSIONS: WNV RL might have aided in the reduction of human WNV cases in Kansas. Development of RL by region can be based on available resources. Timely publication of clear personal prevention measures based on RL was crucial when communicating transmission risk. States or territories without RL could develop thresholds, with available mosquito surveillance data, and might reduce the number of WNV or other arboviral disease cases.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords One Health; Vectorborne Disease; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9676

Abstract Type Breakout

Abstract Title Evaluation of the Illinois Zika Surveillance System, January 2016–October 2017

Abstract

BACKGROUND: Illinois identified its first Zika case in January 2016. As Zika was newly reportable, a module was developed in the Illinois National Electronic Disease Surveillance System (I-NEDSS) to track testing, identify cases and monitor for local transmission. The purpose of this evaluation was to assess the Illinois Zika surveillance system (IZSS) and provide recommendations to improve surveillance of emerging diseases in Illinois.

METHODS: This evaluation utilized the CDC Updated Guidelines for Evaluating Public Health Surveillance Systems. Phone interviews (n=5) were conducted with surveillance staff from the Illinois Department of Public Health (IDPH) and local health departments (LHDs) with high Zika testing volumes to assess the simplicity and flexibility of the IZSS. Data collected during January 2016–October 2017 were evaluated for quality and timeliness. To assess IZSS representativeness, the Spearman rank correlation was used to assess the relationship between the proportion of the population tested for Zika and the proportion of the population born in Latin America by county for the 102 Illinois counties.

RESULTS: Overall, 6,305 individuals tested for Zika were reported to the IZSS with 125 confirmed cases. Interviewed stakeholders indicated that the I-NEDSS module for tracking IZSS data was easy to use, but information sharing between public health agencies and healthcare providers was burdensome with receipt of results both manually and electronically resulting in increased complexity of report follow-up. Data quality for key demographic variables differed by case status: travel history was missing or unknown for 21.7% of non-cases and 2.4% of cases; pregnancy status was missing or unknown for 13.9% of female non-cases and 1.2% of female cases; and ethnicity data were missing or unknown for 55.7% of non-cases and 41.6% of cases. Initial reporting of tested individuals came from 251 different organizations through electronic reporting (36.9%), LHD manual entry (53.8%) and provider reports (9.3%). Once a LHD received a report, the median time until investigation closure was 31 days. The correlation between the proportion of people tested in a county for Zika (range: 0-0.08%) and the population born in Latin America (range: 0-13.6%) was significant ($p=0.36$, $p=0.0002$).

CONCLUSIONS: Although data quality issues were identified, the IZSS captured key data that resulted in effective Zika surveillance. Requiring the collection of risk factor data in IZSS could improve data quality. Improving the proportion of organizations utilizing electronic reporting and streamlining information sharing across agencies could improve timeliness and reduce complexity in future emerging disease scenarios.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Emerging Infections; NEDSS / PHIN; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10077

Abstract Type Breakout

Abstract Title Evaluation of Zika Virus Outreach in Targeted Communities – Chicago Department of Public Health, 2016-2017

Abstract

BACKGROUND: In 2016, the Chicago Department of Public Health's (CDPH) Zika virus outreach campaign targeted travelers through advertisements in airports, subways, buses, and taxi-tops. Analysis of census data identified community areas with high concentrations of immigrants from areas with active Zika virus transmission in the Americas. The 2017 campaign included focused outreach to providers and residents of these communities. This analysis aims to assess whether Zika virus testing for residents in the targeted areas increased as a proportion of total public health tests after the launch of the 2017 outreach campaign.

METHODS: CDPH mapped the spatial distribution by community area of Chicago residents native to countries and territories with ongoing Zika virus transmission using the U.S. Census Bureau's American Community Survey (2010-2014). The 20 community areas with the highest number of immigrants were targeted for enhanced outreach. CDPH enrolled 250 primary care and OBGYN clinics to display Zika educational materials in exam rooms and receive provider guidance documents. Additionally, CDPH advertised on billboards and transit serving residents of these areas. The proportion of total public health tests requested in the targeted communities before the campaign launch (1/1/16 to 7/30/17) was compared against the proportion of total public health tests requested in these areas after the campaign launch (7/31/17 to 11/30/17) using a chi-squared test ($\alpha = 0.05$), and a risk difference and 95% confidence interval were estimated.

RESULTS: Census data showed that immigrants from countries with ongoing Zika transmission were concentrated in the West and Northwest areas of Chicago. There were 184 enrolled clinics located within the 20 community areas targeted. Tests for residents of these community areas represented 47% (725/1552) of all public health tests requested from 1/1/16 through 7/30/17. The chi-squared test showed that the proportion of tests for residents of these areas from 7/31/17 to 11/30/17 increased significantly to 56% (74/133); difference = 9%; 95% confidence interval = 0.1% - 18%).

CONCLUSIONS: For the 20 community areas that received additional outreach engagement, the proportion of total Zika test requests for residents of these areas has significantly increased since the 2017 campaign launch. CDC Zika testing guidance changed in July 2017, and this may have impacted the volume and demographics of patients with tests requests. Continued focus on increasing Zika education and testing in presumably higher risk populations in Chicago will allow CDPH to link more individuals at high-risk to appropriate care.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Emerging Infections; Vectorborne Disease; Underserved Populations

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9323

Abstract Type Breakout

Abstract Title Findings of Animal Rabies Testing and Human Exposure Management—Nebraska, 2006–2016

Abstract

BACKGROUND: Bats and wild terrestrial carnivores (particularly skunks) are implicated as important wildlife reservoirs of rabies in Nebraska. To define rabies epidemiology in Nebraska and to characterize human exposure events and outcomes, we performed descriptive analysis of laboratory results and exposure data from 2006–2016.

METHODS: The Nebraska Department of Health and Human Services manages Nebraska’s Rabies Control Program and captures electronic laboratory reports for results of all Nebraska-origin animals tested for rabies by Kansas State University Rabies Laboratory (KSU-RL) and University of Nebraska-Lincoln Veterinary Diagnostic Laboratory; paper reports are occasionally captured from other laboratories in neighboring states. The Program pays for testing at KSU-RL for animals involved in potential human rabies exposures and issues Rabies Approval (RA) numbers if criteria are met to establish risk as specified by Program requirements; human exposure data are captured at time of RA requisition and recommendations (on the basis of test results) for or against post-exposure prophylaxis (PEP) are documented.

RESULTS: During 2006–2016, 11,579 animals were tested of which 448 (3.9%) were positive. The proportion of positive tests was highest among skunks (219/307 [71.3%]), followed by horses (16/124 [12.9%]), cattle (43/431 [10.0%]), bats (123/6,669 [1.8%]), cats (33/2,030 [1.6%]), raccoons (2/369 [0.5%]), and dogs (6/1,257 [0.1%]). During 2006–2016, median number of bats and skunks testing positive per year was 13 (range, 3–16) and 15 (range, 7–53), respectively. NDHHS paid for 4,932 tests for exposure events with established human risk (median/year, 450; range 371–530). Of these, 4,803 (97.4%) were negative (median/year, 443; range 359–510); risk of rabies was ruled out and costly PEP was avoided. Of the remaining 203 exposure events, 121 (2.5%) were positive (median/year, 11.5; range 7–16 [1.6–4.1%]) and 82 (1.7%) were not testable (median/year, 8; range 4–10 [0.9–2.3%]); PEP was necessary for these potentially exposed, at-risk persons.

CONCLUSIONS: Skunks and bats remain the two primary wildlife reservoirs for the rabies virus in Nebraska. Given ongoing presence of this disease in these reservoir species, rabies remains a potentially serious threat to public health in Nebraska. On the basis of test results from animals associated with potential human exposures, medical professionals and public health officials are able to make well-informed decisions and recommendations for the exposed person(s) regarding need for PEP — an extremely effective intervention to prevent human rabies when administered appropriately. When test results are negative, such findings allow exposed persons to avoid expensive and time-intensive PEP.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; Disease Prevention; Local Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9164

Abstract Type Breakout

Abstract Title Human Rabies Postexposure Prophylaxis Knowledge and Retention Among Health Professionals By Using an Online Continuing Education Module — Arizona, 2012–2015

Abstract

BACKGROUND: Rabies is among the most fatal and preventable communicable diseases, making it an important public health concern. Rabies postexposure prophylaxis (PEP) is administered for rabies prevention after a human exposure to a potentially rabid animal, such as a bite. Previous studies have reported that rabies PEP is often inappropriately administered, incurring unnecessary costs. Health professional education was proposed as one potential solution to address inappropriate PEP use. We assessed baseline knowledge, knowledge gain, and knowledge retention among health professionals of rabies epidemiology and appropriate PEP administration.

METHODS: Maricopa County Department of Public Health created an online scenario-based rabies PEP continuing education (CE) module and measured knowledge before and after module completion using a 10-question test. The same test was administered three times (pretest, posttest, and retention test at ≥ 3 months). To assess knowledge gain and retention, we compared median scores using nonparametric methods.

RESULTS: A total of 302 respondents completed the pretest (median score, 60%) and posttest (median score, 90%; $P < 0.001$); 98 respondents completed all three tests with median scores 60% (pretest), 90% (posttest, $P < 0.01$), and 80% (retention test and compared with pretest, $P < 0.01$). Sixty-nine (70%) respondents improved their pretest to retention test score by a mean of 2.4 points out of a total 10 points (median: 2 points; range: -5–7 points). Only 48% of pretest respondents correctly answered that PEP should not be administered immediately to anyone bitten by a healthy dog. However, 81% and 70% answered correctly on this same question on the posttest ($P < 0.0001$) and retention test ($P = 0.002$), respectively. Correct rabies immune globulin (RIG) administration knowledge increased from 40% correct on the pretest to 92% correct on the posttest. However, this information was not retained and declined to 46% correct on the retention test.

CONCLUSIONS: Respondents demonstrated rabies epidemiology and PEP knowledge gain and ≥ 3 -month knowledge retention after completing the CE module. Low pretest scores among respondents demonstrates the need to effectively educate health professionals about rabies PEP. Based on our findings, knowledge gaps regarding appropriate use of PEP after a dog bite, and RIG placement should be addressed. Local and state health departments and health professionals should have ready access to and a working knowledge of these recommendations and local rabies epidemiology to make correct decisions about PEP administration. CE administrators could consider including rabies topics in physician CE requirements.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Professional Development; Zoonotic Diseases; Prevention

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9863

Abstract Type Breakout

Abstract Title Implementation of a Transfer Protocol for Patients with Rocky Mountain Spotted Fever — Arizona, 2011–2017

Abstract

BACKGROUND: Rocky Mountain spotted fever (RMSF) is a disease caused by *Rickettsia rickettsii* and transmitted by the brown dog tick (*Rhipicephalus sanguineus sensu lato*). Doxycycline administered within 5 days of infection reduces the risk of a severe outcome; $\geq 20\%$ of illnesses among US patients are fatal if treatment is delayed or not provided. In Arizona, cases primarily occur on Native American reservations and residents with severe RMSF are often transferred to Maricopa County (MC) acute care hospitals for a higher level of care; initiation and continuation of doxycycline is crucial to patient survival and a public health priority. Incidence of RMSF in Arizona increased rapidly during 2003–2012, and in July 2012, a new patient transfer protocol was implemented by state, county, and tribal partners to ensure continuation of doxycycline during transfers from Reservation A to MC. This protocol included clinical education to improve recognition of RMSF at Reservation A and MC hospitals and structured communication between state, county, and tribal organizations. We evaluated patient outcomes before and after transfer protocol implementation.

METHODS: Patients with confirmed or probable RMSF (clinically compatible illness with supportive or confirmatory laboratory criteria) transferred from Reservation A to MC hospitals during January 2011–October 2017 were identified through Arizona’s notifiable disease surveillance system. Patients transferred before July 31, 2012, were classified as before protocol implementation; subsequent patient transfers were classified as after. We compared proportion of patients with doxycycline continuation and fatalities before and after protocol implementation using Fisher’s exact test.

RESULTS: Among 282 confirmed or probable RMSF cases, 19 patients were transferred from Reservation A to MC hospitals; 17 had available data on doxycycline treatment (6 before and 11 after). Twelve (71%) patients were female; 8 (47%) were children. Doxycycline continuation occurred for 1/6 (17%) patients before and 8/11 (73%) after protocol implementation ($P = .05$). Fatalities decreased from 5/6 (83%) during the period before protocol implementation to 2/11 (18%) after ($P = .01$).

CONCLUSIONS: Doxycycline continuation among RMSF patients occurred more consistently and fatalities decreased after transfer protocol implementation. This protocol could serve as a model to improve patient care during cross-jurisdictional patient transfers.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Tribal Epidemiology; Vectorborne Disease; American Indians / Alaska Natives

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Submission Type Breakout/Quick/Lightning/Poster

ID 10238

Abstract Type Breakout

Abstract Title Influence of Social Network Structure on Seoul Hantavirus Transmission Among Wisconsin Rat-Housing Facilities, 2016-2017

Abstract

BACKGROUND: In December 2016, a Wisconsin resident breeding pet rats in a home-based rattery was diagnosed with Seoul Hantavirus infection. Seoul virus, a zoonotic pathogen whose reservoir is Norway rats, had not been previously identified in the domesticated rat population of the United States. Subsequent source investigation unveiled a large network of facilities in Wisconsin and other states, with considerable movement of rats between facilities for pet sales and breeding. A trace-back and trace-forward investigation was conducted to identify facilities (ratteries, pet homes, pet stores) that had supplied or accepted potentially infected rats. Rats and humans were tested for Seoul virus infection. Social network analysis techniques were then used to determine how facility network structure influences a facility's risk of infection and to identify strategies to reduce risk.

METHODS: Donor and recipient facilities completed detailed rat-level inventories and movement trackers for the period of 6/1/2016 through the date of facility identification. From these data, a rat movement network was constructed where directed ties represented rat movement between facilities. UCINET, a network analysis program, was used to calculate network metrics. Regression analyses were performed using network metrics and facility-level risk factor data from tested Wisconsin facilities (n=24) using permutation tests in UCINET and in SAS.

RESULTS: Wisconsin's network included 92 facilities and 720 rats; six facilities had confirmed human and/or rat Seoul virus infections. The mean number of facilities supplying rats to each facility (in-degree) was 1.4 (range: 0-14). The number of rats exchanged between facilities ranged from 0 to 22. Being a confirmed Seoul virus-positive facility was statistically associated with using a large number of suppliers (high in-degree), having well connected suppliers (high beta centrality), having other facilities dependent on a facility as a supplier (high betweenness), being part of a tight-knit subgroup of traders (high k-core value), acting as a bridge between subgroups of the network, self-identifying as a rattery, and directly receiving rats from an out-of-state supplier.

CONCLUSIONS: In Wisconsin, network structure and position were strong predictors of facility Seoul virus infection status. Obtaining rats from multiple suppliers increased risk of infection, especially from suppliers located outside of Wisconsin. Facilities can best protect themselves from infection by obtaining rats directly from a small number of Seoul virus-free suppliers and avoiding "middle men" or facilities that obtain and commingle rats from multiple sources. Local Seoul virus-negative closed colony suppliers providing rats bred and raised in-house offer the most protection.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Outbreaks; Infectious Diseases; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9573

Abstract Type Breakout

Abstract Title Investigation of *Brucella Abortus* RB 51 Infection in a North Texas Resident

Abstract

BACKGROUND: *Brucella abortus* RB51 (RB51) is a vaccine strain used to prevent brucellosis in cattle. In July 2017, RB51 infection was confirmed in a symptomatic Texas resident who had consumed unpasteurized (raw) dairy products from a Texas raw milk dairy. A collaborative investigation involving federal, state, and local agencies followed to identify and control the source of RB51, to identify those at risk, and to make post-exposure prophylaxis and testing recommendations.

METHODS: To identify the source(s) of the infection, multiple milk samples were collected from bulk milk tanks and individual dairy cows at the raw milk dairy, and tested by PCR and culture. Potentially exposed individuals were identified from the dairy's customer log and through associated referrals. To identify more exposed individuals, the Texas Department of State Health Services (DSHS) and CDC Bacterial Special Pathogens Branch (BSPB) issued press releases, Laboratory Response Network (LRN) alerts, and health alerts. A notification was developed to assess exposure risk and provide post-exposure recommendations for prophylaxis and symptom monitoring. It was subsequently administered to potentially exposed individuals using available contact information.

RESULTS: Testing of the bulk milk tank samples by PCR and culture yielded positive results for RB51. Testing of milk samples from each dairy cow in the herd identified two RB51-positive cows, which were then removed from the milking herd. The remaining dairy cows were once again individually tested, and were negative for RB51 by PCR and culture. This resulted in a cohort of RB51-negative dairy cows. Subsequent bulk milk tank samples also tested negative. Over 800 patrons of the dairy, from eight states, were identified as having been potentially exposed between June 1st and August 7th. Of these, 577 households (72%) had complete contact information available. A full notification was administered to 377 of the 577 households (65%). At least one exposed household member was identified in 287 (76%) of the contacted households.

CONCLUSIONS: This report describes the investigation that followed the first human case of RB51 identified in the United States from consumption of raw milk products acquired domestically. In Texas, raw milk sales are legal at point of production. Because raw milk is not pasteurized, it can transmit many bacterial pathogens, including *Brucella* spp. Public health workers need to remain alert to potential outbreaks involving raw milk consumption.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords One Health; Foodborne Disease; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9362

Abstract Type Breakout

Abstract Title Is the Juice Worth the Squeeze? Analyzing Immunofluorescence Assay Results and Characterizing the Burden of *Rickettsia Rickettsii* Case Classifications – Georgia, 2016-2017

Abstract

BACKGROUND: Rocky Mountain spotted fever, caused by *Rickettsia rickettsii*, is a nationally notifiable infection transmitted by ticks. Immunofluorescence assay (IFA) is used to diagnose *R. rickettsii*. Empiric treatment with doxycycline is recommended in patients with suspected *R. rickettsii* infection. In Georgia, suspect case-patients (those with positive IFA results) are interviewed and patient information is uploaded into the State Electronic National Disease Surveillance System (SendSS). The current national case definition (2010) requires at least one positive IFA immunoglobulin G-specific antibody titer and clinically compatible symptoms (fever and one or more of the following: rash, headache, myalgia, anemia, thrombocytopenia, or any hepatic transaminase elevation) for a patient to be considered a confirmed or probable case. Georgia, a low-incidence state, quantified the burden of case investigations using the current national case definition.

METHODS: Positive *R. rickettsii* IFA results reported into SendSS during 2016-2017 were characterized according to the national case definitions. Records of patients tested multiple times, out-of-state residents, and duplicates were excluded. Investigations in 2017 were manually reviewed for exposure and treatment history.

RESULTS: A total of 1,135 IFA results were entered into SendSS in 2016-2017, of which 47% were fully investigated; only 11% (126) met the confirmed or probable case definition. Over one-third (36%) of the cases investigated did not meet the clinical criteria. More than half (53%) of the investigations had no clinical information provided. Of all reported cases, only 2% had the convalescent draw required to meet the confirmed case status. A single public health district (of 18 districts) had 40% of the state's total reported positive IFA results yet only 6.2% met the case definitions. Provisionally, data from 2017's investigations indicate 234 of 501 laboratory positive cases were not clinically compatible. Over half (52%) of these individuals were tested because they reported a potential tick exposure; approximately 15% of those who were not clinically compatible were treated with antibiotics.

CONCLUSIONS: Due to the burden of over a thousand laboratory results indicative of *R. rickettsii* reported during 2016-2017, less than half were investigated, meaning many true cases may have gone undetected. Although empirical treatment is recommended for suspected cases, many patients are tested and treated based on exposure, not symptoms - potentially increasing false positive results and unnecessary antibiotic usage. This practice highlights a gap in knowledge, may lead to undesirable outcomes (e.g. side effects for patients, antibiotic resistance), and leaves little room for public health intervention.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Vectorborne Disease; Surveillance

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9835
Abstract Type	Breakout
Abstract Title	Knowledge, Attitudes, and Practices Relevant to Zoonotic Disease Reporting and Infection Prevention Practices Among Veterinarians — Arizona, 2015
Abstract	BACKGROUND: Veterinarians have substantial roles in zoonotic disease detection in animals and infection prevention practices (IPP) in the clinic. In the United States, guidelines exist regarding national, state, and local reporting requirements for animal diseases. However, no published studies exist demonstrating the practice of reporting of suspected zoonoses in animals by veterinarians to public health authorities; reporting is crucial to take actions protecting human and animal health. We examined the knowledge, attitudes, and practices of veterinarians regarding zoonotic disease reporting to public health and associated IPP, and the need for targeted education and outreach for veterinarians in Arizona. METHODS: We developed and distributed an online questionnaire to ~1,100 members of the Arizona Veterinary Medical Association. The survey was divided into four sections, including demographics, education, knowledge and attitudes of zoonotic diseases and reporting, and infection prevention methods in the clinic (e.g., personal protective equipment [PPE] use). RESULTS: In total, 298 (27%) veterinarians from all 15 Arizona counties completed the survey; the majority (70%) were female, practiced small animal medicine (84%), and practiced veterinary medicine for ≥10 years (75%). Only 57% reported they knew when to report a suspected zoonotic disease in an animal; 60% reported they knew how to make such a report. The majority would report plague (99%), rabies (97%), and highly pathogenic avian influenza (91%) to a state agency; however, were less likely to report other reportable diseases, including tularemia (74%) and leptospirosis (41%). The majority used PPE (e.g., masks, gowns, and gloves) when performing surgery (96%) or necropsies (94%), but fewer used PPE for handling clinically ill animals (37%) or healthy animals (17%). Approximately 70% reported always using PPE when in contact with animal birthing fluids, urine, or feces, and 47% for contact with animal blood, saliva, or other body fluids. Only 53% never or rarely ate or drank in animal handling/treatment areas. Only 42% reported having a written infection prevention manual or protocol available in their clinic. More small animal veterinarians reported always washing their hands before eating or drinking (77%) than large animal veterinarians (57%). CONCLUSIONS: Respondents demonstrated suboptimal zoonotic disease reporting and infection prevention practices, including handwashing and PPE use as recommended in the Compendium of Veterinary Standard Precautions for Zoonotic Disease Prevention in Veterinary Personnel. Our findings indicate the need for improvement regarding zoonotic disease reporting and IPP. Public health professionals can have a role to facilitate education and improve communication with veterinarians.
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	One Health; Occupational Health; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9410

Abstract Type Breakout

Abstract Title Lassa Fever in Travelers Arriving from West Africa, 1969-2016

Abstract

BACKGROUND: Originally discovered in 1969, Lassa fever (LF) is a zoonotic viral hemorrhagic fever endemic to West Africa and caused by Lassa Virus (LASV). Diagnosis of LF in patients returning from West Africa may be challenging for providers unfamiliar with the spectrum of its clinical presentation. Additionally, although LASV is not transmitted via casual contact, contact-tracing investigations of returning cases have often been large in scale. To quantify the frequency of case patients presenting with distinctive clinical features, time from patient presentation to clinician suspicion of a LF diagnosis, and the risk for secondary LF transmission, a retrospective review of all 33 LF cases imported to non-endemic countries between 1969 and 2016 was performed.

METHODS: PubMed was searched from August 1 through December 11, 2017 for publications using the terms “Lassa” and “Lassa Fever”. Additional publications were identified by reviewing references in retrieved reports, and official correspondence by epidemiologists involved in these cases. Seventy-four publications discussing clinical or epidemiological aspects of the 33 imported LF cases were selected for review. Information was collected pertaining to case demographics, distinctive clinical features suggestive of LF, time from patient presentation to clinical suspicion, number of total and high-risk contacts traced. Distinctive clinical features were defined as fever and at least one of the following: pharyngitis, sore throat, tonsillitis, conjunctivitis, oropharyngeal ulcers, or proteinuria. High-risk contacts were defined as having unprotected contact with patients or their body fluids.

RESULTS: Of the 28 cases for whom clinical information was available, 15 (54%) had distinctive clinical features and 13 (46%) did not. Time from patient presentation to clinician suspicion of LF ranged from 1 to 22 days (median 4.5 days). In 7 cases, diagnosis of LF was made retrospectively following patient discharge or death. Contact tracing investigation details were reported for 17/33 cases (52%) and ranged from 3 to 552 contacts per investigation. In total, 3,162 contacts were traced, of which 107 were classified as high-risk exposures. Only 2 cases of secondary transmission were reported, both in high-risk contacts in Germany.

CONCLUSIONS: Approximately half of the imported cases of LF had distinctive clinical features, and delays in clinical suspicion of this diagnosis were common. Additionally, there was no secondary transmission of LF to contacts with low-risk exposures, and infection of high-risk contacts was rare. Future public health investigations of returning travelers with LF should focus exclusively on identification and tracing of contacts with high-risk exposures.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; International Health; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 8943

Abstract Type Breakout

Abstract Title Mosquito in a Haystack: Enlisting the Public to Find Aedes in Long Beach, CA

Abstract

BACKGROUND: In 2016, Southern California was preparing for the possibility of local transmission of Zika due to population density, high volume of travel to and from Zika-affected areas, and increasing presence of *Aedes* mosquitoes in the area. Throughout the years of trapping and mosquito abatement, *Aedes* had never been identified in Long Beach, but had already been detected in several cities bordering Long Beach. In spring of 2017, the Long Beach Department of Health and Human Services (LBDHHS) developed a Zika preparedness plan with two goals: (1) identify whether *Aedes* mosquitoes are established in Long Beach and (2) educate and prepare Long Beach residents in the event of local transmission of Zika in Southern California.

METHODS: To determine whether *Aedes* mosquitoes were present in Long Beach, a Zika Hotline was established for residents to call and report day-biting mosquitoes. Outreach strategies to promote the hotline and educate the public on Zika included a social media campaign, billboards on main freeways, messages in the City's utility bill, distribution of Zika kits, and short films aired on public television about Zika. To evaluate whether the campaign was reaching residents, a Zika Community Assessment for Public Health Emergency Response (CASPER) was conducted in July of 2017.

RESULTS: Three months after establishing the Zika Hotline in Long Beach, *Aedes aegypti* mosquitoes were trapped and identified in Long Beach for the first time after a resident called to report day-biting mosquitoes. Since the first discovery, *Aedes aegypti* mosquitoes have been identified in various locations throughout Long Beach, almost all of which were located through calls from residents to the hotline reporting day-biting mosquitoes. Results from the CASPER showed 48% of households were aware of the Zika hotline, and 82% of households in Long Beach had strong knowledge on how to protect themselves from mosquito-borne disease, including Zika.

CONCLUSIONS: Enlisting the public's assistance to find *Aedes* mosquitoes proved to be very valuable, as the mosquitoes were located for the first time in Long Beach during this outreach campaign. The public's participation was instrumental in locating *Aedes*, as the calls coming into the Zika Hotline helped identify where to set traps. In addition, the Zika CASPER proved to be a valuable measurement of residents' knowledge of mosquito-borne diseases. In the event of local transmission of Zika in Southern California, the data and experiences collected will help form more targeted outreach plans and help focus future response efforts.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Community Health Assessment; Vectorborne Disease; Risk Communication

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9776

Abstract Type Breakout

Abstract Title Prioritization of Zoonotic Diseases in the United States Using a Multisectoral, One Health Approach

Abstract

BACKGROUND: Approximately 60% of human infectious diseases are zoonotic, meaning shared between animals (domestic and wildlife) and people. A One Health approach promotes multisectoral, transdisciplinary collaboration with the goal of achieving optimal health outcomes for people and animals and a safer environment. Multisectoral partnerships, with identification of common priorities for collaboration, are essential for zoonotic disease surveillance, prevention, control, and response. A One Health Zoonotic Disease Prioritization (OHZDP) workshop was conducted in the United States (U.S) in December 2017 to identify zoonotic diseases of greatest national concern that should be jointly addressed by the Centers for Disease Control (CDC), U.S. Department of Agriculture (USDA) and Department of the Interior (DOI).

METHODS: CDC's OHZDP tool was used to prioritize zoonoses. Workshop participants selected criteria for prioritization, and developed questions and weights relevant to each criterion. Questions were answered using a comprehensive literature database developed before the workshop and with subject matter experts; each disease was scored resulting in a ranked zoonotic disease list. After the final prioritized zoonotic disease list was agreed upon, participants used components of the One Health Systems Mapping and Analysis Resource Toolkit (OH-SMART™), developed by USDA and the University of Minnesota, to review the procedures and processes for multidisciplinary coordination for the prioritized zoonotic diseases in the U.S.

RESULTS: Workshop participants included nine voting members representing CDC, USDA and DOI plus 27 advisors representing federal and state human, animal, and environmental health sectors. Fifty-six zoonotic diseases were considered for prioritization during the workshop. The five criteria selected to prioritize zoonotic diseases were epidemic or pandemic potential, disease severity, economic impact, introduction or increased transmission potential, and national security. The eight prioritized zoonotic diseases for the U.S were zoonotic influenzas, salmonellosis, West Nile virus, plague, emerging coronaviruses (e.g. SARS, MERS), rabies, brucellosis, and Lyme disease. Participating agencies discussed recommendations to enhance One Health coordination for surveillance, response, prevention, and control of the prioritized zoonoses. Key themes and next steps for furthering implementation of a One Health approach among human, animal, and environmental health sectors were identified.

CONCLUSIONS: The U.S. OHZDP workshop represented the first time a One Health approach was used to prioritize zoonotic diseases in the U.S. This workshop marked a critical step forward for the U.S. federal agencies involved in strengthening One Health approaches for the prioritized zoonoses.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords One Health; Zoonotic Diseases; Collaboration

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9820

Abstract Type Breakout

Abstract Title Seasonal Trends in Zika Virus Testing Among Women of Childbearing Age—Miami Dade County, Florida, December 2015 — September 2017

Abstract

BACKGROUND: Zika virus (ZIKV) infection is typically identified via RT-PCR or the presence of the ZIKV IgM antibody. The virus has been detected in serum, urine, and saliva specimens collected during routine diagnostic consultations and other means. In July 2016, local transmission of ZIKV was identified in Miami-Dade County. As a result, ZIKV testing became routine for pregnant women and individuals presenting with symptoms of ZIKV infection who reported recent exposure to an area with active ZIKV transmission. The purpose of this study was to examine seasonal trends in the incidence of ZIKV positive laboratory results among women of childbearing age during the period of active ZIKV transmission in Miami-Dade County compared to non-active transmission periods.

METHODS: All laboratory result, with collection dates between December 2015 and September 2017, were included in analysis. Our study population of interest were women of childbearing age (15 – 50 years). Variables of interest included age, race/ethnicity, pregnancy status, date of collection, and laboratory performing ZIKV testing (Bureau of Public Health Laboratories or private commercial laboratory). Descriptive statistics were conducted in SAS 9.4.

RESULTS: A total of 20,790 ZIKV laboratory results were reported to DOH Miami-Dade during the timeframe of interest, of which a total of 691 (8.17%) tests were positive. Thirty-nine (1.39%) positive results were identified through BPHL and 652 (3.63%) were identified through commercial clinics. 15, 173 (72.98%) individuals were between the ages of 20 – 34. Race/ethnicities were missing for 19,631 results. among the 120 African Americans who were tested, 77 (64.17%) were positive in comparison to 215 (37.33%) of the 576 Hispanic individuals were tested. Among the 4,665 pregnant women who were tested, 381 resulted in a positive test. The incidence of ZIKV positives were examined by month (using the laboratory collection date). The highest months of RT-PCR positives (> 15% of specimens tested) occurring during December 2015, February, April, May, and July 2016; in contrast, the highest months of IgM detection (>15% of specimens tested) occurred during January, April, July 2016 and September 2017.

CONCLUSIONS: ZIKV testing trends within Miami-Dade County varied by month between December 2015 and September 2017. The increase in testing and positive results coincided with the period of active ZIKV transmission within Miami-Dade County. These results suggest that active and passive surveillance of ZIKV in Miami-Dade County through the monitoring of reported “positive” laboratory results may also be used to monitor for the future occurrence of active ZIKV transmission.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Reproductive Health; Surveillance; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9818

Abstract Type Breakout

Abstract Title Utilization of Dengue IgG for Non-Travel Related Zika Virus Case Investigations

Abstract

BACKGROUND: In July 2016, Florida was the first state to report local cases of Zika virus (ZIKV) infection. While Florida's Bureau of Public Health Laboratories (BPHL) had some ZIKV testing capacity, plaque reduction neutralization testing (PRNT) was unavailable until mid-2017. PRNT testing is costly, takes at least a week to run, and requires specialized training and facilities. Because of limited ZIKV PRNT availability nationwide, testing turn-around times varied, taking several weeks during the time of active local transmission in Miami-Dade County. ZIKV antibodies can cross-react with related flavivirus antibodies such as dengue virus (DENV). To compensate for PRNT testing delays, BPHL performed a two-day DENV IgG antibody test as a proxy for ZIKV IgG. This analysis assesses how useful this proxy was.

METHODS: Florida's reportable disease surveillance system was used to retrieve DENV IgG and DENV and ZIKV PRNT assay results for confirmed and probable cases of local ZIKV infection reported from July 1, 2016 to December 13, 2017. BPHL performed DENV IgG testing while PRNT testing was performed by either BPHL or the Centers for Disease Control and Prevention. DENV IgG enzyme-linked immunosorbent assay results were evaluated for cases with positive ZIKV PRNT results.

RESULTS: Of 33 cases with both positive PRNT and DENV IgG results, 15 (45%) had PRNT titers signifying ZIKV infection (positive ZIKV titer, negative DENV titer). Twelve were symptomatic with samples collected 1-66 days (median 17 days) after onset. Eighteen cases had PRNT titers indicating flavivirus infection (positive ZIKV and DENV titers), with 13 symptomatic and samples collected 0-51 days (median 8 days) after onset. Of 20 cases with no detectable DENV IgG antibodies, 19 (95%) had ZIKV-positive PRNT results and one indicated flavivirus infection. Seventeen cases were symptomatic and samples were collected 1-25 days (median 7 days) after onset. Five DENV IgG seroconversions were identified in individuals with both acute and convalescent samples. Convalescent samples were collected 17-43 days after symptom onset.

CONCLUSIONS: While antibodies against DENV IgG were detectable among cases with confirmed and probable ZIKV infection, past flavivirus infections can complicate laboratory result interpretations. For some patients with reduced risk of past flavivirus exposure, detection of DENV IgG antibodies or IgG seroconversion may serve as a proxy for PRNT testing in conjunction with appropriate ZIKV testing and epidemiological risk assessment. This may have particular value for samples collected after two weeks. Use of DENV IgG testing may lessen the burden of time-consuming and expensive laboratory testing.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Epidemiology; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9831

Abstract Type Breakout

Abstract Title Web-Based Education to Enhance Zoonotic Disease Prevention in Youth Involved with Animal Agriculture

Abstract

BACKGROUND: Several animal related disease outbreaks, such as variant influenza A virus of swine (H3N2v) and enteric diseases caused by E. coli and Campylobacter, have been associated with fairs in recent years. Children infected with these pathogens are at increased risk for severe complications. Youth agriculture programs, including raising and showing livestock, help youth develop responsibility, learn good sportsmanship, gain confidence, and teach the public about animal agriculture. However, zoonotic diseases can affect exhibitors and spectators, especially when people have close contact with animals. Youth involved in animal agriculture, teachers, volunteer leaders, and parents, should understand disease risks and preventive measures to reduce zoonotic disease occurrence. Accessible, free, web-based education can engage youth and be easily incorporated into current agriculture or science curricula.

METHODS: Excellence in Exhibition: Preventing Disease in Animals and People (www.BlueNotFlu.org) is a web-based, interactive, educational course that was developed by the Center for Food Security and Public Health in collaboration with the Iowa Department of Public Health and with support from the CDC and CSTE. The course, which includes 6 lessons designed to be completed in 20–30 minutes each, may be taken independently by anyone at any time, but is targeted at youth aged 13–18 years. The first 3 lessons cover specific zoonotic diseases, such as influenza, and ways to prevent transmission to humans and animals. The remaining lessons review case studies, agencies, and career opportunities in One Health. Learning objectives, PowerPoint slides, supplemental materials, and class activities are also available. The course is designed to be used widely and in a variety of ways, including incorporation into classroom, chapter, and club curricula; into 4-H projects on animal and human health; as preparation for FFA contests; and/or as prerequisites for showing at local or state exhibitions or fairs.

RESULTS: Real-time information on user data associated with course web page views has shown extensive national and international distribution since release in March 2017. Course website tracking has indicated 3,590 unique homepage views and 661 users from 31 states accessing the course. An optional evaluation component has indicated an increase in knowledge and intentions to adopt disease prevention habits upon post-course completion.

CONCLUSIONS: Web-based education presents an opportunity to promote youth involvement in animal agriculture, increase disease prevention practices, and reduce zoonotic disease risks. Requiring completion of this course prior to showing animals may increase disease prevention behaviors and further reduce zoonotic disease risks.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; Children and Adolescents; Influenza / Pandemic Influenza

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9224
Abstract Type	Breakout
Abstract Title	Zika Testing Behaviors and Risk Perceptions Among Pregnant Women in Miami-Dade County, One Year after Local Transmission

Abstract

BACKGROUND: There is limited knowledge regarding the Zika virus (ZIKV) testing perceptions and practices of pregnant women. This study sought to describe the knowledge and perceptions of pregnant women in Miami-Dade County concerning the risk of ZIKV in their community, to characterize the behaviors of pregnant women regarding testing, and to identify any barriers that would keep a pregnant woman from seeking testing.

METHODS: The Florida Department of Health in Miami-Dade County (DOH-Miami-Dade) partnered with the Healthy Start Coalition of Miami-Dade to administer an original assessment survey in the waiting rooms of eight OBGYN clinics from June to August 2017. The survey captured demographics, preferred sources of health information, past ZIKV testing practices, attitudes towards testing, risk perception of ZIKV in the participants' community, and ZIKV-related knowledge. The data were analyzed using SAS version 9.4. Descriptive analyses were performed on variables of interest. Chi-squared tests examined associations between categorical variables.

RESULTS: A total of 363 participants were included in the analysis. Of these, 55.9% thought they should be tested for ZIKV, and less than half of the participants reporting having been previously tested (41.9%). Of those who were tested, the majority reported having been tested through their OBGYN or primary care physician (70.3%). Participants with some high school education were significantly more likely than those with higher education levels to see ZIKV as a "big problem" in the community ($p = 0.0026$). There was a significant association ($p < 0.0001$) between women who thought that they should be tested, and those who perceived ZIKV to be a medium or big problem in their community. Over two-thirds of participants did not list any reasons and/or barriers that would keep them from seeking ZIKV testing, and risk perception was not associated with higher knowledge levels regarding ZIKV.

CONCLUSIONS: Health interventions that focus on increasing ZIKV knowledge should also place greater emphasis on risk communication when targeting the pregnant population. Having a higher risk perception of ZIKV as a community problem may be more predictive of testing behaviors than having a lack of barriers or a high level of ZIKV-related knowledge. Risk communication messages should also be tailored to fit different educational backgrounds. OBGYNs and primary care physicians should be encouraged to continue discussing the risk of ZIKV and testing options with their patients.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Barriers to Care; Risk Communication; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9138

Abstract Type Breakout

Abstract Title Zika Virus Disease Cases —U.S. States and the District of Columbia, January 1–December 31, 2016

Abstract

BACKGROUND: Zika virus is a flavivirus primarily transmitted to humans by *Aedes aegypti* mosquitoes. Zika virus infections also have been documented through intrauterine, intrapartum and sexual transmission; blood transfusion; and laboratory exposure. Before 2015, local mosquito-borne transmission of Zika virus had been reported in Africa, Southeast Asia, and the Pacific Islands, but only 14 Zika virus disease cases had been diagnosed in returning U.S. travelers. In 2015, local mosquito-borne transmission of Zika virus was identified for the first time in the Americas, and subsequently spread throughout the region. We report national surveillance data for Zika virus disease cases reported from U.S. states and the District of Columbia (DC) in 2016.

METHODS: We reviewed data for noncongenital Zika virus disease cases reported to ArboNET with onset in 2016. Zika virus disease became nationally notifiable in February 2016; confirmed and probable cases are reported using standard definitions that include clinical and laboratory criteria.

RESULTS: A total of 5,168 noncongenital Zika virus disease cases with illness onset in 2016 were reported from 49 states and DC; almost half were reported from three states, including Florida (1,107; 21%), New York (1,002; 19%), and California (421; 8%). Cases peaked in July and declined rapidly after August. The median age of cases was 37 years (range = 10 months–89 years), with 4,118 (80%) aged 20 to 59 years; 3,310 (64%) were female. Overall, 153 (3%) cases were hospitalized; one hospitalized male patient died. Travelers to areas with Zika virus transmission accounted for 95% (4,897) of cases. A total of 224 (4%) patients were infected through presumed local mosquito-borne transmission in Florida (n=218) and Texas (n=6); 103 (46%) were female. Forty-seven (1%) cases were acquired through other routes, including sexual transmission (n=45), laboratory transmission (n=1), and person-to-person through an unknown route (n=1).

CONCLUSIONS: Following the introduction and spread of Zika virus in the Americas in 2015, the number of travel-associated cases in the continental U.S. increased substantially during the first half of 2016. Most cases were among travelers recently returning from locations outside the continental United States. Local mosquito-borne transmission was geographically limited to small areas of Florida and Texas. Despite the presence of *Aedes aegypti* in multiple states, other factors (e.g., use of air conditioning and window screens, temperate climate, lower human population density, and reduced mosquito habitat) likely limited the local transmission risk.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease; Outbreaks; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10187

Abstract Type Breakout

Abstract Title Zika Virus Infection in Asymptomatic Pregnant Women with Prolonged Exposure

Abstract

BACKGROUND:

Zika infection during pregnancy has been associated with adverse birth outcomes. The District of Columbia Department of Health (DC DOH) started investigating cases of Zika virus infection among DC residents in January 2016. We examined our data to identify populations that warranted special recommendations and follow-up in our jurisdiction.

METHODS:

Pregnant women were screened and reported by healthcare providers to DC DOH for Zika virus testing. Zika virus exposure was defined as travel to, residence in, or sexual contact with an individual who traveled to or resides in a “Zika-affected” country as described by the Centers for Disease Control and Prevention (CDC) and World Health Organization (WHO). CDC guidelines for testing initially classified pregnant women as symptomatic or asymptomatic, but in July 2017 further defined these categories into symptomatic, asymptomatic with a single exposure, and asymptomatic with ongoing exposure. DC DOH added an additional category of asymptomatic with prolonged exposure, defined as women who lived in a Zika-affected area for greater than six months. Inclusion criteria for the CDC United States Zika Pregnancy Registry (USZPR) included a broad population of pregnant women and infants with positive or equivocal laboratory results of Zika virus infection. Data on maternal health, delivery information, birth outcomes, and infant development during the first 12 months of life was collected through the USZPR.

RESULTS:

Of 991 pregnant women tested through the DC DOH, 33 had positive or equivocal laboratory results and were enrolled in the USZPR. Fifty-seven percent (n=19) of cases were exposed periconceptionally and 21% (n=7) were exposed in their first trimester. Of the 33 cases in the USZPR, 24 (73%) had prolonged exposure and 21(87.5%) were asymptomatic. Of the 21 asymptomatic pregnant women with prolonged exposure, 4 delivered babies with health outcomes that warranted additional follow-up: developmental delays (n=2), and abnormalities on head ultrasound (n=2).

CONCLUSIONS:

We identified the population of asymptomatic pregnant women with prolonged exposure as important for consideration in our jurisdiction. DC healthcare providers were given specific guidance for pregnant women with prolonged exposure. The USZPR helped identify mother infant pairs that warranted additional follow-up in DC and highlighted that understanding the needs of this special population is a vital component of planning further outreach programs and health education activities in DC to identify and mitigate the effects of Zika virus infection.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Registry; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10207
Abstract Type	Lightning
Abstract Title	Are Increasing Temperatures and Precipitation Affecting Transmission of Murine Typhus in Travis County during 2007-2016?

Abstract

BACKGROUND: Murine typhus is a disease caused by the *Rickettsia typhi* bacteria, it can infect different species of wild mammals, including rodents, opossums, cats, and dogs. It is spread to people through contact with infected fleas. Murine typhus is endemic in temperate climates, especially coastal areas. Studies have shown the majority of cases occur during warmer weather, while infection is very low or almost zero during colder months. Most cases of murine typhus in the United States are reported from California, Hawaii, and Texas. The study aims to explore the climate dynamics of confirmed or probable murine typhus cases in Travis County from 2007 to 2016, and if the increase in temperature and the amount of precipitation is related to the number of cases.

METHODS: All cases of murine typhus from 2007 to 2016 were extracted from the National Electronic Disease Surveillance System for Texas, the weather variables from the same time period (precipitation, snow, and average temperature) were requested from the National Centers for Environmental Information. To explore the dynamics between murine typhus incidence and environmental variables the cases were mapped by Zip Code and statistical analysis was performed using ArcGis.

RESULTS: Between 2007 and 2016 a total of 225 confirmed or probable cases of murine typhus were reported to Travis County. The majority of cases were reported each year between May and October, with peak incidence during June, almost every year. The spatiotemporal dynamics of murine typhus varied over the 10 year period with more cases identified in the years with warmer annual average temperatures. There were more cases when the average annual temperature was 1° F over 68°F even during the colder months. The relation between precipitation and the number of cases was inconclusive.

CONCLUSIONS: The results of this study indicate that increase of murine typhus in some years may be related to the increase of temperatures on average, especially during the colder months. A more in depth analysis is necessary to determine if the areas with warmer temperatures had more mammals during those years. More importantly, by analyzing annual spatiotemporal clustering we will be able to determine and implement targeted interventions.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Climate; Infectious Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10014

Abstract Type Lightning

Abstract Title Challenges in Early Diagnosis and Treatment of Rocky Mountain Spotted Fever – a Case Report

Abstract

BACKGROUND: Rocky Mountain spotted fever (RMSF) is a tickborne disease caused by the bacterium *Rickettsia rickettsii* that is fatal in 5–10% of cases. Early signs and symptoms include fever, headache, myalgia, and maculopapular rash; laboratory findings include thrombocytopenia, hyponatremia, and elevated transaminases. Doxycycline is most effective at preventing fatalities if begun within five days of symptom onset.

METHODS: We report a fatal case of RMSF in a pediatric patient in Indiana.

RESULTS: A pediatric patient presented to the emergency department (ED) with a two-day history of fever and lethargy. While in the ED, the patient developed a transient maculopapular rash. A complete blood count (CBC) tested within normal limits, and a chemistry panel revealed low normal sodium (135 mmol/L) and elevated transaminases. The patient was diagnosed with a viral illness. Four days later, the patient presented to a second ED with fever and a maculopapular rash; a rapid test for Group A *Streptococcus* was positive and no other testing was done. The patient was diagnosed with scarlet fever and prescribed amoxicillin. Two days later, the patient presented to a third ED with altered mental status and a petechial rash. A history of outdoor exposure was elicited, but no tick bites were reported. A CBC and chemistry panel revealed anemia, lymphopenia, thrombocytopenia, hyponatremia, and elevated transaminases. The patient was admitted and treated with vancomycin and ceftriaxone. Although RMSF was suspected, doxycycline was not started until infectious disease consultation one day later. The following day, the patient succumbed to anoxic brain injury. Serum tested positive for *R. rickettsii* by polymerase chain reaction.

CONCLUSIONS: This case report illustrates the challenges of diagnosing RMSF in its early stages. The clinical presentation in this patient was consistent with other common diseases, and laboratory testing supported an alternate diagnosis. Providers are encouraged to ask about history of outdoor exposure and should not rule out tickborne disease even if no specific tick exposure is reported. Testing and treatment should be initiated immediately upon clinical suspicion of RMSF even if other potential diagnoses are identified. The Indiana State Department of Health provided these recommendations to healthcare providers statewide via the Indiana Health Alert Network following the investigation of this case.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Children and Adolescents; Communication; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9510

Abstract Type Lightning

Abstract Title Implementation of a REDCap Database to Monitor Rabies Consultations in a State Health Department, Tennessee

Abstract

BACKGROUND: Infection with rabies virus causes a rapidly progressive, fatal encephalitis. Despite a significant burden of disease worldwide, human rabies cases are rare in the United States. In Tennessee, the last reported case of human rabies was in 2002; however, the virus remains present in skunk, bat, and raccoon reservoirs in the state. The Tennessee Department of Health (TDH) provides 24/7 consultation for members of the public, healthcare providers, veterinarians and others. We sought to describe the characteristics and volume of rabies consultations to target stakeholder education.

METHODS: An electronic database was created using Research Electronic Data Capture (REDCap) software to track all telephone rabies consultations received by TDH. Calls were entered into the database by staff taking calls, or their proxy. Data were collected on the caller, characteristics of the call, and public health recommendations; consultation categories were not mutually exclusive.

RESULTS: During August 9–December 11, 2017, 85 telephone rabies consultations were completed by TDH staff. The highest proportion of calls were received from the general public (n=30/85; 35.3%); followed by veterinarians (n=23/85; 27.1%), healthcare providers (n=15/85; 17.6%), and local/regional public health staff (n=13/85; 15.3%). The majority of consultations assessed the need for human rabies post-exposure prophylaxis (n=43/93; 46.2%) or animal testing (n=32/93; 34.4%). Rabies post-exposure prophylaxis was recommended in approximately 50% of consultations assessing the need for post-exposure prophylaxis (n=21/43; 48.8%). A total of 18 hours and 45 minutes were spent on consultations; the median amount of time spent on each call was 10 minutes (interquartile range: 5–15 minutes).

CONCLUSIONS: Despite an extremely low incidence in the United States, rabies consultations comprised a substantial call volume in the state health department. Public health consultation services were a resource for the general public, veterinarians and healthcare providers regarding rabies animal testing and human post-exposure prophylaxis guidelines. The development of a REDCap database allowed for timely and accurate data collection by numerous staff members. Routine tracking of rabies consultations assisted in allocating resources needed, and in identifying stakeholder groups to target for education.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Epidemiology Capacity; Zoonotic Diseases; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9307

Abstract Type Lightning

Abstract Title Prevalence of *B. Canis* in Stray and Previously Owned Dogs Entering a Minnesota Animal Rescue Organization

Abstract

BACKGROUND: Canine brucellosis, caused by the bacterium *Brucella canis*, is a zoonotic and largely reproductive disease of dogs. The disease is a recognized problem in canine breeding populations, and the risk to individuals assisting with birthing is well described. Prior to 2015, all cases of canine brucellosis reported to the Minnesota Board of Animal Health were in dogs used for breeding. In 2015, canine brucellosis was identified in eight Minnesota rescue dogs, all originating from two discreet geographic areas in South Dakota. Our objective was to measure the prevalence of *B. canis* in stray and previously owned dogs entering a large Minnesota animal rescue organization.

METHODS: A stratified random sample of stray and previously owned dogs entering the largest Minnesota animal rescue organization between November 1, 2016 and November 7, 2017, was tested for *B. canis* antibodies by the 2-Mercaptoethanol Rapid Slide Agglutination Test (2ME-RSAT) (Zoetis D-TEC® CB kit). Sample sizes for each strata were calculated using previously published prevalence estimates. Blood from selected dogs was collected, serum harvested, and transported to the Minnesota Veterinary Diagnostic Laboratory for testing. Positive samples in the 2ME-RSAT were shipped to Cornell University for confirmation by Agarose Gel Immunodiffusion (AGID) testing. Demographics, state and setting of origin, and health status were collected on study-dogs.

RESULTS: Of the 10,654 dogs arriving at the rescue during the study timeframe, 943 (8.9%) were selected for testing. A majority of tested dogs arrived from Oklahoma (28%) and Alabama (18%). The median age of tested dogs was 1.5 years; 303 (32%) tested dogs were intact males and 294 (31%) were intact females. Most tested dogs were strays (n=716, 76%); 227 (24%) were previously owned. Of these, 22 (3%) stray and eight (4%) previously owned dogs were presumptively positive by RSAT. One (0.14%) stray was positive by 2ME-RSAT and confirmed by AGID. The positive dog was a healthy 1 year-old neutered male beagle from Texas.

CONCLUSIONS: The prevalence of canine brucellosis in dogs entering Minnesota from multiple states appears to be low. Due to the low overall prevalence, the appearance of a minimal increase or cluster of canine brucellosis cases could indicate a geographic area where targeted disease control interventions and prioritized canine brucellosis screening is needed. Although this study included dogs from states other than Minnesota, a larger, multi-state prevalence study representative of the national canine population is needed to further understand the burden of this important zoonotic disease.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Veterinary Public Health; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10236

Abstract Type Lightning

Abstract Title Proportion of Tickborne Illness Classified As Non-Cases, Saint Louis County 2013 to 2017

Abstract

BACKGROUND: In Saint Louis County, as in Missouri and nationally, the majority of vectorborne illness is tickborne. Additionally, Missouri is a “hotspot” for certain tickborne conditions, such as ehrlichiosis and Rocky Mountain spotted fever (RMSF). Given this public health burden, Saint Louis County Department of Public Health (DPH) staff devote significant time and resources to investigating cases of tickborne illness. Upon further investigation, however, initial reports (e.g., positive laboratory tests) of many potential cases of tickborne illness in Saint Louis County residents are downgraded to non-cases. We sought to determine the proportion of reported cases of tickborne illness subsequently classified as non-cases and examine whether this proportion, or the reasons for a non-case classification, differed by condition.

METHODS: Data were obtained from WebSurv, Missouri’s communicable disease surveillance system. All potential cases of six tickborne illnesses (anaplasmosis, ehrlichiosis, Lyme disease, acute Q fever, RMSF, and tularemia) among Saint Louis County residents that were reported to DPH between 01/01/2013 and 12/31/2017 and entered into WebSurv were included in this analysis. Descriptive statistics were calculated using Microsoft Excel 2013.

RESULTS: Of the 420 total cases included in this analysis, 228 (55.5%) were deemed non-cases and 187 as suspect, probable, or confirmed cases. Both the number of potential cases and the proportion deemed non-cases varied substantially by condition: anaplasmosis– 30 total cases with 66.7% classified as non-cases; ehrlichiosis– 131 total cases, 26.7% non-cases; Lyme disease– 62 total cases, 75.8% non-cases; Q fever– 8 total cases, 100.0% non-cases; RMSF– 183 total cases, 66.7% non-cases; and tularemia– 6 total cases, 16.7% non-cases. Not meeting the clinical requirements of the case definition (e.g., no fever) was the most common reason for a non-case classification for anaplasmosis (75.0%), ehrlichiosis (93.8%), and RMSF (87.3%). For Lyme disease, not meeting laboratory diagnostic criteria resulted in the highest proportion of non-cases (60.5%). A lack of exposure history (25.5% of Lyme disease and 8.1% of total non-cases) and an alternate diagnosis (15.0% of anaplasmosis and 6.3% of total non-cases) were also common reasons for a non-case classification.

CONCLUSIONS: In Saint Louis County, more than half of all reported cases of tickborne illness are ultimately classified as non-cases, a situation resulting from such factors as surveillance case definitions and testing and reporting practices. Conversations are warranted at all levels of public health to optimize limited resources, while maintaining, or even improving, the ability to collect accurate and timely surveillance data on tickborne illness.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9856

Abstract Type Lightning

Abstract Title Tick-Borne Relapsing Fever Outbreak Among Writing Workshop Attendees in an Urban Setting-Austin, Texas, 2017

Abstract

BACKGROUND: Tick-borne relapsing fever (TBRF) is an uncommon cause of febrile illness in Texas. *Borrelia turicatae* bacteria that cause TBRF are transmitted to humans through the bite of infected “soft ticks”. During February 2017 an outbreak of TBRF occurred in a group of workshop attendees in Austin, Texas. The investigation goals were to identify the location of exposure, confirm any additional cases, and prevent further disease.

METHODS: A probable case was defined as a presence of fever with headache and muscle and/or joint pain who was present at the workshop during the weekend of February 24-26. A confirmed case had evidence of infection by EIA and/or Western Blot testing using *B. hermsii* antigen. Interviews were conducted over the phone, to collect data regarding demographics, symptoms since attending the workshop, doctor’s visits and treatment given, and risk factors, including activities and sleeping location. Copies of laboratory tests were requested. An environmental assessment of the property was conducted.

RESULTS: During February 2017, a total of 28 persons (21 attendees and 7 staff) attended a writing retreat located in an urban area in Austin, Texas. Almost all (96%) attendees and staff were interviewed. The attendees reside throughout the United States and Canada. No staff reported symptoms. Eleven ill attendees were identified; four confirmed and seven probable cases. Onset dates ranged from February 26 through March 4. Eight of the 11 ill persons reported insect bites, primarily on the feet, ankles, and legs. Illness was associated with reporting of insect bites (OR=6.4, 95% CI:1.2-34.6). Eight ill slept on-site and three ill slept off-site. Sleeping on-site was not associated with illness (OR=3.8, 95% CI:0.7-19.7). Three persons experienced a relapse. Three persons experienced Bell’s palsy. Onset of Bell’s palsy was 12 to 17 days after onset of fever. Six persons reported testing positive for Lyme disease. During the environmental assessment collection efforts conducted in late April 2017, failed to recover any ticks or rodents.

CONCLUSIONS: The occurrence and ecologic setting of this outbreak was unexpected. Being in Texas, reporting insect bites, the occurrence of Bell’s palsy, and positive serology tests for Lyme disease influenced incorrect diagnoses of Lyme disease. Increased awareness of current epidemiology and features of TBRF among medical providers and public health practitioners can lead to early and effective diagnosis and treatment of patients.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10184
Abstract Type	Lightning
Abstract Title	Timing of Rabies Postexposure Prophylaxis Initiation in Relation to Rabies Exposure, Fairfax County, Virginia, July 2009-December 2016

Abstract

BACKGROUND: Human rabies cases are preventable with timely treatment. The current Advisory Committee on Immunization Practices (ACIP) recommendations on human rabies prevention advise that administration of rabies postexposure prophylaxis (PEP) is a medical urgency, not an emergency. The term urgency, however, is not defined and studies analyzing the time between exposure and initiation of PEP are lacking. Patients and healthcare providers often inquire about the timing of PEP initiation after exposure.

METHODS: Fairfax County Health Department PEP records for July 2009-December 2016 were reviewed. Those patients who were determined by health department personnel to meet case definition of rabies exposure (bite and nonbite exposures as described in the ACIP recommendations) were included. The number of days between a patient's rabies exposure and when PEP was initiated was calculated. The average number of days for high risk patients (those bitten by a laboratory confirmed rabid animal or high risk species for rabies) was compared to average number of days for low risk patients using a t-test. Patients who reported a previous rabies vaccination series were compared to those not previously immunized.

RESULTS: During the study period, 2024 patients were reported as having received PEP. Health department personnel assessed that PEP was indicated for 1440 (71%) patients. Data from 331 patients was removed as there was either no evidence that they initiated the series (n=296) or the exposing animal was later confirmed as not rabid (n=35). Of the 1109 exposures analyzed, there was an average of 5.5 days between exposure and initiating PEP (range, 0-366). The number of days from exposure to vaccination for patients meeting the high risk exposure definition (n=211) averaged 2.3 days (range, 0-168), which was significantly different ($p=0.0002$) than the average of 5.5 days (range, 0-366) for those patients reporting low risk exposure (n=1020). For patients reporting previous vaccination (n=89), there was an average of 5 days between exposure and initiating PEP (range, 0-28) which did not differ significantly from those not previously immunized ($p=0.55$). No patients were reported to have developed rabies.

CONCLUSIONS: Patients with high risk exposures to rabies had significantly shorter times from exposure to PEP initiation than those with lower risk exposures, but even with high risk exposures, at least two days, on average, passed before initiation of PEP. The data from this limited series and future, similar study of this kind, may inform the ACIP in defining the term urgency.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Veterinary Public Health; Vaccine-Preventable Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10322
Abstract Type	Lightning
Abstract Title	Zika Test Ordering Practices of Healthcare Providers in Washington State, January 2016-November 2017

Abstract

BACKGROUND: Laboratory testing for Zika virus infection is complicated by a short period of viremia and waning IgM antibodies over time. Nucleic acid testing (NAT) testing is only useful during the period of viremia, and negative results do not rule out recent infection; NAT should be followed by serum IgM testing. During the recent Zika epidemic, Washington State Department of Health (WA DOH) requested electronic commercial laboratory reporting of both negative and positive Zika test results in order to better understand healthcare provider ordering practices for patients in WA. We compared Zika tests ordered through commercial laboratories and through Public Health Laboratories (PHL) over time to determine whether patients were being appropriately tested for this emerging disease.

METHODS: We collected patient Zika NAT and IgM test results from the WA Public Health Reporting Electronic Database (PHRED), and from WA DOH databases of tests performed through the Public Health Laboratories (PHL) for WA residents. We compared numbers of tests performed by type and proportions of tests handled over time.

RESULTS: Zika tests were performed for 2509 WA patients from January 2016 through November 2017. NAT tests constituted 36.9% (1212/3284) of the tests performed; the remainder were for Zika IgM antibodies. Of the NAT tests, 43.2% (524/1212) were performed through commercial laboratories and the remainder through PHL. The majority of NAT tests were negative (96.9%). Zika IgM testing was performed for 38.1% (197/517) of the negative NAT tests from commercial laboratories and 86.6% (569/657) of those performed through PHL. The proportion of negative NAT tests that were coupled with IgM tests varied monthly at commercial laboratories, peaking to 57% in November 2016, roughly four months after commercial testing began, and to 50-57% from June-September 2017, after PHL began limiting testing to patients for whom cost was a barrier in June 2017. The majority of patients received both NAT and IgM testing at a single facility; only 2% of the tests were split between commercial facilities and PHL.

CONCLUSIONS: Completeness of Zika testing using NAT in combination with testing for Zika IgM antibodies differed substantially by testing site, with much higher completeness when testing through PHL. NAT testing alone cannot rule out Zika virus infection. This data demonstrates tremendous and ongoing need for healthcare provider education on appropriate test types to order for Zika virus.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9745

Abstract Type Poster

Abstract Title *Borrelia Miyamotoi* Infection Rate in Black-Legged Ticks Recovered from White-Tailed Deer Heads in Pennsylvania

Abstract

BACKGROUND: *Borrelia miyamotoi* is a tickborne bacterial pathogen responsible for the emerging zoonosis *Borrelia miyamotoi* disease (BMD). Clinically, BMD-infected individuals present similarly to those with Lyme disease but lack the characteristic erythema migrans rash. *Borrelia miyamotoi* was first detected in the United States in 2001, and has since been detected in all regions of the US where Lyme disease is endemic. The first US human cases were diagnosed in 2013, and while no BMD cases have been found in Pennsylvania to date, several cases have been diagnosed in surrounding states. This study aims to determine the statewide prevalence of *Borrelia miyamotoi* -infected ticks in Pennsylvania.

METHODS: During the fall hunting seasons of 2013-2015, 1,990 *Ixodes scapularis* ticks were recovered from white-tailed deer heads submitted to the six Pennsylvania Game Commission regional chronic wasting disease sampling stations located throughout Pennsylvania. The *I. scapularis* ticks were grouped into 409 pooled samples and tested for presence of *B. miyamotoi* via PCR. Maximum Likelihood Estimations (MLE) were used to determine the regional and statewide prevalence rates of *B. miyamotoi* from the pooled tick samples.

RESULTS: Testing results from the 409 pooled tick samples showed the statewide MLE infection rate of *B. miyamotoi* to be 7.64/1000 (95% CI, 4.46-12.29) for *I. scapularis* ticks in Pennsylvania. The MLE infection rates for the six regions from which ticks were collected ranged from 0/1000 in the Southwest region to 16.84/1000 in the Northeast region.

CONCLUSIONS: The results of this study confirm the presence of *B. miyamotoi* -infected ticks throughout Pennsylvania. This finding raises concern from a public health perspective as *Borrelia miyamotoi* disease (BMD) can result in severe illness similar to other tickborne zoonoses also transmitted by *I. scapularis* ticks endemic within the Commonwealth. Given the statewide presence of *B. miyamotoi* -infected ticks, clinicians should be aware of this emerging zoonosis and state and local health departments should consider implementation of surveillance activities for *Borrelia miyamotoi* disease in Pennsylvania.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Epidemiology; Zoonotic Diseases; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9250

Abstract Type Poster

Abstract Title Eastern Equine Encephalitis Virus in the United States, 2003–2016

Abstract

BACKGROUND: Eastern equine encephalitis virus (EEEV) is a zoonotic mosquito-borne alphavirus found in the eastern United States. EEEV infection in humans is rare but can result in severe, often fatal, disease. We report national EEEV surveillance data for 2003–2016, including human disease cases and non-human infections.

METHODS: We reviewed data reported to ArboNET, the national arboviral disease surveillance system. ArboNET collects data on human disease cases, veterinary disease cases, and infections in mosquitoes, dead birds, and sentinel animals. EEEV disease in humans is a nationally notifiable condition; cases are reported using CSTE's arboviral case definition that include clinical and laboratory criteria. Categorical variables were summarized using counts and proportions; continuous variables were summarized by using median and interquartile range (IQR). Incidence rates were calculated using neuroinvasive disease cases and 2010 U.S. Census Bureau data.

RESULTS: Over the 14 year period, 633 counties from 33 states reported EEEV activity; 559 (88%) of those counties reported EEEV activity only in non-human species. Counties reporting activity were located primarily along the Atlantic and Gulf coasts. Of 3,112 veterinary cases reported, 3,016 (97%) were equines. A total of 121 human cases of EEEV disease were reported, with a median of eight cases reported annually (range 4–21). Overall, 99 (82%) case-patients had illness onset during July–September. Eighty-five (70%) case-patients were male. The median age of case patients was 52 years (IQR 13–68 years), but most were aged <20 years (n=36, 30%) or ≥60 years (n=46, 38%). Of the 121 reported cases, 119 (98%) were classified as neuroinvasive disease and 118 (98%) were hospitalized. Overall, 50 (41%) case-patients died; however, 75% (21/28) of patients aged ≥70 years died compared to 31% (29/93) patients aged <70 years (p<0.01). The national average annual incidence of EEEV neuroinvasive disease was 0.03 cases per million population. States with the highest average annual incidence included New Hampshire (0.82 per million population), Massachusetts (0.31), Vermont (0.27), Maine (0.13) and Alabama (0.12). EEEV neuroinvasive disease incidence was highest among males and among persons >60 years.

CONCLUSIONS: EEEV continues to cause rare but serious neurologic infections. Non-human surveillance data indicate the geographic range of the virus is much greater than human cases alone might suggest. In areas where the virus circulates, health-care providers should consider EEEV infection in patients with aseptic meningitis and encephalitis during the summer, and should report suspected cases to their public health department to facilitate diagnosis.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Surveillance; Vectorborne Disease

Consider for Different Presentation? No

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Submission Type Breakout/Quick/Lightning/Poster

ID 9995

Abstract Type Poster

Abstract Title Increase in Reported Rocky Mountain Spotted Fever Cases — Indiana, 2017

Abstract

BACKGROUND: Rocky Mountain spotted fever (RMSF) is caused by the bacterium *Rickettsia rickettsii*, which is transmitted in Indiana by the American dog tick. RMSF is fatal in 5–10% of cases. On June 8, 2017, a fatal RMSF case in a pediatric Indiana resident was widely reported in local, state, and national media. We analyzed surveillance data to determine whether this event had an effect on case reporting.

METHODS: RMSF cases reported to the Indiana National Electronic Disease Surveillance System (I-NEDSS) during 2012–2017 that met the confirmed and probable national surveillance case definitions were analyzed. Because case reports for 2017 were not finalized at the time of this writing, analysis was restricted to cases with specimen collection date during January 1–September 30 for each year for consistency. Overall case counts and proportions of pediatric patients, hospitalized patients, and emergency department (ED) visits for 2017 were compared with the averages for 2012–2016 using chi-square statistics with one degree of freedom. An alpha level of 0.05 was used to determine statistical significance.

RESULTS: During 2012–2016, 155 RMSF cases were reported (average: 31/year; range: 28–38); none were fatal. Specimens were collected before June 8 in 44 (28%) cases (average: 9/year; range: 4–13) and after June 8 in 111 (72%) cases. Twelve (8%) cases occurred in pediatric patients, 38 (25%) were hospitalized, and 60 (39%) patients visited an ED. In 2017, 79 RMSF cases were reported ($X^2=74.32$; $p<0.00001$). Specimens were collected before June 8 in 21 (27%) cases and after June 8 in 58 (73%) cases ($X^2=0.0001$; $p=0.992021$). Six percent of cases occurred in pediatric patients ($X^2=0.005$; $p=0.943628$), 20% were hospitalized ($X^2=0.01$; $p=0.920344$), and 41% visited an ED ($X^2=0.0003$; $p=0.987385$). The case reported in the media was the only fatality.

CONCLUSIONS: There was a statistically significant increase in reported RMSF cases in Indiana in 2017 that began prior to the media reporting of a fatality on June 8. The lack of a statistically significant increase in the proportion of cases reported after June 8 suggests that media coverage had minimal impact on case reporting. The stable proportions of hospitalized cases and ED visits suggests that overall illness severity did not increase in 2017. The cause of the increase in reported cases remains unknown.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Surveillance; Vectorborne Disease; Epidemiology

**Consider for
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Presentation?** Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10117
Abstract Type	Poster
Abstract Title	Investigation of Mosquito Populations in Relation to Human West Nile Virus Case Cluster

Abstract

BACKGROUND: West Nile virus (WNV) was first detected in Virginia residents in 2002. In 2004, a Virginia city reported 4 human cases of WNV, 3 of which were clustered close together. A nearby sewage treatment plant (STP) was identified as a potential source of the vector mosquitoes. Between 2004 and 2016, 4 more human WNV cases were identified in this city, all clustering within a radius of 0.5 to 1.5 miles from the same STP. In response, the Virginia Department of Health (VDH) conducted a mosquito survey at the STP and in surrounding neighborhoods.

METHODS: In 2004, VDH used gravid traps to collect *Culex pipiens/restuans* mosquitoes at the STP and at patient residences. In 2017, the VDH set an array of 23 traps in four concentric groupings, from the STP property out to two miles from the STP to evaluate *Culex* populations and WNV infection rates at different distances from the STP. These trap data were compared to averages collected during the 2004 mosquito survey. Larval surveillance was also conducted at the STP by sampling with 250 ml dippers in the STP's settlement ponds.

RESULTS: The average trap catch at the STP was similar in 2004 and 2017 with approximately 100 mosquitoes collected per trap night. The results from the 2017 survey indicated that trap catches and minimum WNV mosquito infection rates declined at distances > 1 mile from the STP. The results of larval surveillance with 250 ml. dippers revealed that some STP treatment tanks were producing moderate numbers of *Culex* mosquitoes (5 to 10 larvae per dip), but among the STP's large sludge settlement ponds, those that contained surface water yielded at least 100 to 200 larvae per dip for most dip samples taken along the margins of these ponds.

CONCLUSIONS: Based on the known flight ranges of *Cx. pipiens* mosquitoes, the decline in trap catch averages at greater distances from the plant suggests that a significant proportion of the mosquito population, out to one mile or more from the plant, originated from the plant. All 7 of the human WNV cases in the cluster resided within 1.5 miles of the STP. The results of the larval surveillance indicated that the 5 settlement ponds totaling approximately 21 acres of water surface area have the potential to produce tremendous numbers of *Culex* mosquitoes. At least 3 of these ponds contained surface water at the time of our 2017 survey.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Surveillance; Environmental Health
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9675
Abstract Type	Poster
Abstract Title	Kentucky's Participation with Influenza and Zoonoses Education Among Youth in Agriculture Grant

Abstract

BACKGROUND: Novel influenza viruses can emerge after re-assortment of two or more viruses in a host animal. Swine are especially adept at this. Since identified in US pigs in 2010, several swine flu human outbreaks have occurred from exposure to swine at fairs. Other zoonoses can also be transmitted in this setting. Young people with close animal contact are at increased risk for infection and complications from zoonotic diseases. Influenza is one of these diseases of concern. Our objective is to teach the adults that lead the 4-H students, about zoonotic diseases, disease transmission and prevention with a “Train the Trainer” approach, and motivate them to adopt preventive behaviors.

METHODS: The project focused primarily on education regarding influenza prevention in youth from swine and other animal exposure at agricultural fairs. Collaboration was with the University of Kentucky College of Agriculture and their 4-H Extension to develop training opportunities and materials. Training was accomplished with lectures, hands on activities that leaders can repeat with their 4-H students and take home materials. Training effectiveness will be measured by pre and post tests given to the 4-H leaders being trained. The 4-H students’ knowledge will be measured at the annual “Skillathon”. This test 4-H participants take to judge animal knowledge. Skillathon questions are from trainings we provide to 4-H Leaders. Analysis will be based on the mean difference of pre and post tests and Skillathon results. Frequency of test question results will help determine focus for future trainings.

RESULTS: Participant results increased 10% after training. The pre-test average was 84.5% correct, post-test was 95.4% correct (10% increase). In a second training mean, mode and median were all 90%. A pre-test was not given. In test frequency analysis, 15 of 30 participants (50%) answered incorrectly they believed “A key symptom of swine flu is diarrhea”, and 11 of 30 (37%) did not believe “People can also give animals illnesses”. Other questions had better results. A complete breakdown of the questions and answer frequency would be included.

CONCLUSIONS: Knowledge of Zoonotic diseases and especially swine influenza was increased after each training. Information about transmission and prevention of illnesses was increased and measured using the pre-test and post-test methods. Future trainings can be guided by missed test responses. Additional analysis from future trainings will be included in the poster, including results from 4-H participants’ responses in the February Skillathon.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Veterinary Public Health; Influenza / Pandemic Influenza
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9392

Abstract Type Poster

Abstract Title Knowledge, Attitudes, and Practices about Zoonotic Diseases and Novel Influenza Among Adults Involved in Agricultural Fairs in Michigan, 2017-18

Abstract

BACKGROUND: Since 2014, The Michigan Department of Health and Human Services (MDHHS) has received funds from a CDC/CSTE Project Development Grant for Influenza Education among Youth in Agriculture. The funding supports pilot projects designed to educate youth participating in agricultural organizations about zoonotic diseases with public health impact. MDHHS has collaborated with the Michigan State University Extension (MSUE) to educate youth about zoonotic diseases and biosecurity through Michigan 4-H. These relationships proved instrumental in the State's response to an outbreak of H3N2v influenza in swine and people at agricultural fairs in the summer of 2016. In 2017, MDHHS partnered with the Michigan Association of Fairs and Exhibitions (MAFE) to bring information about zoonotic disease prevention to Michigan adult fair organizers and 4-H leaders through a series of meetings organized at the local level.

METHODS: MDHHS and MAFE organized a series of "Zone Meetings" to be held around the state. Meetings were held in the evening to accommodate the mostly volunteer fair workforce. Invitees included local fair organizers and superintendents, fair veterinarians, adult 4-H leaders, MSUE staff, state and local public health staff, and state animal health staff. MDHHS developed survey tools to determine participant's knowledge, attitudes, and practices around zoonotic diseases in the fair setting. Anonymous surveys were administered to all attendees at the beginning and end of each meeting, which consisted of two hours of educational presentations and discussion.

RESULTS: In 2017, six meetings were hosted, with a total of 185 attendees. Pre-meeting surveys show a high level of support for prohibitions on eating or drinking in the swine barns (75%), and providing access to hand washing stations (73%). Relative to pre-meeting surveys, post-meeting surveys show increased knowledge about influenza and increased perception of personal risk of swine influenza. Participant support for disease prevention practices also increased, with support for distance swine auctions rising by 22% (from 16% to 38%) and support for limiting the time swine are kept at the fair to ≤ 72 hours rising by 20% (from 25% to 45%).

CONCLUSIONS: Local fair organizers and stakeholders are broadly supportive of disease prevention practices such as handwashing and not eating and drinking in the swine barns. Knowledge about influenza and support for additional disease control measures at fairs increased significantly after only a single two-hour meeting.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords One Health; Influenza / Pandemic Influenza; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9384

Abstract Type Poster

Abstract Title Mosquito Surveillance and Arbovirus Testing in Kentucky, 2017

Abstract

BACKGROUND: Diseases transmitted by mosquitoes and other arthropods are an important public health concern. Recent outbreak events, such as the Zika virus outbreak that emerged in 2015, have raised public awareness of vector-borne diseases. To better understand the threat of potential mosquito-borne disease events, public health partners in Kentucky initiated a mosquito surveillance program to identify and describe mosquito species present across the state. Prior to 2017, routine statewide mosquito surveillance activities had not been conducted.

METHODS: A multi-agency workgroup, stemming from Kentucky's One Health Awareness coalition, was convened to develop a surveillance strategy. Local health departments (LHDs) in each region were identified to participate in mosquito collection. Each week between June 12 and October 2, environmental health staff at 19 LHDs covering 28 counties set and retrieved mosquito traps at one or more collection sites. LHD staff prepared and shipped specimens to a designated laboratory that performed mosquito speciation and arbovirus testing. Select species were tested for St. Louis Encephalitis virus (SLE), West Nile virus (WNV), or Zika virus based on the anticipated presence of mosquito species and historical disease transmission patterns. Timely mosquito control actions were planned following any positive pools. All data were submitted to the Kentucky Department for Public Health and subsequently reported to CDC's ArboNET and MosquitoNET surveillance systems.

RESULTS: In total, 28 species were identified in 8,015 mosquitoes from 493 mosquito pools. The most commonly identified species was *Culex pipiens* (3,416), a known vector of WNV and SLE. No *Aedes aegypti* mosquitoes, the primary vector of Zika virus, were identified; but many *Aedes albopictus* (1,301), another vector, were collected and subsequently tested. 112 mosquito pools were tested for WNV with 17 testing positive in three distinct geographic areas. 104 mosquito pools were tested for SLE virus with no positives. 120 mosquito pools were tested for Zika virus with no positives.

CONCLUSIONS: This initiative produced valuable information about the distribution of mosquito species in Kentucky. We established a baseline for vector surveillance activities and gained new insight about potential disease vectors. For example, a higher than expected presence of *Culex nigripalpus* (441) was noted in the western half of the state; increasing populations may indicate overwintering is occurring and may precede a rise in human or veterinary disease events. These and other findings will be instrumental in identifying and addressing potential health threats. Continued efforts are planned for summer 2018, building upon knowledge gained in 2017.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords One Health; Surveillance; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10217

Abstract Type Poster

Abstract Title Spatially Associated Coincident and Asynchronous La Crosse Encephalitis – North Carolina

Abstract

BACKGROUND: La Crosse encephalitis (LACE) is the most commonly reported pediatric arboviral encephalitis in the United States. The etiologic agent, La Crosse virus (LACV), is a California serogroup bunyavirus that is transmitted by container-inhabiting *Aedes* mosquitoes, namely *Ae. triseriatus*, *Ae. albopictus*, and *Ae. japonicus*. In North Carolina, LACE is the most common endemic arboviral disease reported in humans, with an average annual incidence rate of 6.22 per million children during 2003-2012. Within the state, the disease geography is highly regional with seven western counties accounting for more than 80% of the confirmed LACE cases since 1997. In August 2017, the NC Division of Public Health was notified of probable LACE in a sibling pair (2 and 11-year-old boys) with exposure likely at the same residence.

METHODS: In response to the sibling cases, an interagency team conducted an environmental assessment of the residence. Because coincident LACE infections in siblings are expected to be rare, we also reviewed 323 confirmed or probable LACE reports in the NC Electronic Disease Surveillance System (NCEDSS) for evidence of additional instances of coincident or residentially linked case pairs from 1997 to 2017.

RESULTS: The environmental investigation identified multiple risk factors associated with the increased risk of LACV transmission at the siblings' residence (e.g., presence of LACV vectors, close proximity to mixed hardwood forest, multiple windows lacking effective screens). The NCEDSS review revealed two additional coincident case pairs (one sibling pair and one caregiver/child pair) linked spatially by place of residence and occurring during the same MMWR epiweeks. We also identified two instances where LACE was confirmed in children residing at the same residence, but during different years (spatially linked asynchronous cases). In one instance the cases had no familial relationship but were linked by residence following a change in homeownership.

CONCLUSIONS: This report indicates that LACV neuroinvasive disease risk is highly focal and disease may occur coincidentally or asynchronously in siblings and non-sibling pairs linked by the same physical residence. Public health agencies should coordinate environmental assessments and modification (e.g., filling tree holes, installing and repairing window or door screens, and removing water filled containers) and consider mosquito control measures when a LACE case is identified. If siblings are present at a newly identified LACE case residence, personal protection measures, sustained mosquito control efforts, and long-term environmental management should be recommended.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10220

Abstract Type Poster

Abstract Title Survey: How Much Do You Know about Zika Virus?

Abstract

BACKGROUND: The Arkansas Department of Health Office of Health Communications conducted a survey in April, 2017 to assess knowledge and risk perceptions of Zika virus among individuals planning to travel to Zika affected areas. The purpose of the survey was to determine interventions to educate key population groups in the state, using mass media communication strategies.

METHODS: A convenience sample of 220 respondents was obtained from those who visited the ArkansasBride.com website, including those who planned to travel to Zika affected areas. Zika affected areas included any country, state, or territory with a travel notice issued by the Centers for Disease Control and Prevention (CDC) prior to the time of travel. The multiple-choice survey questions were designed based on Zika knowledge and risk perception questions used in a Harvard Opinion Poll. Data were managed and analyzed using SAS.

RESULTS: Survey respondents were predominantly female (95%) and aged 21-39 (85%). Respondents reported that they learned about Zika primarily from national/local TV, online news/research, and social media. But the survey results showed that 44% of the respondents knew very little or nearly nothing about Zika; 41% did not know that Zika transmission could occur through vaginal or anal sex and 80% did not know it could occur by having oral sex without condom; and 47% did not know Zika virus infection during pregnancy could cause brain damages in infants. Over 50% of the respondents reported that they planned to be pregnant within next two years or believed getting pregnant was a possibility and 4% reported to be pregnant at the time of survey. Sixty-two percent planned to travel within a year of the survey, of which 47% had not done any research to ascertain Zika status in their destinations. Almost 46% expressed little or no concern of getting infected with Zika during travel. Yet, according to CDC reports, 60% of the destinations chosen by the respondents had evidence of local Zika transmission.

CONCLUSIONS: Survey results revealed gaps in the knowledge of Zika virus infection among women of childbearing age. Results also underscored the need for targeted interventions in educating women potentially planning to travel to Zika affected areas for honeymoon or vacation. Results suggest, future media communications should explicitly focus on improving awareness of modes of Zika virus transmission, adverse outcomes associated with infection during pregnancy, and Zika preventive behavior during travel.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Maternal and Child Health; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9465

Abstract Type Poster

Abstract Title The First 5 Years of National Surveillance for Babesiosis—United States, 2011–2015

Abstract

BACKGROUND: Babesiosis is caused by intraerythrocytic parasites, which are tickborne in nature but also are transmissible via blood transfusion. National surveillance for babesiosis began in January 2011. Health departments in states where babesiosis is a reportable condition notify the Centers for Disease Control and Prevention (CDC) of cases via the National Notifiable Diseases Surveillance System (NNDSS) and using a babesiosis-specific case report form (CRF).

METHODS: We analyzed babesiosis surveillance data available through NNDSS and CRFs for the first 5 years of national surveillance. We combined data for confirmed and probable cases and calculated incidence rates using population data from the U.S. Census Bureau.

RESULTS: For 2011–2015, CDC was notified of 7,612 cases of babesiosis. CRFs were submitted for 7,434 cases (98%). Case counts fluctuated from year to year (1,126 for 2011; 909 for 2012; 1,761 for 2013; 1,742 for 2014; 2,074 for 2015); however, the annual number of reported cases increased 84% from 2011 to 2015. Although the number of states conducting surveillance increased over time from 22 in 2011 to 33 in 2015, the 11 additional states reported a total of only 21 cases (0.3%). Cases were reported by 27 states, 9 of which (CT, MA, ME, MN, NH, NJ, NY, RI, and WI) reported 98% (n=7,495/7,612). Among the 27 states, the 5-year incidence rates by state ranged from <0.01 to 12.0 cases per 100,000 persons, with the highest rates and largest rate increases from 2011 to 2015 in some of the northeastern states. The case-patients' median age was 63 years (range, <1–99 years); 65% were male. Among the 5,930 case-patients with available data, 4,901 (83%) had symptom onset dates during June–August. The median interval from the earliest available patient date (e.g., illness onset or diagnosis date) to the initial submission of data via NNDSS was 87 days and to the submission of CRF data was 369 days.

CONCLUSIONS: The reported cases of babesiosis occurred primarily but not exclusively in residents of the Northeast and upper Midwest, during spring and summer. Changes in incidence rates over time warrant further investigation to identify contributing factors (e.g., changes in tick density or testing/surveillance methods) and inform prevention strategies. Timely and complete surveillance data will enable public health authorities to continue to monitor the frequency and distribution of babesiosis cases. The development of tools for electronic submission of CRF variables is expected to facilitate timely receipt of surveillance data.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Epidemiology; Surveillance; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	10066
Abstract Type	Poster
Abstract Title	Utilizing Human and Sentinel Tick Surveillance Data to Understand Increased Lyme Disease Reporting, West Virginia 2013-2016

Abstract

BACKGROUND: To determine the burden of Lyme disease (LD) in West Virginia (WV), it is important to identify and monitor trends of human case reporting and presence of the tick vector in WV, *Ixodes scapularis* (*IS*). In 2013 the WV Bureau for Public Health began the West Virginia Veterinary Tick Submission Project (WVVTSP), a sentinel surveillance system that engages veterinarians in tick surveillance activities. Data collected from WVVTSP can be used in conjunction with human surveillance to identify areas at risk for increased LD.

METHODS: LD case surveillance data for confirmed and probable cases from 2013-2016 were obtained from the WV Electronic Disease Surveillance System for analysis. WVVTSP participating veterinarians submitted ticks from animal hosts for identification by genus, species, sex, and life stage. A corresponding form containing demographic and geographic information about hosts was also included. *IS* collected during 2014-2016 underwent an initial real-time PCR (qPCR) followed by a confirmatory PCR and sequencing for *Borrelia burgdorferi*.

RESULTS: Human cases of LD increased every year except in 2014 (143 in 2013, 136 in 2014, 289 in 2015, and 368 in 2016). Of these cases, 737 (78%) did not report travel history. County-level distribution of human cases increased from 23 (42%) counties reporting human cases in 2013 to 42 (76%) counties in 2016. Berkeley (n=209), Jefferson (n=124), Morgan (n=111), Hampshire (n=97) and Hancock (n=46) counties reported the most LD cases. *IS* collected through WVVTSP increased each year (12 in 2013, 134 in 2014, 371 in 2015, and 435 in 2016). A total of 547 *IS* were screened for presence of *B. burgdorferi*, of which 11 tested positive of *Borrelia* species by qPCR. Of these 11, 4 were sequenced and confirmed to be *B. burgdorferi*. Four *IS* collected in 2016 from cats in Hardy, Mercer, and Monongalia counties tested positive for *B. burgdorferi*, no travel history was reported outside of home county within two weeks.

CONCLUSIONS: The density of reported LD cases along with detection of LD-positive *IS* suggests an expansion of LD-infected animal hosts into WV counties that border high incidence states of Maryland, Pennsylvania, and Virginia. Sentinel tick surveillance data mirrored human LD case data during the study period, evidenced by marked increases in both the number and distribution of human LD cases reported and *IS* identified. Counties with increasing LD activity in humans and animals should be targeted for LD training and outreach to improve disease recognition and prevention efforts.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9378
Abstract Type	Poster
Abstract Title	What's All the Buzz about- Using Statewide and Regional Mosquito Surveillance Indicators to Predict Human West Nile Virus Risk in Nebraska
Abstract	BACKGROUND: The Nebraska Department of Health and Human Services (DHHS) employs a comprehensive mosquito surveillance program to monitor vector populations and West Nile virus (WNV) activity among them. This study examined the use of mosquito surveillance indicators, specifically percent of pools positive and vector index (VI), to determine which indicator is best suited to determine human risk in Nebraska, both at statewide and regional levels (Central, East, and West). METHODS: Human surveillance data for Nebraska from MMWR weeks 24-40 for the years 2007-2016 was used. Mosquito trapping occurred weekly across the state throughout summer months (MMWR weeks 22-39) each year with half of the participating trap counties trapping on even MMWR weeks and the other half on odd MMWR weeks. A similar number of counties in each Nebraska region were represented during even and odd weeks. <i>Culex</i> mosquitos were identified, counted and pooled for testing using PCR. By using a two week moving window, statewide and regional weekly percent of pools positive and VI values were calculated from the previous two weeks of trapping data. The relationship between these weekly indicators and number of human cases occurring the following week was explored using Spearman's correlation at both statewide and regional levels. RESULTS: Both mosquito indicators showed significant correlation with the number of human cases occurring one week after mosquito sampling ($p < 0.001$) at statewide and regional levels. Moderate ($r_s = 0.40-0.59$) to strong ($r_s = 0.60-1.00$) relationships were seen between weekly percent of pools positive and human cases occurring one week later for statewide ($r_s = 0.83$) and regional data (Central $r_s = 0.61$; East $r_s = 0.52$; West $r_s = 0.71$). Weekly VI data showed similar relationships to the number of human cases occurring one week later at state ($r_s = 0.80$) and regional levels (Central $r_s = 0.54$; East $r_s = 0.55$; West $r_s = 0.69$) when compared to the percent of pools positive. CONCLUSIONS: Active mosquito surveillance has provided weekly indicator data that significantly correlates with human cases. From the data, each indicator was determined to accurately estimate the number of human cases that occur the following week after mosquito sampling in Nebraska, and therefore determine human risk in the state. Using these indicators, threshold values can be established at both state and regional levels to better focus strategies to prevent mosquito exposure several weeks in advance.
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Indicators; Surveillance
Consider for Different Presentation?	No
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Submission Type Breakout/Quick/Lightning/Poster

ID 9341

Abstract Type Quick

Abstract Title An Evaluation of Health Care Provider Suspected Arboviral Reporting in Florida, 2014-2016

Abstract

BACKGROUND: In 2016, Florida had 74 cases of dengue fever, 8 cases of chikungunya fever, and 1,456 cases of Zika fever. Timely reporting of diseases to county health departments (CHDs) is necessary as local introductions of these viruses can occur. Upon report of a suspected dengue, chikungunya, or Zika infection, CHDs notify local mosquito control so proper vector control measures can be initiated. As per the Florida Administrative Code, health care providers and hospitals are required to report all suspected arboviral cases to CHDs immediately.

METHODS: Dengue, chikungunya, and Zika passive surveillance reports dated between January 1, 2014-December 31, 2016 were extracted from Merlin, Florida's reportable disease system, and the electronic laboratory reporting system using their respective disease codes. Sample collection date and CHD reporting date were investigated. An analysis of reports from one county is presented here; analysis will be expanded to examine reporting practices in all 67 Florida counties.

RESULTS: Between 2014-2016, 295 individuals were tested for dengue virus, 175 tested for chikungunya virus, and 1,575 tested for Zika virus. Health care providers notified the CHD first in 129 (43.7%), 90 (51.4%), and 901 (57.2%) of these instances, respectively. Among reports that were entered in Merlin, dengue infections were mostly reported first through laboratory result reports (66.7%). Most chikungunya infections (58.2%) and Zika infections (62.8%) were first reported by health care providers, but the proportion of Zika reports from health care providers decreased over time. For both dengue and chikungunya, there were no changes in reporting practices over time. The average reporting time was 7.2 days after initial suspicion of dengue infection, 6.3 days for chikungunya infection, and 1.6 days for Zika infection; CHDs were notified of suspicion before health care providers obtained laboratory results in greater than 85% of instances. Local cases of dengue and chikungunya and hospitalized cases of chikungunya were associated with faster reporting times. Case pregnancy status was not associated with increased reporting or reporting timeliness.

CONCLUSIONS: Health care provider reporting for the three arboviruses is delayed, with the largest delay in reporting suspected dengue fever cases. More timely reporting was driven by testing; Zika reporting was quicker in the first half of 2016 when all testing occurred at the public health laboratory and CHDs approved Zika testing. After transitioning primarily to commercial testing, health care provider reporting decreased. Increased outreach to health care providers to improve their awareness of disease reporting should occur.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Surveillance; Electronic Case Reporting; Vectorborne Disease

Consider for Different Presentation? Yes

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State Public Health Agency

Submission Type Breakout/Quick/Lightning/Poster

ID 9277

Abstract Type Quick

Abstract Title Assessing the Frequency of False Positive Zika Virus Results Tested at Commercial Laboratories – Florida, January 2016 – December 2017

Abstract

BACKGROUND: The spread of Zika virus (ZIKV) into the Americas presented several challenges, including accurately identifying individuals with the infection. ZIKV is linked to serious birth defects in women infected during pregnancy. Since an estimated 80% of individuals with ZIKV infection are asymptomatic, the need for a sensitive and specific screening test is paramount. ZIKV testing became available to commercial laboratories in June 2016.

METHODS: A total of 634 samples collected between June 2016 and October 2017 were included in this analysis if they were reverse transcriptase-polymerase chain reaction (RT-PCR) or IgM enzyme-linked immunosorbent assay (ELISA) positive at Laboratories A or B with re-testing at a reference laboratory; either the Florida Department of Health Bureau of Public Health Laboratories or the Centers for Disease Control and Prevention (CDC). Positive RT-PCR results were considered confirmed true positives if the acute sample tested RT-PCR positive at a reference laboratory or if an acute or convalescent serum sample tested positive for ZIKV IgM antibodies. Acute and convalescent samples (collected at least five days after an acute sample) that tested negative for ZIKV RT-PCR and IgM at a reference laboratory were designated false positives. Positive IgM ELISA results from Laboratories A or B were confirmed true positives if repeat testing at a reference laboratory was positive for IgM ELISA. A commercial laboratory result was determined to be a false positive if the sample tested IgM ELISA or Plaque Reduction Neutralization Test (PRNT) Zika negative at a reference lab.

RESULTS: The lowest false positive IgM ELISA rate was 59% for both laboratories in 2016 and 2017. The percent of IgM ELISA false positives decreased from 72.6% in 2016 to 59.1% in 2017. For Laboratory B, the percent of ELISA IgM false positives remained constant from 2016 to 2017. The positive predictive value (PPV) for RT-PCR for Laboratory B decreased by 62% from 2016 to 2017 while Laboratory A remained consistently high above 97%.

CONCLUSIONS: Factors such as time of sample collection, cross-reactivity of the IgM antibodies with other flaviviruses or non-specific reactivity, and changes in the type of assay used could affect the accuracy of the tests. Timeliness of accurate results is especially important for pregnant women, a sensitive population due to potential consequences of congenital infection. Providers should be reminded that the Zika IgM test is a screening test only and confirmatory testing should be performed before making a final diagnosis of Zika infection in pregnant women.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9547

Abstract Type Quick

Abstract Title Brucella Abortus Strain RB51: Exposures and Public Health Challenges

Abstract

BACKGROUND: Brucellosis is a zoonotic disease, caused by gram-negative coccobacilli known as *Brucella* spp. In humans, brucellosis can present with non-specific symptoms similar to influenza-like illnesses; with more complicated cases, focal organ involvement is possible. In animals, infection can be asymptomatic or present with non-specific symptoms; fetal loss, stillbirth, fertility issues, and abortion are possible. *Brucella abortus*, *Brucella melitensis*, *Brucella suis*, and *Brucella canis* are commonly known to cause human disease. RB51, a vaccine strain of *B. abortus*, though attenuated, is also pathogenic in humans.

METHODS: We aim to inform the audience about RB51 and associated challenges with human exposures and cases, increase awareness about exposures to RB51 in non-veterinary settings, and provide an overview of post-exposure follow-up guidelines and testing recommendations for RB51 through examples that did not occur in veterinary settings or via travel.

RESULTS: In 2017, the CDC Bacterial Special Pathogens Branch (BSPB) assisted with risk assessment of exposures to RB51 in non-veterinary settings. In February, samples containing RB51 were sent to diagnostic laboratories as part of a clinical proficiency testing panel. These samples were distributed across 134 diagnostic laboratories, 32 states, Bermuda, Trinidad & Tobago, and the US Virgin Islands. In July, BSPB confirmed an isolate from a Texas patient as RB51; this individual's only exposure was to raw milk obtained from a local dairy in Texas. In October, BSPB learned of another case of brucellosis in New Jersey, caused by exposure to RB51 in raw milk acquired from a local dairy on the east coast. Unlike the field strain of *B. abortus*, the RB51 vaccine strain cannot be detected with serological assays. It is also resistant to rifampin, which is a common treatment option for most types of brucellosis. This presents challenges in post-exposure follow-up as well as in testing and treatment for RB51.

CONCLUSIONS: Exposures to RB51 are not limited to veterinary settings, underscoring the need for complete risk factor history when evaluating brucellosis cases. Awareness of the differences in detection and treatment of RB51, compared to other strains of *Brucella*, is vital to proper medical follow-up. Communications strategies targeted towards physicians, health departments, laboratories, and at-risk groups can increase awareness about RB51, potentially mitigating the use of inappropriate testing and treatment.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; Infectious Diseases; Communication

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9513
Abstract Type	Quick
Abstract Title	Ecological and Environmental Factors Impacting Flea-Borne Typhus in Texas

Abstract

BACKGROUND: Twenty-three patients with Murine Typhus were identified in Tarrant County, Texas, USA in 2017. Murine Typhus, a flea-borne disease often transmitted to humans through contact with rats, opossums and cats, is endemic to south Texas and California. Fewer than 5 cases per year were reported in Tarrant County prior to 2016. A new cluster of murine Typhus cases in north Texas represents a possible expansion of the area of endemic Typhus fleas.

METHODS: Murine Typhus is a mandatory reportable disease in the state of Texas. Data of interest for this study will be collected from Texas NEDSS system for 2013-2017. For case identification, we will use the flea-borne typhus Epi Case Criteria 2017 case definition/case classification of the Texas Department of State Health Services. For those identified, we will abstract the medical records to obtain data on demographics and epidemiology; comorbid conditions; symptoms and physical findings; laboratory results, antimicrobial drug treatment; response to treatment; and duration of hospital stay. Additionally, we will review and compare historical weather trends downloaded from National Oceanic and Atmospheric Administration national weather service digital library for the same time period. Basic descriptive statistics will be calculated and comparison between the counts and rates of Tarrant County and Texas murine Typhus cases will be calculated with Fisher exact test or Chi-squared, when appropriate.

RESULTS: Preliminary analysis of the 41 Typhus-positive patients showed, 59% were female; 93% were white and 20% were Hispanic. Ages ranged from 7 to 79 years, with an average of 35.3 years of age. A review of the case investigations showed that 49% of patients had some relevant animal exposure, most commonly to dogs or cats. Four people during this period reported exposure to an opossum, and 22% of reports noted fleas in the investigation. Only two patients recalled travelling outside of Tarrant County during the exposure period, reaffirming local transmission.

CONCLUSIONS: In this study, we will describe the epidemiological and environmental features of a newly emerging vector-borne infectious disease in north Texas. With the increase in reported cases and geographic expansion, we want to highlight the importance of raising healthcare providers and the public awareness to identify and treat suspected cases of murine Typhus.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Infectious Diseases; Vectorborne Disease; Environmental Health
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9398

Abstract Type Quick

Abstract Title Evaluation of Access to Care and Pregnancy Outcomes of Pregnant Zika Cases Reported to the Florida Department of Health, January 2016 – December 2017

Abstract

BACKGROUND: Exposure to Zika virus (ZIKV) during pregnancy can result in fetal abnormalities. In the continental U.S., Florida has one of the highest numbers of pregnant women exposed to ZIKV either through travel or local exposure. Due to the potential impact on fetal health, it is essential that these women are aware and have access as needed to pre- and post-natal care programs, such as Healthy Start and Early Steps.

METHODS: Data were obtained from the Florida Department of Health (FDOH) Merlin reportable disease system. ZIKV infection cases involving pregnant women or their infants were identified between January 1, 2016 and December 12, 2017 using national criteria developed by the Centers for Disease Control and Prevention and the Council of State and Territorial Epidemiologists. Processes to ensure connection with care were developed by FDOH and tracked in Merlin.

RESULTS: Four-hundred twenty pregnant women were identified as ZIKV infection cases in Florida. Of those pregnant women, 348 (83%) were connected to prenatal care and 335 (80%) were connected to Healthy Start. Thirty-four (8%) cases were not referred to any additional services, due to lost to follow-up (29) or patient refusal (5). As of December 12, there were 371 (88%) live births, 15 (4%) fetal losses, 17 (4%) ongoing pregnancies, and 17 (4%) lost to follow-up. Eighty-four percent of infants were tested for ZIKV. Of the travel-associated cases, 8 out of 286 (2.8%) had liveborn infants with laboratory evidence of congenital ZIKV infection compared to 1 out of 30 cases (3.3%) with local ZIKV exposure. Fifty-five livebirths were born to women with ZIKV exposure that could have occurred in Florida or outside of the continental U.S. None of these women had infants with laboratory evidence of congenital ZIKV infection. Of the nine infants with demonstrated congenital ZIKV infection, seven had congenital symptoms such as microcephaly (6), limb anomalies (2), and intracranial calcifications (2). All nine congenitally infected infants were referred to the Early Steps program. Additionally, three fetal losses, delivered to women with travel-associated exposure, tested positive for ZIKV infection.

CONCLUSIONS: Nearly all ZIKV positive pregnant women (92%) were advised of local pre- and post-natal care programs and most chose to use these types of services. Fortunately, more than 96% of all liveborn infants appeared healthy and tested negative for ZIKV at birth. Ensuring families are informed of local resources will help facilitate identification and management of any delayed congenital symptoms in ZIKV positive infants.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infant Health; Infectious Diseases; Maternal and Child Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9815

Abstract Type Quick

Abstract Title Evidence of Powassan Virus (POWV) in Adult Black-Legged Ticks (*Ixodes scapularis*) Recovered from Hunter-Harvested White-Tailed Deer (*Odocoileus virginianus*) Heads in Pennsylvania

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 meningoencephalitis in humans. POWV is transmitted by the black-legged tick, *Ixodes scapularis*. In recent years the incidence of POWV infection in humans appears to be increasing, and there have been over 100 cases of POWV disease reported in the United States since national surveillance began in 2003. There have been a total of four human cases of POWV reported to the Pennsylvania Department of Health, one case in 2011 and three cases in 2017. The aim of this study was to determine if POWV was circulating in Pennsylvania *I. scapularis* tick populations.

METHODS: During the late Fall of the 2013, 2014, and 2015 hunting seasons, adult ticks were recovered from hunter-harvested white-tailed deer (*Odocoileus virginianus*) heads presented to the six regional Pennsylvania Game Commission chronic wasting disease sampling stations. Ticks identified as adult *I. scapularis* were grouped into pooled tick samples by year and region of collection. Real time polymerase chain reaction testing was performed to determine the presence of POWV. Ticks making up a positive pool were then tested individually for POWV.

RESULTS: During 2013-2015, 1,990 adult *I. scapularis* ticks were recovered from 9,930 hunter-harvested white-tailed deer. One of 409 (0.2%) pooled tick samples tested positive for POWV. Subsequent testing identified a single positive tick, recovered in 2014 from the southeast region of Pennsylvania. 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 *I. 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, it is imperative for primary care physicians to become familiar with signs and symptoms of this emerging pathogen in order 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.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease; Zoonotic Diseases; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9082
Abstract Type	Quick
Abstract Title	First Report of <i>Yersinia Pestis</i> Transmission to a Human from the Bite of a Gunnison's Prairie Dog (<i>Cynomys gunnisoni</i>)

Abstract

BACKGROUND: The use of a One Health approach to zoonotic disease investigations aids in identifying unusual routes of zoonotic disease transmission. The state of New Mexico has the highest rates of human and animal plague (*Yersinia pestis*) infection in the United States. The New Mexico Department of Health (NMDOH) Zoonotic Disease Team investigates every suspect, probable, or confirmed case of animal or human plague in the state. These investigations have detected novel means of bacterial zoonoses transmission including the first documented case of plague transmission to a human from a wild prairie dog bite.

METHODS: By state statute, every confirmed or suspected case of *Yersinia pestis* infection of humans or animals must be reported emergently to NMDOH. The Zoonotic Disease Team investigates each report using standardized data collection tools. An environmental investigation is conducted at the site(s) of possible exposure, and detailed interviews and history are collected from the patient, family member/next-of-kin, animal owner, medical provider, and/or veterinarian as appropriate. Confirmatory testing by PCR, culture, or serology is performed by New Mexico's Scientific Laboratory Division (SLD).

RESULTS: A contractor hired to relocate wild Gunnison's prairie dogs (*Cynomys gunnisoni*) from an airport in a plague-endemic area to a national wildlife refuge in another part of the state developed plague, with right axillary bubo, after a bite to the right hand from an animal in a quarantine facility. The human infection was discovered by Zoonotic Disease Team staff after the biting animal died and tested positive for *Y. pestis* at SLD. The patient did not seek medical care until encouraged to do so by NMDOH epidemiologists. Genomic analysis found no difference in *Yersinia pestis* isolates from the human and the prairie dog. The animals and their holding area had been treated with insecticide and no evidence of fleas or flea bites were found.

CONCLUSIONS: Environmental investigation and in-person interviews are valuable tools in zoonotic disease investigations. Collecting both human and animal data, in accordance with a One Health approach, can provide valuable information about risk and exposure to disease. This case of *Y. pestis* infection caused by the bite of a wild animal highlights that safety precautions should be taken against zoonotic disease by anyone in contact with wild animals. The risks inherent in translocating animals from a zoonotic disease endemic area should be carefully considered.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Vectorborne Disease; One Health
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10224
Abstract Type	Quick
Abstract Title	Francisella Tularensis Transmitted through Solid Organ Transplantation – Environmental Investigation and Follow-up Preventive Measures

Abstract

BACKGROUND: Tularemia is a zoonotic infection that occurs sporadically throughout the United States. Human infection can occur via direct contact with infected animal tissue, tick or deerfly bite, inhalation of infectious aerosols, or other routes. Human-to-human transmission has never been reported. In July 2017, two kidney recipients from a common donor developed *F. tularensis* sepsis. Archived tissue from the organ donor was subsequently cultured and also grew *F. tularensis*. Strain typing and whole genome sequencing confirmed the isolates from the organ donor and two recipients were indistinguishable *F. tularensis* A2 strains, demonstrating that infection was transmitted by solid organ transplant. In collaboration with the Centers for Disease Control and Prevention (CDC) and other federal, state, and local health agencies, the Southern Nevada Health District (SNHD) initiated an epidemiologic investigation to identify a potential environmental exposure source for the donor and mitigate any ongoing risk to other community members.

METHODS: Medical records from all patients were reviewed. The organ donor's family members were interviewed to capture additional information about his illness and potential exposures to *F. tularensis*. A team of disease investigation and environmental health specialists worked with community leadership to conduct an environmental investigation near the organ donor's residence and search for signs of animal die-off or prominent vector activity.

RESULTS: The organ donor was hospitalized in June 2017 for acute alcohol withdrawal syndrome, fever, pneumonia, and sepsis; and died 12 days after admission. Interviews with his family members did not reveal an obvious exposure source for tularemia; however, two rabbit carcasses were found near his residence and tested positive by PCR for *F. tularensis* type A (A2). To prevent illness due to exposure to infected animals, an educational presentation and fact sheets were provided to residents in the organ donor's community. A fact sheet for health care providers was distributed via the state Health Alert Network to improve awareness and recognition of potential cases.

CONCLUSIONS: Environmental investigation following the first reported tularemia transmission through solid organ transplantation helped identify a likely source of exposure for the organ donor. Two rabbit carcasses with evidence of *F. tularensis* infection suggest a recent epizootic near the organ donor's home. Although the specific route of the donor's infection could not be identified, infection could have been transmitted by inhalation, direct inoculation of the skin by infected tissue, or arthropod bite. Environmental investigation also helped target direct educational efforts to protect community members.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Risk Assessment; Collaboration
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9422
Abstract Type	Quick
Abstract Title	Health Care Provider Prescription Practices of Treatment for Confirmed and Probable Rickettsial Diseases Reported to the Florida Department of Health, 2015-2016
Abstract	BACKGROUND: Rickettsial diseases are a group of bacterial infections that can lead to severe medical complications and ultimately death if not treated promptly. Thus, the Centers for Disease Control and Prevention (CDC) recommends treatment with doxycycline upon suspicion of a rickettsial infection, rather than waiting until test results are reported. Three tickborne rickettsial diseases, anaplasmosis, ehrlichiosis, and Rocky Mountain spotted fever/spotted fever rickettsioses (RMSF/SFR) are reportable in the state of Florida. Florida is a low-incidence state for these diseases; therefore, health care providers in Florida often do not see many cases and may be unfamiliar with CDC treatment recommendations. This study analyzes health care provider treatment practices for rickettsial illnesses reported to the Florida Department of Health. METHODS: Confirmed and probable cases of anaplasmosis, ehrlichiosis, and RMSF/SFR reported between January 1, 2015 and December 31, 2017 were reviewed in Merlin, Florida's reportable disease database. Case classification was based on national case definitions published by the Council of State and Territorial Epidemiologists. Data collected included antibiotic recommended, prescription date, date of sample collection for rickettsial disease testing, number of health care visits during illness, and the state in which treatment was recommended and provided. RESULTS: Eighty-seven cases of rickettsial diseases were reported; 53 cases (61%) were treated in Florida and had laboratory and treatment information. Fifty-one cases (96%) were prescribed doxycycline, one (2%) was prescribed other antibiotics due to doxycycline allergy, and one (2%) was not prescribed antibiotics. Of the 53 cases, six (11%) were treated after laboratory results were reported. These cases were treated an average of 3.5 days after seeking care. In addition, nine cases (17%) were not treated at the first health care visit, and consulted with two to four health care providers before rickettsiosis was considered. Eight of these nine cases were hospitalized before receiving appropriate treatment. One of the 53 cases reviewed died, however treatment delay was attributed to the case not seeking care immediately. CONCLUSIONS: The majority of rickettsiosis cases were prescribed doxycycline before lab results were reported and on the first health care visit. However, nearly 30% of cases experienced delays in diagnosis and treatment. In eight cases (15%), these delays likely resulted in more severe illness and hospitalization. Additional outreach to providers is planned to increase awareness of tickborne rickettsiosis and CDC treatment recommendations, particularly in counties where delays in diagnosis and treatment were reported.
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Standards; Vectorborne Disease; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9545

Abstract Type Quick

Abstract Title Human Tularemia Associated with Exposure to Domestic Dogs — United States, 2006–2016

Abstract

BACKGROUND: Tularemia is a potentially serious zoonotic infection caused by the gram-negative coccobacillus, *Francisella tularensis*. Human infection via cat bite is well documented; however, the role of dogs in transmitting infection is much less understood. The objective of this study was to characterize the scope and patterns of human tularemia cases with exposures linked to domestic dogs to promote health care provider and public awareness and targeting of prevention methods.

METHODS: We reviewed available confirmed and probable human tularemia case investigation records supplemental to national electronic surveillance data from 2006–2016 and extracted those with potential evidence of domestic dog involvement – specifically, history of a pet dog that was recently ill, died, or brought home dead animals, or written comments that provided other evidence of dog-related exposure to *F. tularensis*. Two independent reviewers further evaluated the records in detail to select those demonstrating probable or possible dog-related *F. tularensis* exposure based upon strength of available evidence.

RESULTS: Among 735 tularemia case investigation records reviewed, 24 (3.3%) were identified as dog-related. Median age of patients was 51 years (range: 1–82); 54% were female compared with 32% of all reported cases. Two-thirds (67%) of cases were ulceroglandular/glandular in presentation followed by pneumonic (13%) and oropharyngeal (13%). Among 20 patients with known clinical outcomes, 18 (90%) recovered from illness and two (10%) died. Illness was attributed to three main exposure types: direct contact via dog bites, scratches, or face snuggling/licking (n = 12; 50%), contact with dead animals retrieved by domestic dogs (n = 8; 33%), and dogs bringing infected ticks into contact with humans (n = 4; 17%). Four (17%) case records indicated exposure to ill dogs, but only one dog was evaluated for laboratory evidence of exposure to *F. tularensis*.

CONCLUSIONS: Although uncommon, dog-related tularemia infections highlight specific modifiable risk factors for pet owners. Veterinarians play a key role in ensuring that pet owners are aware of these risks and opportunities for disease prevention, including use of appropriate tick-control products on dogs, precautions in disposal of animal carcasses retrieved by dogs, caution in direct facial contact with pets who hunt or roam, and seeking veterinary care for ill pets. Using a One Health approach to tularemia case investigations, public health officials should be alert to the potential for dogs as a source of human infection and encourage veterinary evaluation of dogs linked to human cases.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords One Health; Vectorborne Disease; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 10198

Abstract Type Quick

Abstract Title Innovative Strategies for Patient Contact Following Bat Exposures

Abstract

BACKGROUND: Rabies in humans is almost 100% fatal once symptoms develop. Therefore it's vital to treat anyone potentially exposed to rabies with rabies post exposure prophylaxis (RPEP). The Kentucky Department for Public Health received a weekend consult regarding RPEP for girls who woke up to a bat in their cabin during a one week camp. Further investigation revealed exposure occurred to three different groups of campers from throughout the state over three weeks. Preventing rabies is crucial, but it's also important not to give RPEP indiscriminately due to side effects, cost and availability. Each camper was contacted and interviewed to determine bat exposure, rabies risk and need for RPEP. Contact information was lacking for most campers. Innovative strategies were employed to ensure 100% contact.

METHODS: Interviews were conducted by phone, each camper was assigned a risk category of "high" (direct bat contact, awoke to the bat, slept on top bunk, deep sleeper, on medications), "medium" (unsure of contact, asleep on lower bunk) or "low" (awake, in another room). High or medium risk campers were encouraged to get RPEP, whereas low risk campers were not recommended for RPEP. This private camp did not keep contact information on campers and three different camp leaders had only partial information. The State Health Operations Center was activated to coordinate the response between state and 16 different Kentucky counties. University of Kentucky students, epidemiologists, nurse investigators, and STD investigators assisted with interviewing. School-based data bases, social media and Lexus-Nexus background databases were used to gather information.

RESULTS: 100% contact of campers was achieved. A total of 87 campers were potentially exposed with 39 (44.8%) receiving RPEP. Of those, seven were not recommended RPEP, but chose to, three refused interviews, six were high risk and did get RPEP, one of medium risk refused RPEP.

CONCLUSIONS: Innovative strategies were employed to reach all potentially exposed campers. Our goal of 100% contact was achieved using a variety of contact methods and organizations to assist in locating and contacting each family. This brought to light that the campground did not maintain proper documentation on campers. Were they licensed and following state law, information would have been available, campers could have been contacted in a timely and efficient process. The collaboration of different departments and communication between health departments was essential to protecting the campers. Using the State Health Operations Center and ICS structure was vital in orchestrating our response.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; Infectious Diseases; Veterinary Public Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9280

Abstract Type Quick

Abstract Title Inpatient Hospitalizations of Zika Virus Cases in Florida

Abstract

BACKGROUND: In 2016, Florida had the second highest number of imported Zika virus (ZIKV) infection cases and was the first state with local ZIKV transmission. Most infections are asymptomatic and clinical illness is usually mild with symptoms lasting for several days to a week. Severe disease requiring hospitalization is considered uncommon and ZIKV related deaths are rare. A potential association between ZIKV infection and Guillain-Barré syndrome (GBS) has also been reported.

METHODS: Data from the Florida Department of Health reportable disease reporting system and data collected through medical record review were used to summarize inpatient hospitalizations for cases of ZIKV disease between 1/1/16-11/14/17. Hospitalizations for congenital ZIKV disease cases were not included in this analysis.

RESULTS: Thirty-two cases were hospitalized following development of Zika-like illness (2.5% of all disease cases reported). Onset dates ranged from 1/8/16-10/19/17. The majority of hospitalized cases were female (63%), white (84%), Hispanic (66%), and ranged in age from 1-81 years (median 45 years). ZIKV ribonucleic acid was detected by polymerase chain reaction for most hospitalized cases (81%). Cases commonly reported fever (94%), rash (91%), arthralgia (59%), conjunctivitis (56%), myalgia (41%), and diarrhea (38%). Hospitalized cases were more likely than non-hospitalized cases to report fever (OR 6.93) and diarrhea (OR 6.99). Two confirmed cases met GBS criteria (one level 2 and one level 3), with lower extremity weakness beginning 5-7 days after symptom onset. Three hospitalized cases reported paresthesias starting 5-10 days after symptom onset; one tested positive for Zika IgM antibodies in cerebral spinal fluid. Additional workup at the hospital identified 13 cases with leukopenia, seven with thrombocytopenia, and nine with elevated liver enzymes. Length of stay ranged from 1-18 days (average 3.2). Most cases were admitted with a differential diagnosis of febrile illness or viral syndrome. Several cases were also evaluated for upper respiratory infection, pneumonia, or gastroenteritis based on reported symptoms. Some also tested positive for influenza (1), rhinovirus/enterovirus (2), or coronavirus (1). Half of the cases (53%) had underlying medical conditions. Hospitalized cases were first reported to the county health department by health care providers (72%), followed by laboratories (22%).

CONCLUSIONS: Hospitalizations due to ZIKV infection were uncommon in Florida and most cases had a short length of stay. Co-infections, symptoms consistent with other illnesses, and both common and uncommon symptoms may complicate ZIKV diagnosis. Physicians should consider Zika fever when evaluating patients with travel to areas where the virus is active.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9291

Abstract Type Quick

Abstract Title Kissing a Chick Will Make You Sick: A Fowl Outbreak of Salmonella

Abstract

BACKGROUND: Live poultry is a common source for the transmission of *Salmonella* bacteria to humans. Maintaining a backyard flock of chickens, ducks, turkeys or other poultry has become a popular activity in recent years. The 2017 multi-state *Salmonella* outbreak associated with live poultry exposure, 1704MLTDK-1, is the largest to date with 1120 reported cases. Eighteen (1.6%) of these cases occurred in Vermont, where an increase in *Salmonella* infections associated with live poultry has been reported in the last two years. The objective of this study was to identify additional risk factors for human *Salmonella* infections associated with live poultry in Vermont and to inform targeted interventions.

METHODS: Confirmed salmonellosis cases with live poultry exposure or with indistinguishable pulsed-field gel electrophoresis (PFGE) patterns for known implicated isolates during 2011–2017 were included. Patients were interviewed using a poultry-specific questionnaire developed by the Centers for Disease Control and Prevention (CDC). Information from case interviews was reviewed and summarized to consider potential risk factors, such as patient age and poultry housing practices.

RESULTS: During 2011–2017, 59 cases of salmonellosis associated with live poultry exposure were reported in Vermont; a median of 5 cases per year (range, 2–20). The highest number of cases (n=20, 34%) occurred in 2016, a 5-fold increase from the previous year. Of the 56 cases with complete sex information, 55% were female. Fifty-seven cases had complete age information, for which 42% were in children less than 10 years of age; median patient age was 21 years (range, 0–73 years). Of the 40 cases with complete chick count data, 95% reported owning less than 25 chicks. Of those with peridomestic exposure (n=44), 77% reported keeping poultry inside the house.

CONCLUSIONS: Salmonellosis cases associated with exposure to live poultry in Vermont have increased during 2016–2017. The disproportionate burden of disease among children is likely due to more frequent physical contact with juvenile poultry, closer interactions with birds such as hugging and kissing, and less stringent personal hygiene practices including infrequent hand washing. Targeting backyard flock owners with messaging to always wash hands thoroughly right after touching live poultry or anything in their environment, supervise children during poultry interactions and hand washing, and to refrain from keeping poultry indoors could help reduce the number of salmonellosis cases in Vermont.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Outbreaks; One Health; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9299
Abstract Type	Quick
Abstract Title	Knowledge, Attitudes, and Beliefs about Agritourism and Zoonotic Diseases Among Minnesota State Fair Attendees, 2016

Abstract

BACKGROUND: Agritourism continues to grow in popularity as a source of supplemental farm income. Although agritourism provides an important opportunity for the public to learn about animals, food production, and the importance of agriculture, there is also risk for zoonotic enteric disease transmission to visitors. The *Compendium of Measures to Prevent Disease Associated with Animals in Public Settings* provides national best practices for operators; however, it is unclear to what extent how well or uniformly these practices have been adopted. We conducted a survey to measure health behaviors and baseline knowledge of agritourism and zoonotic diseases among Minnesota State Fair attendees with and without an agricultural background.

METHODS: An anonymous survey was administered via iPad to a convenience sample of Minnesota State Fair attendees. The survey contained questions regarding participants' agricultural background, conceptual knowledge of agritourism, knowledge of zoonotic diseases, hygiene practices, and demographics.

RESULTS: There were a total of 1,105 survey respondents, and 318 (29%) had an agricultural background. Overall, 829 (89%) respondents knew that animals and people could share diseases, 627 (58%) knew these pathogens could be transmitted fecal-orally, and 1064 (97%) knew handwashing was the best way to prevent illness. Only 674 (61%) understood that hand sanitizer and handwashing were not equally effective. Of all participants, 413 (37%) individuals were familiar with the term agritourism, but this differed significantly between those with and without an agricultural background (46% vs. 34%, $p < 0.001$). Overall, 40% of respondents had visited an agritourism venue in the past 12 months. Of those who attended an agritourism venue, 388 (35%) reported not washing their hands; the most common reason given was the inability to find handwashing stations ($n=131$, 34%). Only 28% of respondents could correctly identify activities that can make people sick while visiting animals, and only 31% were able to correctly identify groups at highest risk for severe illness. The ability to identify "high risk" groups differed significantly between those with and without an agricultural background (25% vs. 34%, $p = 0.008$).

CONCLUSIONS: General knowledge about zoonotic diseases and handwashing among respondents was high. However, reported barriers to handwashing indicated that greater access to handwashing stations and education around the importance of handwashing still remain important issues. There was a lack of specific knowledge regarding high risk behaviors and high risk populations. Educational efforts should focus on recognition of high risk activities and "high risk" groups to raise awareness, the first step in prevention.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Behavioral Health; Disease Prevention
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	9211
Abstract Type	Quick
Abstract Title	Postexposure Prophylaxis Use Among Veterinary Staff Exposed to Tularemia-Infected Animals — Wyoming, 2012–2017

Abstract

BACKGROUND: Tularemia, a bacterial zoonosis caused by *Francisella tularensis*, is a reportable disease in Wyoming. Because animal tularemia is an occupational risk to veterinary staff, the Wyoming Department of Health (WDH) recommends antibiotic postexposure prophylaxis (PEP) for high-risk exposures (e.g., bodily fluid contact or aerosol inhalation). However, anecdotal reports indicate PEP might be overused among veterinary staff. Because PEP patterns for occupational tularemia exposure are poorly understood, we evaluated PEP use involving animal contact among veterinary staff in Wyoming.

METHODS: We invited staff from the 9 veterinary clinics with animals having laboratory-confirmed tularemia infection reported during 2012–2017 to complete a questionnaire electronically or by phone regarding nature of exposure, use of personal protective measures (PPM), and use of PEP. Risk for infection (high or low) was assigned based on exposure type and PPM use. We analyzed frequencies of animal exposures, correct PPM use, individual risk, and PEP.

RESULTS: Thirteen veterinary staff from 6/9 (67%) clinics completed the survey. The three most commonly reported interactions included petting (6/13; 46%), restraining the animal (5/13; 38%), and performing a physical exam (5/13; 38%). Protective measures reported included handwashing after touching the animal (8/13; 62%) and wearing gloves (6/13; 46%). One veterinarian (8%) was at a high risk for contracting tularemia based on exposure type (performed a necropsy) and incomplete PPM use (gloves, but no face mask or goggles), but did not seek health care for PEP. However, 7/13 (53.8%) respondents reported using PEP despite low-risk exposures.

CONCLUSIONS: PEP was used incorrectly among veterinary staff exposed to tularemia-infected animals. Provider education and consultation with WDH can help to identify high-risk exposures and need for PEP while reducing incorrect use. WDH will create a letter for veterinary clinics on potential exposure notifications and an algorithm for health care providers for use of PEP.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Veterinary Public Health; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 9067

Abstract Type Quick

Abstract Title Prevalence of *Francisella Tularensis* in Minnesota *Dermacentor Variabilis* Ticks, 2017

Abstract

BACKGROUND: Human and animal cases of tularemia in Minnesota have increased in the last 2–3 years. *Dermacentor variabilis* (American dog tick) has a suspected role in the enzootic cycle and transmission of *Francisella tularensis* (FT) to humans; however, the prevalence of FT in this tick species in Minnesota is unknown. In 2017, we collected *D. variabilis* ticks at an apparent tularemia epizootic site, and other sites, to determine the prevalence of FT in *D. variabilis* populations.

METHODS: *D. variabilis* ticks were collected from two adjacent properties at an epizootic site weekly from May 11 through July 6, 2017. *D. variabilis* ticks were also incidentally collected from five routine *Ixodes scapularis* surveillance sites across Minnesota (sites A-E). Ticks were collected into vials of 70% ethanol then sorted by species, life stage, and sex, and pooled (maximum, 10 ticks/pool). Ticks were bisected and homogenized; supernatant was tested by real-time PCR for FT. Additional live ticks were collected during two weeks, and the supernatant plated for culture. The minimum infection rate (MIR) with FT was calculated for each site.

RESULTS: A total of 3,527 adult *D. variabilis* ticks were collected and tested for FT, including 1,601 males and 1,926 females. Across all sites, 128 (34%) of 378 pools were FT-positive (range, 0–66% of pools per site). The epizootic and two other sites had FT-positive pools. The MIR was 4.1% across all positive sites (range, 2.1–7.2% per site). FT was isolated from 10 (25%) of 40 pools by culture (MIR=2.7%). Ninety-six (75%) of the 128 FT-positive pools were able to be subspeciated and all were FT type A. The MIR significantly differed by week at the epizootic site and site B, but not at site A. The MIR was significantly lower at the epizootic site compared to site A (3.9% vs. 7.2%, $p=0.01$) but was not significantly different between the epizootic site and site B (3.9% vs. 2.1%, $p=0.49$). Within the epizootic site, the MIR was significantly higher at the second property compared to the other property (5.7% vs. 2.3%, $p<0.001$).

CONCLUSIONS: The MIR of FT in *D. variabilis* ticks varied temporally and geographically, but the variation was relatively small (0–10%). Our findings support the hypothesis that *D. variabilis* plays an important role in the natural history of tularemia in Minnesota. Further ecologic studies are needed to better understand the importance of this and other tick species in the maintenance and transmission of FT in Minnesota.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Epi / Lab Capacity (ELC); Zoonotic Diseases; Vectorborne Disease

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9759

Abstract Type Quick

Abstract Title Rabies Postexposure Prophylaxis Among Persons with Known Rabies Exposure — Wisconsin, 2013–2015

Abstract

BACKGROUND: Rabies is a zoonotic virus that is usually fatal. Persons with rabies exposure receive postexposure prophylaxis (PEP) with rabies immunoglobulin (RIG) and 4 or 5 rabies vaccine doses; persons with prior completed vaccination receive 2 booster vaccinations without RIG. In Wisconsin, rabies PEP is not reportable, but providers can report vaccine and RIG administration in the Wisconsin Immunization Registry (WIR). The Wisconsin State Laboratory of Hygiene performs all nonhuman rabies testing. We examined PEP completion among Wisconsin residents with exposure to animals with laboratory-confirmed rabies.

METHODS: Records of animals with laboratory-confirmed rabies during 2013–2015 and WIR data for PEP receipt were reviewed. A case was defined as receipt of PEP within 14 days of an animal being received for rabies testing in a resident who matched name in both datasets or found to be exposed on follow-up. PEP completion was defined as RIG receipt within 7 days of vaccine initiation and vaccination on Days 0, 3, 7, and 14, or on Days 0 and 3 if previously vaccinated. Cases with incomplete WIR-documentation were followed-up with local health departments or medical record review.

RESULTS: During 2013–2015, 81 animals tested positive for rabies, including 41 (51%) tested because of human exposure; 35 persons matched in WIR, including 3 previously vaccinated persons. Median age was 38 years (range: 1.9–89 years). Median time between exposure and PEP initiation was 3 days (range: 0–8 days). WIR and medical records confirmed PEP completion for 25/29 (86%) persons; 4 persons did not receive RIG; records were unavailable for 6 persons.

CONCLUSIONS: Persons with rabies exposure received PEP within 8 days of exposure; however in 4 cases RIG was not administered. Although no illnesses resulted, incorrect PEP administration is concerning and highlights the need for public health involvement and clinician education.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type	Breakout/Quick/Lightning/Poster
ID	9305
Abstract Type	Quick
Abstract Title	Rapid Rule-out of Local Vector-Borne Zika Transmission in a Household, Los Angeles County, California

Abstract

BACKGROUND: Cases of Zika virus have been identified in Los Angeles County (LAC) as well as the species of mosquito that is capable of transmitting Zika virus. In October of 2016, the LAC Department of Public Health (DPH) Acute Communicable Disease Control Program (ACDC) identified Zika-like illness in two household members of Zika virus case, prompting concerns of local vector-borne Zika transmission.

METHODS: The ACDC program 1) interviewed the case and ill household members for illness history, symptoms and Zika risk factors 2) requested the local vector control agencies to assess the neighborhood for the presence of aedes mosquitos 3) request Community Health Services program staff to provide education and collect specimens on household members 4) notify DPH laboratory of the testing priority of collected specimens.

RESULTS: The case (Zika RNA positive) interview was completed one day after DPH received the laboratory report (Day 1) for this case resident. The case reported being symptomatic after returning to the US from a Zika affected area (Day 2). The case also reported two adult household contacts (HHC), both ill with Zika-like symptoms eight days after the case's return to the US. HHC1 reported conjunctivitis, coughing, sneezing and sore throat. HHC2 reported conjunctivitis, fever, chills and sore throat. HHC1 also reported having unprotected sexual contact with the case in the week prior to onset, suggesting possible sexual transmission of Zika. Neither HHCs had recently travelled to a Zika-affected area. *Aedes aegypti* mosquitos had been identified within five miles of the case's residence earlier in the year. Over 100 properties were inspected and mosquito traps (ova cups) were placed around the case's residence (Day 2). No *Aedes* were observed at any stage of growth and Ova cups were negative (Day 5). CHS nurses to obtain urine specimens from the HHCs for Zika testing (Day 4). Both HHCs tested negative for Zika virus RNA, with testing performed by LAC Public Health Laboratory (Day 7).

CONCLUSIONS: The investigation found no evidence suggesting local transmission had occurred in this household. Rapid communication and collaboration among multiple LAC DPH departments and other governmental agencies was required to assess the risk of local vector-born transmission. This assessment was completed within one week of the DPH notification of the case.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Zoonotic Diseases; Vectorborne Disease
Consider for Different Presentation?	Yes
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Submission Type Breakout/Quick/Lightning/Poster

ID 10172

Abstract Type Quick

Abstract Title Surveillance for a Newly Recognized Tickborne Disease: A Description of *Borrelia Miyamotoi* Infections in Vermont

Abstract

BACKGROUND: *Borrelia miyamotoi* is a newly recognized tickborne disease in the United States. The first reported case occurred in 2013 and fewer than 60 well-documented cases have been recorded by the Centers for Disease Control and Prevention (CDC). In June 2016, the Vermont Department of Health began receiving *Borrelia miyamotoi* laboratory results from a commercial laboratory specializing in tickborne disease testing. Surveillance activities were initiated to capture standardized information on Vermont residents reported with this disease.

METHODS: A review of the biomedical literature was conducted to identify symptoms and clinical outcomes associated with previously documented *Borrelia miyamotoi* infections. A case report form was developed to capture information on patient demographics, symptoms, clinical and laboratory findings, exposure history and treatment regimens. Laboratories were asked to submit positive *Borrelia miyamotoi* results to the Health Department and providers were asked to complete case report forms.

RESULTS: Three commercial laboratories reported twenty *Borrelia miyamotoi* positive lab results in Vermont residents, between May 2016 and September 2017. Cases ranged in age from 4-80 years, with a median age of 63. Half of the cases were female. Onsets ranged from mid-May through early October. The most commonly reported symptom was fever (95%), followed by myalgia (75%), fatigue (75%), chills (65%), headache (60%) and nausea (50%). Eight cases reported a relapsing fever; there were no reports of dyspnea, jaundice, photophobia, vertigo or lymphadenopathy. Over a third of cases had abnormal lab findings including thrombocytopenia, leukopenia and elevated liver enzymes. Fifteen percent of cases were hospitalized for their infections.

CONCLUSIONS: Since 2016, *Borrelia miyamotoi* infections have become the fourth most commonly reported tickborne disease in Vermont. Infections were clustered in the southwestern part of the state where the highest incidence of Lyme disease, anaplasmosis and babesiosis exist, but this area is also within the service area of the commercial lab that specializes in tickborne disease testing. Across the state, tick collecting and testing for *Borrelia miyamotoi* is currently underway and should better elucidate the distribution of this disease. Greater awareness among health care providers about the existence of *Borrelia miyamotoi* may lead to increased clinical testing, which, along with a standardized case definition, could help us better understand the public health impact of this disease.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease; Surveillance; Infectious Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9264

Abstract Type Quick

Abstract Title The Importance of Laboratory Confirmation of Human Orf Virus Infection – a Case Report

Abstract

BACKGROUND: Orf virus is a zoonotic parapoxvirus that is associated with small ruminants (e.g., sheep). Human orf infections occur after direct contact with infected animals. Orf infection typically presents as ulcerative skin lesions on the fingers, hands, or forearms that resolve without treatment. Orf lesions can resemble clinical manifestations associated with other infections of public health importance (e.g., anthrax). Laboratory confirmation of orf virus infections is therefore encourage

METHODS: We report a case of orf virus infection in an Indiana resident.

RESULTS: In April, a 19-year-old woman presented to an urgent care clinic with a dermatologic complaint of two weeks' duration; she reported being bitten by a sheep 3 weeks prior. A painful 1 cm lesion was noted on the tip of her left index finger. The patient was diagnosed with cellulitis and prescribed oral amoxicillin/clavulanic acid. A different provider added sulfamethoxazole-trimethoprim the next day. The lesion subsequently ulcerated, became more painful, and increased in size, reaching a diameter of 3 cm. After 3 days, the patient presented to the emergency department, where she was given intravenous and oral clindamycin and received consultation for surgical debridement. Orf infection was suspected, but testing was not ordered. The patient's mother contacted the Centers for Disease Control and Prevention (CDC) the next day to request orf testing. The Indiana State Department of Health coordinated collection of a fluid specimen from the lesion and submitted it to CDC. The specimen was positive for orf virus by polymerase chain reaction (PCR); results were reported 14 days after the patient's initial presentation. The lesion resolved 4 weeks later without surgical debridement.

CONCLUSIONS: The patient received antibiotic treatment and surgical consultation for a typically self-limiting viral infection. Given the patient's exposure history and lesion, the initial differential diagnosis should have included several zoonotic diseases of public health importance. Providers are encouraged to confirm suspected cases of orf with laboratory testing to facilitate prompt diagnosis and appropriate treatment. Orf testing at CDC can be arranged by state health departments.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9782

Abstract Type Quick

Abstract Title Toxoplasmosis Associated with Venison Consumption during a Retreat — Wisconsin, September–October 2017

Abstract

BACKGROUND: On October 19, 2017, a physician contacted the Wisconsin Division of Public Health (WDPH) regarding a patient with fever, myalgia, leukopenia, and thrombocytopenia of undetermined etiology. One week before illness onset, the patient and 11 other persons attended a retreat during September 28–October 1 in northwestern Wisconsin. The patient reported consuming venison during the retreat and that other attendees had similar illnesses. After consultation with WDPH, the patient and 2 other attendees were tested for *Toxoplasma* -specific antibodies; results indicated a recent infection. We investigated to determine outbreak magnitude and illness-related factors.

METHODS: We interviewed 10 of 12 attendees, and assessed signs, symptoms, and exposures and coordinated *Toxoplasma* testing. A clinical toxoplasmosis case was defined as fever, fatigue, muscle aches, or sweats (≥ 3 symptoms) in an attendee with onset during October 3–21; a confirmed case included serologic test results consistent with recently acquired *Toxoplasma* infection. Raw, frozen venison from the same deer was tested at the Palo Alto Medical Foundation Toxoplasma Serology Laboratory.

RESULTS: All 10 persons interviewed were male; median age was 55.5 years (range: 34–75 years). One attendee did not consume venison and was not ill. All 9 attendees who consumed venison reported it was definitely or possibly undercooked; 8 (89%) had illnesses meeting the clinical case definition with onsets during October 5–8. All 8 patients sought health care, 8 were laboratory-confirmed; none were hospitalized. The venison served at the retreat was refrigerated since being locally harvested on September 21. *Toxoplasma gondii* DNA was detected in the venison sample by polymerase chain reaction.

CONCLUSIONS: Evidence implicated consumption of undercooked venison as the illness source. Based on this outbreak, WDPH seeks to increase awareness that game meat should be frozen to -4°F for 2 days and cooked to 160°F to kill *Toxoplasma*.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Foodborne Disease; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9423

Abstract Type Quick

Abstract Title Trends in Reported West Nile Virus Infections Among Elderly Georgia Residents, 2012-2017

Abstract

BACKGROUND: West Nile virus (WNV) is primarily transmitted to humans through *Culex* species mosquitos. Although most people infected with WNV are asymptomatic, some develop a febrile illness with headache, myalgia, and rash. A small number of infected people (approximately 1%) develop neuroinvasive illness, exhibiting symptoms such as encephalitis or meningitis, which can result in death. In Georgia, WNV infections are reportable to the Georgia Department of Public Health (GDPH). GDPH epidemiologists analyzed WNV data to determine trends among elderly (65+) Georgians with WNV infections.

METHODS: All arboviral illnesses identified in the U.S. are reported to ArboNET, a national passive surveillance system managed by the Centers for Disease Control and Prevention. GDPH's ArboNET data from 2012 through mid-December 2017 were exported into Excel for analysis. Asymptomatic individuals were not included in this study.

RESULTS: From 2012 to 2017, Georgia reported 100, 17, 13, 15, 6, and 46 WNV cases annually, respectively. Of the total number of cases reported yearly between 2012 through 2017, 39 (39%), 6 (35.3%), 5 (38.5%), 6 (40%), 4 (66.7%), and 26 (56.5%) were at least 65 years old, respectively. Infections were classified as neuroinvasive in 20 (51.3%), 2 (33.3%), 3 (60%), 4 (66.7%), 4 (100%), and 25 (96.2%) of all reported cases in elderly patients from 2012 through 2017, respectively. Among all WNV-attributed fatalities reported between 2012 and 2017, 5 (83.3%), 0 (0%, no fatalities), 0 (0%, 1 nonelderly fatality), 0 (0%, no fatalities), 1 (100%), and 7 (100%) were reported in elderly patients, respectively.

CONCLUSIONS: Reported WNV cases in elderly patients account for at least 35% of all yearly reported cases in Georgia between 2012 and 2017; in fact, over half of all reported WNV infections in 2016 and 2017 were among the elderly. Additionally, the majority of elderly case-patients had neuroinvasive infections during the study period (58 of 86, 67.4%). Strikingly, WNV-attributed fatalities in Georgia were overwhelmingly associated with elderly patients (13 of 15, 86.7%). These limited data suggest that the elderly may be more likely to develop neuroinvasive WNV infections and subsequently expire. Epidemiologists can use this information to target prevention education to this demographic group, including using mosquito repellent and other mosquito bite avoidance interventions.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Vectorborne Disease; Epidemiology

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9810

Abstract Type Quick

Abstract Title Two Cases of Hantavirus Pulmonary Syndrome in Washoe County, Nevada, 2017

Abstract

BACKGROUND: Two confirmed cases of Hantavirus Pulmonary Syndrome (HPS) were reported in Washoe County, Nevada in September 2017. Previously Washoe County had only had four confirmed cases of HPS reported between 1995 and 2006, with never more than one case in a given year. Two of six reported cases were fatal including one death in 2017. Surveillance of deer mice (*Peromyscus maniculatus*) for hantavirus had been conducted in Washoe County in past years. While the percent positive varied from year to year, overall this past surveillance indicated that about 17% of deer mice had been infected with hantavirus. However, regular testing was discontinued in 2013. A joint epidemiologic and environmental investigation was conducted to identify potential risk factors and to inform public health prevention messaging.

METHODS: Epidemiologic case investigations were conducted through interviews of cases' immediate family members. Medical records were also reviewed to gather information related to the cases' clinical presentation, course of illness, testing, and treatment. Environmental health specialists did site visits and trapped mice on and around the cases' properties. Trapped mice were serologically tested for hantavirus.

RESULTS: The cases were serologically confirmed to have infection with Sin Nombre hantavirus. Both cases of HPS resided in the same neighborhood and were likely exposed to mice and their urine or droppings. Both cases had trapped mice on their property and had exposure to dust or aerosols in buildings known to be contaminated with rodent droppings. Specimens were collected from 22 trapped mice: 21 deer mice and 1 harvest mouse (*Reithrodontomys megalotis*). Four deer mice (19%) tested positive for Sin Nombre hantavirus.

CONCLUSIONS: Joint epidemiologic and environmental investigations can provide evidence to support known risk factors for disease and to provide a clearer understanding of the risk within a community. Cases of HPS are rare in Washoe County; however, the disease vector, the deer mouse, is widely found throughout Washoe County. Furthermore, the 2016-2017 water year was the wettest on record for Washoe County, potentially impacting the contact between deer mice and humans. The identification of two confirmed cases geographically co-located prompted a coordinated epidemiologic and environmental response. Epidemiologic and environmental data collected during the investigation confirmed the presence of hantavirus within the community and identified known risk factors for disease. Press releases and media interviews were conducted to inform the public about the continued presence of hantavirus within the community and to provide risk reduction and prevention messages.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Local Epidemiology; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9527

Abstract Type Quick

Abstract Title Unnecessary and Incorrect Administration of Postexposure Prophylaxis for Rabies — Illinois, 2016

Abstract

BACKGROUND: Rabies is a fatal neurological illness transmitted by the bite of infected mammals. Human rabies cases are rare in the United States, partly attributable to the availability of postexposure prophylaxis (PEP). The Advisory Committee on Immunization Practices (ACIP) provides recommendations for initiating and administering PEP, which consists of 1 dose of rabies immunoglobulin (RIG) and multiple doses of vaccine at specific times and body locations. PEP administration is costly and following the vaccine schedule is complex. We examined unnecessary and incorrect PEP administration in Illinois.

METHODS: Using data reported to the Illinois National Electronic Disease Surveillance System from 2016, we calculated prevalence of unnecessary (i.e., initiated when it should not have been) and incorrect (i.e., improper timing or injection location on ≥ 1 occasion) PEP administration and potential risk factors. We calculated risk ratios (RRs) and 95% confidence intervals (CIs) to identify factors associated with unnecessary PEP administration and reasons for incorrect administration.

RESULTS: Among 670 persons for whom PEP was initiated, records for 638 contained sufficient information to determine if PEP was necessary; PEP was determined unnecessary for 257 (40.3%) persons. Risk for unnecessary PEP was higher when the health care provider did not consult with the health department (RR = 3.0; 95% CI = 2.3–4.0; $P < .0001$). PEP was administered incorrectly for 236 (51.6%) of 457 persons whose records contained sufficient information to determine if PEP was administered correctly. The most common reasons for incorrect administration were incorrect vaccination timing (55.5%) and incorrect injection location of vaccine (21.6%) or RIG (18.2%).

CONCLUSIONS: Rabies PEP is often administered unnecessarily and incorrectly in Illinois. Health care providers might benefit from targeted education concerning ACIP recommendations and proper PEP administration. Improving communication between health care providers and health departments might reduce the burden of unnecessary and incorrect PEP administration.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Immunization; Zoonotic Diseases; Veterinary Public Health

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9404

Abstract Type Quick

Abstract Title Using Syndromic Surveillance to Identify Unreported Incidents of New York City Residents Seen in Emergency Departments for Exposures to Rabies Vector Species, May 2017–November 2017.

Abstract

BACKGROUND: Rabies is a fatal neurotropic virus typically transmitted to humans through the bite of an infected animal. In NYC, the virus is maintained in rabies vector species (RVS) including raccoons, bats, or skunks. Rabies can be prevented with proper administration of rabies postexposure prophylaxis (rPEP). Animal bites and other potential rabies exposures are reportable to the New York City (NYC) Department of Health and Mental Hygiene (DOHMH). An average of 32 exposures to RVS are reported annually and each individual is interviewed and followed to ensure appropriate and complete rPEP administration. This study evaluates the use of text-based queries of emergency department (ED)-based chief complaints (CC) to identify unreported RVS exposures and assess whether rPEP was appropriately administered in these patients.

METHODS: The DOHMH syndromic surveillance system receives information, including CC text, from ED visits from all 53 NYC hospitals daily. An automated program extracted all records with CC including the keywords “raccoon,” “bat,” or “skunk” between May 2017 – November 2017. Manual review of extracted records was performed to determine if the CC represented a legitimate unreported RVS exposure event (e.g., not “raccoon eyes” or “hit by baseball bat”). RVS events identified through the CC surveillance system were cross-checked with known, reported RVS exposures. Unreported RVS exposure patients were assigned to DOHMH investigators for routine RVS exposure follow-up including gathering exposure details, and assessing clinical management and rPEP administration.

RESULTS: Between May 1 and November 30, 2017, the program identified 43 persons presenting to an ED with at least one keyword in the chief complaint text. Of these, 21 (49%) were legitimate exposures to RVS, 17 (81%) of which, from 15 different EDs, were not previously reported to DOHMH. All 17 patients had documented rPEP administration during the initial ED visit, though it was administered inappropriately for two (12%) patients.

CONCLUSIONS: ED-based CC surveillance is a novel method to identify unreported RVS exposures. Our study demonstrates that a large proportion of RVS exposures are not reported as required by standard reporting mechanisms in NYC. While all identified RVS exposure patients started rPEP, it was administered inappropriately for two patients. The resources invested in identifying unreported RVS exposures were considered reasonable in relation to the benefit of ensuring rPEP administration and completeness to prevent death from rabies virus in NYC. These findings will also help direct outreach to improve mandated reporting and educate providers on proper rPEP administration.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Zoonotic Diseases; Syndromic Surveillance; Surveillance

Consider for Different Presentation? Yes

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Submission Type Breakout/Quick/Lightning/Poster

ID 9413

Abstract Type Quick

Abstract Title Viral Hemorrhagic Fever Preparedness, Kween and Kapchorwa Districts, Uganda, 2017

Abstract

BACKGROUND: On October 17, 2017, a case of Marburg Virus Disease (MVD) was confirmed in a recently deceased patient from Kween District, eastern Uganda. Initial suspicion of a viral hemorrhagic fever (VHF) by local health workers and confirmatory testing led to the declaration of the first MVD outbreak in eastern Uganda. A mixed methods assessment of existing VHF readiness capacity was conducted to improve VHF surveillance and outbreak response in this region.

METHODS: An 11-part, point-based questionnaire focusing on epidemiology and laboratory aspects of VHF preparedness and allowing a maximum score of 76 was developed. The questionnaire was administered to physicians, laboratorians and hospital administrators at two health facilities in Kween and neighboring Kapchorwa Districts, and at five other health facilities with existing VHF surveillance programs across Uganda. A six-question qualitative assessment of the MVD outbreak response was also administered to Kween and Kapchorwa District health facility staff.

RESULTS: Kween and Kapchorwa District health facilities scored 39/76 and 21/76 points, respectively. Established VHF surveillance sites scored an average of 49/76 points (range 42-63). Identified gaps in VHF readiness included lack of comprehensive training in VHF surveillance, missing clinical specimens from deceased patients due to rapid collection of bodies by families, staff uncertainty and lack of awareness that an outbreak alert could be issued before testing clinical specimens. Responses to the qualitative assessment indicated that factors leading to the successful identification of this MVD outbreak were recognition of an epidemiological link between two patients with hemorrhagic symptoms and rapid blood sample submission for laboratory testing.

CONCLUSIONS: Despite limited VHF readiness in Kween and Kapchorwa Districts, health officials successfully identified the first cases of a VHF MVD outbreak. Earlier recognition of future VHF cases may be enabled by expanding the VHF surveillance program in Uganda.

Committee Infectious Disease

Topic Vector-Borne & Zoonotic Diseases

Keywords Infectious Diseases; Outbreaks; Zoonotic Diseases

Consider for Different Presentation? Yes

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Submission Type	Roundtable
ID	9866
Abstract Type	Roundtable
Abstract Title	Future Updates for Arboviral Case Definitions

Abstract

Key Objectives:

- Review current case definitions for arboviral diseases.
- Discuss possible future updates to both the “Zika virus” and “Arboviral diseases” case definitions.
- Obtain feedback from participants on current case definitions and potential future updates.

Brief Summary:

Domestic neuroinvasive and non-neuroinvasive arboviral disease has been nationally notifiable since 2004. In 2015, the case definition was updated to include chikungunya virus, an imported arbovirus. In 2016, to address the increasing risk to travelers and the potential for local transmission in some areas of the United States, a standalone case definition for Zika virus disease and infection was approved and implemented. Similar to chikungunya virus, Zika virus disease incidence appears to be declining in most areas of the Americas but will likely become endemic to many areas frequented by US travelers. In this context, we would like to review and discuss possible future updates to the current case definitions for both “Zika Virus Disease and Zika Virus Infection” and “Arboviral Diseases, Neuroinvasive and Non-neuroinvasive”.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Vectorborne Disease
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9860
Abstract Type	Roundtable
Abstract Title	Lyme Disease Surveillance in High Incidence States: Is It Time to Rely on Laboratory-Based Reporting?

Abstract

Key Objectives:

- Define the purpose(s) of surveillance in a high-incidence jurisdiction;
- Describe and discuss laboratory-based surveillance as an approach to surveillance in high-incidence states;
- Discuss the expected impact on surveillance numbers.

Brief Summary:

With over 30,000 cases reported to CDC annually, Lyme disease is the most common vector-borne disease in the U.S. and there are data indicating that this figure undercounts the true number of cases by a factor of ten. The vast majority (>96%) of these cases occur in the high-incidence states of the Northeast, Mid-Atlantic, and the upper Midwest. National surveillance data collected over several decades show areas of high incidence, emergence/expansion, and low incidence. There are barriers to more complete Lyme disease surveillance. First, the current national case definition requires clinical, exposure and laboratory information for classification, and the large volume of reports received, usually through laboratory reporting, places a major burden on health departments and healthcare providers. Secondly, patients in early disease with an erythema migrans are unlikely to have a positive laboratory test, requiring healthcare providers to initiate reporting to the health department rather than relying on health departments to follow-up. In order to create more sustainable surveillance systems, some jurisdictions have modified their process (e.g., dropping laboratory reporting or sampling a proportion of reported cases to generate estimates) or altered reporting requirements (e.g., only requiring reporting of patients with erythema migrans). Although this has reduced burden, these modifications have undermined one of the primary purposes of making a disease nationally notifiable, standardized case counting. The lack of standardization makes it impossible to compare incidence across jurisdictions and has not improved the ability to measure the true burden of disease. In light of this, the Lyme disease case definition for high incidence states should be revised. As part of this revision, the purpose surveillance serves in high-incidence versus emerging versus low-incidence areas should be re-evaluated. One proposal is to rely on laboratory-based reports for high-incidence areas, as this standard may be more sustainable and comparable across jurisdictions. This would not prevent jurisdictions from continuing individual case investigations if desired. Efforts are ongoing to understand: 1) if this method serves an appropriate surveillance purpose in high-incidence areas; and 2) the potential impacts of this proposed case definition change on the number of cases reported by individual jurisdictions, as well as in aggregate.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Surveillance; Infectious Diseases; Vectorborne Disease
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9613
Abstract Type	Roundtable
Abstract Title	National Surveillance of Spotted Fever Rickettsioses: What We Know, What We Don't Know, and What We Could Learn

Abstract

Key Objectives:

- Discuss best practices for spotted fever rickettsiosis serology: differentiating between persistent antibodies and incident infections
- Discuss the increased use of polymerase chain reaction (PCR) assays for spotted fever rickettsiosis, now available through the Laboratory Response Network (LRN)
- Discuss differences in spotted fever rickettsiosis case investigations at state and local level health departments

Brief Summary:

Incidence of spotted fever rickettsiosis (SFR) has been increasing for decades, with preliminary case counts for 2017 exceeding any previous year of reporting. SFR are common in the United States, with national serosurveys finding detectable antibodies in 5-10% of the population. Differentiation of persistent and incident antibodies requires the use of indirect immunofluorescence antibody assays (IFA) on paired samples, taken 2-4 weeks apart, performed at the same laboratory. However, laboratory criteria for the majority of SFR cases fall short of this standard, resulting in a skewed understanding of SFR epidemiology. Reliance on serologic techniques stems from the previous lack of sensitive acute diagnostic assays. Due to the endothelial nature of *Rickettsiae*, PCR techniques were thought to have minimal diagnostic value until late stages of infection. However, more sensitive and less resource-intensive real-time PCR assays are now available through the LRN. While the true utility of these tests is largely unknown, they could contribute significantly to our understanding of SFR, providing species-specific diagnoses. Investigation of suspected SFR in support of a case classification substantially burdens state and local health departments. High incidence states have taken different steps in how they process and gather information on SFR cases in order to limit undue effort. Sharing of these practices may be helpful for other health departments investigating large numbers of SFR cases. Currently, fewer than 1% of SFR cases are confirmed, and most of our understanding of SFR is based on incomplete, and often times uninterpretable diagnostic evidence including single serologic titers and/or qualitative antibody results. Improvements in the diagnostic criteria can provide opportunities to identify specific SFR and differentiate between incident cases and persistent serologic titers. A Roundtable would be an ideal opportunity to discuss current challenges in SFR reporting and to identify possible ways to reduce inconsistencies through improved guidance.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Vectorborne Disease; Surveillance
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9821
Abstract Type	Roundtable
Abstract Title	One Health Approach to Optimizing Outcomes for Humans, Animals, and the Environment

Abstract

Key Objectives:

The objective of this roundtable presentation is to explore collaborative, systems-based approaches for developing interventions that reduce risks from emerging diseases and balance the needs of humans, animal agriculture, wildlife, and the environment. Presenters and participants will discuss practical skills and tools and consider best practices for health professionals to use to break down agency silos and create inter-disciplinary scientific approaches to manage emerging and high consequence zoonotic disease risks within a One Health framework.

Brief Summary:

Emerging infectious diseases of wildlife origin pose profound threats to human, animal, and environmental health by increasing burdens on public health systems, negatively impacting the economy, causing declines and extinctions of animal species, and damaging ecological processes. The concept of One Health, defined as the collaborative effort of multiple disciplines—working locally, nationally, and globally—to attain optimal health for people, animals, and the environment has been growing in recognition. One Health recognizes that human, domestic animal, and wildlife health are all interconnected within the context of a shared environment, and provides a useful conceptual framework for the development of solutions to public health challenges. To date, however, health-promoting interventions have focused largely on single sector outcomes. Using One Health concepts as a framework, disease management and regulatory strategies should seek to optimize outcomes for humans, animals, and the environment. We will use a series of emerging disease case studies, including highly pathogenic avian influenzas in wild birds; zoonotic viruses of bats; and sylvatic plague in grassland ecosystems to explore using a collaborative, systems-based approach to develop interventions that reduce risks and balance needs of humans, wildlife, and the environment. This case series will illustrate various interventions, including temporal and spatial separation of humans and wildlife, risk communication, and other preventative strategies that allow humans, domestic animals, and wildlife to co-exist in mutually healthy ways. The examples will also highlight gaps in current capabilities such as upstream surveillance, wildlife vaccination, and other tools to prevent pathogen spillover, and governance structures and leadership qualities that facilitate collaboration. The ultimate goal is to encourage health professionals to define clear multi-sector outcomes and use a systems-based, scientific approach to develop interventions that reduce risks and balance the needs of humans, animals, and the environment.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Emerging Infections; One Health; Zoonotic Diseases
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9122
Abstract Type	Roundtable
Abstract Title	Partnerships for Zoonotic Disease Awareness and Prevention

Abstract

Key Objectives:

- Identify audiences and methods to communicate zoonotic disease risk and prevention practices
- Learn more about the roles of industry and corporate partners in zoonotic disease prevention
- Discuss collaborations that can engage industry and corporate partners in public health campaigns

Brief Summary:

In January 2017, an outbreak of Seoul virus associated with pet Norway rats resulted in 17 human cases with three hospitalizations in 11 states. While Seoul virus was found in wild Norway rats in the United States previously, this was the first time that pet rats were found to be the source of human infections. Early in the outbreak investigation, communication and education was needed, particularly targeting pet rat owners, breeders, retailers, and veterinarians. Partnerships were sought with veterinary associations, veterinary teaching hospitals, fancy rat networks, and industry groups, including the Pet Industry Joint Advisory Council (PIJAC). PIJAC represents the commercial pet trade, and advocates for responsible pet ownership, including the production and dissemination of zoonotic disease information targeting retail store associates. PIJAC helped alert the pet industry to the presence of Seoul virus in the United States through a Pet Industry Health Alert, and members of the PIJAC Zoonoses Committee worked with public health authorities during the trace back phase of the investigation to help identify affected facilities. During the investigation PIJAC hosted a call with CDC, State Public Health veterinarians and rat breeders to discuss findings of the investigation and disseminated accurate information to interested stakeholders to alleviate misinformation. Members of the PIJAC Zoonosis Committee have continued to work with CDC to help establish guidelines for testing rat breeding facilities and rat distribution facilities for the presence of Seoul virus. Through the efforts of multiple partners, rats at more than 30 facilities were identified with Seoul virus infection, and many breeders were able to successfully control the disease. Although the Seoul virus outbreak investigation has now come to a close, the work of the partners goes on through continued promotion of best management practices for safely handling and testing pet rats, and by ensuring that national hantavirus surveillance will detect new human cases as they occur.

Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	Communication; Zoonotic Diseases; One Health
Consider for Different Presentation?	No
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Submission Type	Roundtable
ID	9308
Abstract Type	Roundtable
Abstract Title	Promoting One Health Collaboration with Youth Agricultural Education Organizations to Enhance Zoonotic Disease Prevention and Response
Abstract	Key Objectives: • Discuss current challenges to education, prevention, detection, and monitoring of zoonotic diseases in agricultural venues • Explore convenient means of sharing educational resources, including print templates, social media messages, interactive games, and online learning options • Describe current initiatives to facilitate One Health collaborations and improve youth education efforts related to zoonotic disease prevention • Identify innovative approaches and best practices in leveraging these frameworks within other areas of public health importance Brief Summary: The Centers for Disease Control and Prevention (CDC), United States Department of Agriculture (USDA), and Council of State and Territorial Epidemiologists (CSTE) have developed an ongoing partnership to educate youth on the transmission and prevention of zoonotic disease (e.g., influenza, <i>Salmonella</i>, <i>E. coli</i> O157:H7). The <i>Influenza Education Among Youth in Agriculture Pilot Project</i> was developed from this partnership and launched in 2013. Through this project, state-based collaborations between public health, animal health, and youth organizations develop education initiatives focused on preventing zoonotic disease transmission at agricultural fairs and other venues. The primary goals of this project are to (1) help empower millions of youth in agricultural organizations like 4-H and National FFA Organization to enjoy time spent with their animals while reducing the risk of zoonotic diseases and (2) facilitate a more effective and efficient response to important public health issues by strengthening relationships among key stakeholders. CDC, CSTE, USDA, and multiple state organizations including departments of public health and agriculture, academic institutions, and youth agricultural programs have been working together to develop hands-on activities (zoonotic disease kits, a board game, and a card game), zoonotic disease curricula, educational workshops, and One Health meetings to achieve these goals. Products from this project have been shared between pilot states in order to leverage resources and expertise. This roundtable will provide an overview of this collaboration, describe project accomplishments, explore unique partnership networks to improve knowledge about zoonotic diseases among youth, and discuss opportunities for expanding this framework to address other diseases or areas of public health importance.
Committee	Infectious Disease
Topic	Vector-Borne & Zoonotic Diseases
Keywords	One Health; Collaboration; Veterinary Public Health
Consider for Different Presentation?	No
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