

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

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Epidemiology; Food Safety
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10847
Abstract Type	Breakout
Abstract Title	A Shared Effort to Better Attribute Illnesses to Foods – 9 Years of the Interagency Food Safety Analytics Collaboration (IFSAC)

Abstract

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

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

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

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

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Epidemiology; Foodborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Association between Communities of Color, Poverty, Unemployment and Salmonella and E. coli Rates in 20 Large American Cities

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Epidemiology; Health Disparities; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Comparing Shiga Toxin-Producing <i>Escherichia coli</i> O157 and Non-O157 Outbreaks, National Outbreak Reporting System — 2010–2017

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	NORS (National Outbreak Reporting System); Outbreaks; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Cyclosporiasis Outbreak Associated with Vegetable Tray Consumption

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Emerging Infections
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10952
Abstract Type	Breakout
Abstract Title	Epidemiology of Campylobacteriosis, Salmonellosis, and Shigellosis—Miami-Dade County 2012-2017

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Local Epidemiology; Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Epidemiology of <i>Listeria Monocytogenes</i> , Miami-Dade County, 2001—2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Maternal and Child Health; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Estimating the Burden of Waterborne Disease in the United States

Abstract

BACKGROUND: The routine treatment of drinking water is one of the greatest US public health achievements of the twentieth century and provides a safe, reliable water supply. Treated water is used in many complex ways that can affect disease transmission. Waterborne disease and outbreaks continue to occur in the United States and are associated with a variety of water sources (drinking, recreational, environmental) and exposure routes (ingestion, contact, inhalation). An estimate of the burden of waterborne disease in the United States, measured through numbers of illnesses, emergency department (ED) visits, hospitalizations, deaths, and associated costs, will direct prevention activities and set public health goals.

METHODS: We chose 18 waterborne diseases for which surveillance data, billing data, or literature estimates indicated domestic waterborne transmission was plausible, substantial burden of illness or death was likely, and data were available. We classified diseases as primarily enteric (campylobacteriosis, cryptosporidiosis, giardiasis, norovirus infection, salmonellosis, and shigellosis) or primarily respiratory (Legionnaires' disease, nontuberculous mycobacteria [NTM] infection, and *Pseudomonas* pneumonia). Adapting previously developed methods, we used a series of disease-specific multipliers to adjust the reported/documented number of cases of each disease for under-reporting, under-diagnosis, proportion domestically acquired, and proportion transmitted via water to generate point estimates with 95% credible intervals (CrI). Sources for multipliers included surveillance data, population studies, and expert judgment when no other data were available. We estimated the number of illnesses, ED visits, hospitalizations, and deaths, and the costs of ED visits and hospitalizations due to waterborne disease transmitted in the United States in 2014.

RESULTS: An estimated 7.2 million waterborne illnesses (CrI 3.9–12.0 million) occur annually, including 601,681 (CrI 365,061–866,093) ED visits, 117,342 (CrI 85,805–150,070) hospitalizations, and 6,559 deaths (CrI 4,373–8,932) deaths, incurring US\$3.2 billion (2014 dollars) in direct healthcare costs. Otitis externa and norovirus infection were the most common illnesses. Hospitalizations and deaths were predominantly caused by environmental pathogens that are commonly associated with biofilm in plumbing systems (NTM, *Pseudomonas*, *Legionella*) costing US\$2 billion annually.

CONCLUSIONS: Millions of domestically-acquired waterborne illnesses from these 18 infections occur in the United States each year, and incur billions of dollars in healthcare costs. This analysis highlights the shifting roles of enteric and environmental pathogens in waterborne disease in the United States.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Emerging Infections; Water; Waterborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Evidence-Based Practices to Inform the Conduct of Enteric Disease Interview and Questionnaire Design

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Surveillance; Data Collection; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11659
Abstract Type	Breakout
Abstract Title	Food Security Versus Food Safety: <i>Salmonella</i> Enteritidis Outbreak Linked to a Pop-up Food Pantry

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Food Safety; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Hypothesis Generation during a Foodborne Illness Outbreak Investigation: Tools and Resources from the Integrated Food Safety Centers of Excellence

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Outbreaks; Epidemiologic Methods
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	International Travel-Associated <i>Campylobacter</i> , <i>Salmonella</i> , and <i>Shigella</i> Infections — Foodborne Diseases Active Surveillance Network, 2008–2017

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Food Safety; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Investigation of a Multistate Outbreak of <i>Salmonella</i> Enteritidis Associated with Shell Eggs Using Whole Genome Sequence Analysis

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Food Safety; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Is a Positive Shiga Toxin Test a Shiga Toxin-Producing <i>E. coli</i> Infection? — Foodborne Diseases Active Surveillance Network (FoodNet) — 2012–2017

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Surveillance; Foodborne Disease; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	It Must Have Been Something I Ate...Two Outbreaks at One Facility

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Collaboration; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11680
Abstract Type	Breakout
Abstract Title	Multi-Serotype Outbreak of Salmonella Infections Linked to Kratom — United States, 2017–2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Food Safety; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Multiple Pathogen Gastroenteritis Outbreak Associated with an Outdoor Recreational Facility — Tennessee, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Outbreaks; Waterborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Multistate Outbreak of <i>Salmonella</i> Infections Linked to Raw Turkey Products — United States, 2017–2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Outbreaks; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10985
Abstract Type	Breakout
Abstract Title	Multistate Outbreak of Shiga Toxin-Producing <i>E. coli</i> Infections Associated with Romaine Lettuce

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Environmental Health; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Breakout
Abstract Title	Outbreak of <i>Salmonella</i> Enteritidis Associated with Eggs – a Local Public Health Response, August 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Outbreaks; Local Epidemiology; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID Breakout/Quick/Lightning/Poster 11514

Abstract Type Breakout

Abstract Title Sexual Transmission of *Shigella* in the Portland Oregon Metropolitan Area 2008-2018: Case Case Analyses of Related Pathogens and Classic STIs

Abstract

BACKGROUND: *Shigella* is a bacterial pathogen that causes severe and often bloody diarrhea, fever, and sepsis. Infections are spread via the fecal-oral route and humans are the sole reservoir. Sex-dependent fecal-oral transmission is a known *Shigella* risk factor especially among men who have sex with men (MSM) and sexual networks have enabled the emergence and dissemination of drug resistant *Shigella*. However, the risk of shigellosis during sexual activity among heterosexual men and women is poorly defined. Similarly, limited data exist on the role of sexual transmission for other closely related bacterial pathogens. We hypothesized that sex-dependent fecal-oral transmission mirrors sexual transmission among other sexually transmitted infections (STIs) and this represents a unique epidemiological niche for *Shigella* compared to other fecal-oral bacterial pathogens.

METHODS: To investigate the burden of illness due to sexual activity for *Shigella* relative to: *Salmonella*, Shiga Toxigenic *E. coli* (STEC), and *Campylobacter* we analyzed data from domestically acquired, "at risk" (>14 years), sporadic cases from July 2008-July 2018. Using STI diagnoses as a proxy for high risk sexual behavior we performed a broad case-case analysis comparing the odds of having an STI diagnosis among representative fecal-oral pathogens as well as traditional STIs including *Chlamydia*, *Gonorrhea*, *Syphilis*, and HIV. Multiple logistic regression analyses were performed to model the odds of having an STI diagnosis between diseases.

RESULTS: Since 2008, the Portland Metropolitan Area had 343 cases of *Shigella*. 76% were male and 23% were female. 51% of *Shigella* cases had an STI diagnosis including 63% of males and 16% of females. After stratifying by sex and adjusting for confounding factors including age, county, race, and year, we found that cases of *Shigella* were significantly more likely to have an STI diagnosis compared to all other fecal-oral pathogens (males adjusted Odds ratio [OR] 15.9-24.7 p<0.01; females OR 2.4-4.0 p<0.02). Conversely, male *Shigella* cases had similar odds of having an STI diagnosis compared to the STIs (OR 0.8-2.3 p>0.1), and 92% of cases with an STI were MSM.

CONCLUSIONS: Our evidence strongly suggests that the majority of domestically acquired *Shigella* infections were acquired sexually, predominantly among MSM. However, we found no evidence that other fecal-oral bacterial pathogens are consistently transmitted sexually. Given the overlap of *Shigella* with other STIs, we recommend foremost consideration of domestically acquired *Shigella* infections as being sexually acquired. Shigellosis cases, especially MSM, should be tested for other STIs and provided fecal-oral sexual health education.

Submission Complete? Yes

Committee Topic Infectious Disease
Enteric Diseases

Keywords Epidemiology; Sexually Transmitted Diseases; Enteric Infectious Diseases

Consider for Different Presentation? Yes

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

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Epidemiologic Methods; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11383
Abstract Type	Breakout
Abstract Title	"It Didn't Taste Right, but I Ate It Anyway" ...an Investigation of Foodborne Botulism

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Infectious Diseases
Consider for Different Presentation?	No
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11836
Abstract Type	Lightning
Abstract Title	Detecting a Multi-State Outbreak Using Environmental Sampling, Whole Genome Sequencing, and Data Sharing Platforms

Abstract

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

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

www.ncbi.nlm.nih.gov/Structure/tree/#!/tree/Salmonella/PDG000000002.1230/PDS000001865.145?key=xlpIqULLh7_U9bRZtZXRRf-zlgxCL_VWzSi9QdwMh0bFCYtJ6wk

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

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

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Collaboration; Epidemiologic Methods; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11022
Abstract Type	Lightning
Abstract Title	Use of a Health Alert Network's (HAN) Mass Text Messaging Functionality to Investigate Foodborne Outbreaks – Tennessee, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Emergency Preparedness & Response; Outbreaks; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10617
Abstract Type	Poster
Abstract Title	A Collaborative Outbreak Investigation of Salmonella Enteritidis Linked to Chicken with Multiple Exposure Locations

Abstract

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Food Safety; Outbreaks; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	10949
Abstract Title	Poster
	An Outbreak of Gastrointestinal Illness Associated with a Thanksgiving Potluck, Williamson County, Texas, 2018

Abstract

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	Enteric Infectious Diseases; Outbreaks; Infectious Diseases
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	Local Public Health Agency

Submission Type	Breakout/Quick/Lightning/Poster
ID	11576
Abstract Type	Poster
Abstract Title	Campylobacteriosis Outbreak at a Workplace Cafeteria in Pennsylvania – August 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11297
Abstract Type	Poster
Abstract Title	Characteristics of Infections with Common Salmonella Serotypes in Georgia, 2000-2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Epidemiology; Foodborne Disease; Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11519
Abstract Type	Poster
Abstract Title	Ciguatera Fish Poisoning in Puerto Rico

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Outbreaks; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11865
Abstract Type	Poster
Abstract Title	Evaluating Impacts of Enhanced Salmonella Surveillance By Student Disease Investigation at the Hawaii State Department of Health, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Affiliation	Academic Institution

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

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Surveillance; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11452
Abstract Type	Poster
Abstract Title	Foodborne Outbreak Shows Gaps in Food Safety

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Food Safety
Consider for Different Presentation?	No
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	11038
Abstract Title	Poster
	Giardiasis Reported to the National Notifiable Diseases Surveillance System — United States and the Commonwealth of Puerto Rico, 2017

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	Enteric Infectious Diseases; Surveillance
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	11430
Abstract Title	Poster
Abstract Title	How Often Did PFGE Identify Clusters Worth Investigating? A Cluster Comparison of Indistinguishable PFGE Patterns and Whole Genome Sequencing Analysis

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease
Keywords	Enteric Diseases
Consider for Different Presentation?	Foodborne Disease; Epi / Lab Capacity (ELC); Surveillance
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11135
Abstract Type	Poster
Abstract Title	Is Less Really More? an Analysis of Georgia's Routine Salmonella Case Interview Protocols

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11227
Abstract Type	Poster
Abstract Title	Norovirus and Acute Gastroenteritis-Associated Deaths — United States, 2001-2015

Abstract

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

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

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

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

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; ICD
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11350
Abstract Type	Poster
Abstract Title	Outbreak of <i>Salmonella</i> Typhimurium Linked to Chicken Salad

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Epidemiology; Food Safety
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10638
Abstract Type	Poster
Abstract Title	Post-Infectious Sequelae after <i>Campylobacter</i> Enteric Infection: A Pilot Study in Maricopa County, Arizona, USA

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Chronic Disease; Foodborne Disease; Research
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10895
Abstract Type	Poster
Abstract Title	Potential Impact of Multiplex Molecular Panel Testing on Surveillance of Cyclosporiasis, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Surveillance; Foodborne Disease; Data Collection
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11857
Abstract Type	Poster
Abstract Title	Risk History Surveillance Assessment of Campylobacteriosis Cases in Hawaii from August 2018 to November 2018

Abstract

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

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

RESULTS: During the assessment period, HDOH received laboratory confirmation of 144 cases. We were able to contact 134 and successfully interviewed 114 (84%). Of the interviewed cases, 37 (33%) stated they travelled (20 internationally, 17 within the U.S.) during the incubation period. Among in-state cases, 35 (46%) claimed to have direct or indirect close contact with live chickens and/or droppings. Cases residing on islands other than Oahu were significantly associated ($p<0.01$) with having more live chicken exposure (87%) than cases residing on Oahu (30%). Comparison between 86 foods listed on our questionnaire and FoodNet Atlas showed chicken ($p<.01$), pork ($p<.01$), hamburger ($p<.05$), and eggs ($p<.05$) were foods likely to be associated with campylobacteriosis in our study population.

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10740
Abstract Type	Poster
Abstract Title	Salmonella Outbreak in an Elementary School from Home-Made Ice-Cream, Nebraska - October 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Foodborne Disease; Enteric Infectious Diseases; Epidemiology
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11049
Abstract Type	Poster
Abstract Title	Shigellosis Prevention and Control Efforts: A Needs Assessment of State and Local Health Departments

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10817
Abstract Type	Poster
Abstract Title	Timely Identification of Alfalfa Sprouts As the Source of a <i>Salmonella</i> Newport Cluster Prevents Ongoing Cases -- Nebraska, 2018

Abstract

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

Submission Complete?	Yes
Committee Topic	Infectious Disease 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	10892
Abstract Type	Quick
Abstract Title	A Multi-Disciplinary Response to a <i>Shigella</i> Flexneri Outbreak Among Persons Experiencing Homelessness in Long Beach, CA

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Special/Vulnerable Populations; Enteric Infectious Diseases; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11477
Abstract Type	Quick
Abstract Title	Coordinating Chaos: Strategies Utilized during a Large Cluster of Cyclosporiasis Outbreaks, Illinois, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Epidemiology; Foodborne Disease; Outbreaks
Consider for Different Presentation?	Yes
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Affiliation	State Public Health Agency

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

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Genomics; Epidemiologic Methods; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Differential Food and Non-Food Exposures Reported By Pennsylvania Salmonella and Campylobacter Case-Patients in Urban and Rural Areas, 2011-2016

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Rural Health; Epidemiology; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Evaluating the Impact of Multiplex PCR Use on Shiga Toxin-Producing <i>Escherichia coli</i> (STEC) Surveillance, New York City, 2016–2018
Abstract	BACKGROUND: Historically, diagnostic testing for Shiga toxin-producing <i>Escherichia coli</i> (STEC) infections included antigen detection of Shiga toxin or PCR-based testing for Shiga toxin genes, and bacterial culture. In June 2015, laboratories in New York City (NYC) began adopting multiplex PCR (mPCR) panels for enteric diseases, including STEC. We assessed the impact of mPCR on surveillance activities for STEC cases. METHODS: Health care providers and laboratories must report STEC infection among NYC residents to the NYC Health Department, with specimens forwarded to the NYC Public Health Laboratory for additional testing. We attempt to interview all patients with STEC. Cases with only an antigen or PCR-based test were classified as unconfirmed, while cases with a positive culture were classified as confirmed. We analyzed confirmed and unconfirmed STEC cases among NYC residents diagnosed during 2016–2018. Risk ratios (RRs) were used to assess differences (1) by case classification in age, sex, race/ethnicity, residential county, census tract poverty level, diagnosis year, and international travel history, and (2) by first reported test type (mPCR or non-mPCR) in case classification and interview completeness. Wilcoxon rank-sum tests were used to assess differences by first reported test type in days between first specimen collection and report dates, and first report and interview attempt dates. RESULTS: mPCR was the first test reported for 62% of 1,011 cases (confirmed: 344; unconfirmed: 667). Annual confirmed case numbers remained stable across the three years (range: 109–123). Cases first reported by mPCR increased from 36% (91/253) in 2016 to 76% (343/453) in 2018. Unconfirmed cases occurred more frequently among Hispanic vs. white, non-Hispanic patients (RR: 1.21, 95% confidence interval (CI): 1.10–1.34), ≥20 year-olds vs. <20 year-olds (RR: 1.49, 95% CI: 1.32–1.67), Manhattan vs. Queens residents (RR: 1.24, 95% CI: 1.09–1.39) and those diagnosed in 2018 vs. 2016 (RR: 1.27, 95% CI: 1.12–1.43). Cases first reported by mPCR were more likely to be unconfirmed (RR: 2.19, 95% CI: 1.90–2.51) and reported more quickly (median days from collection to report date, mPCR: 2, non-mPCR: 3, $p < 0.0001$). No difference by first reported test was observed for interview completeness or timeliness of first attempted interview. CONCLUSIONS: mPCR testing increased reporting of only unconfirmed cases. Geographic areas served by labs performing mPCR may explain demographic differences in culture confirmation. Cases reported first by mPCR did not differ in interview timeliness or completeness. We are evaluating methods to address the increased staff burden of investigating unconfirmed cases.
Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Surveillance; Foodborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	False-Positive Culture-Independent Diagnostic Test Reports and Effects on <i>Vibrio</i> Surveillance — Nebraska, 2017–2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Waterborne Disease; Surveillance
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Gastrointestinal Illness Associated with a Community Food Truck Event — Nebraska, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Food Safety; Foodborne Disease; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type ID	Breakout/Quick/Lightning/Poster
Abstract Type	Quick
Abstract Title	Impact of Culture-Independent Diagnostic Tests (CIDTs) on Vibriosis Surveillance and Epidemiological Factors Associated with Culture Confirmation, Illinois, 2016–2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Epi / Lab Capacity (ELC); Waterborne Disease; Enteric Infectious Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11272
Abstract Type	Quick
Abstract Title	Implementation of Prospective Whole Genome Sequencing for Enteric Pathogens: The Canadian Experience

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Genomics; Foodborne Disease
Consider for Different Presentation?	Yes
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Affiliation	International Health Agency

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

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Outbreaks; Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10894
Abstract Type	Quick
Abstract Title	Multiple Cyclosporiasis Outbreaks, United States, 2018

Abstract

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

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

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

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

*As of 12/21/2018.

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Outbreaks; Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10904
Abstract Type	Quick
Abstract Title	Multistate Outbreak of <i>Listeria monocytogenes</i> Infections Linked to Ready-to-Eat Country Deli Ham

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10995
Abstract Type	Quick
Abstract Title	Novel Serotype of Enteroinvasive <i>Escherichia coli</i> Associated with a Party — North Carolina, June–July 2018

Abstract

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

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

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

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

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

ID 11447

Abstract Type Quick

Abstract Title Outbreak of *Staphylococcus Aureus* and *Clostridium Perfringens* Associated with a Meal Served at a Workplace, Kansas 2018

Abstract

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

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

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

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

Submission Complete? Yes

Committee Topic Infectious Disease
Enteric Diseases

Keywords Foodborne Disease; Outbreaks

Consider for Different Presentation? Yes

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Institution Affiliation Kansas Department of Health and Environment
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11818
Abstract Type	Quick
Abstract Title	Outbreak of Cryptosporidiosis Associated with Dining at a Taco Restaurant – San Diego, California, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Local Epidemiology; Enteric Infectious Diseases; Foodborne Disease
Consider for Different Presentation?	Yes
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Affiliation	CDC/CSTE Fellow

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

Abstract

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

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

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

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

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Outbreaks; Waterborne Disease; Food Safety
Consider for Different Presentation?	Yes
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Affiliation	State Public Health Agency

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

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Food Safety; Zoonotic Diseases
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11618
Abstract Type	Quick
Abstract Title	Raw Milk Outbreaks in Pennsylvania – a Systematic Review, 2005-2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Foodborne Disease; Food Safety
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11059
Abstract Type	Quick
Abstract Title	Shigellosis at a Wedding — Oregon, 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Foodborne Disease; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10678
Abstract Type	Quick
Abstract Title	Stec O157:H7 Outbreak in Childcare Provides Opportunity for Infection Control Education

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Infection Control; Local Epidemiology; Outbreaks
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	11286
Abstract Type	Quick
Abstract Title	Using Student Interviewers to Enhance Capacity for Salmonellosis Investigations in Texas

Abstract

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

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

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

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Epidemiology Capacity; Foodborne Disease
Consider for Different Presentation?	Yes
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Submission Type	Breakout/Quick/Lightning/Poster
ID	10913
Abstract Type	Quick
Abstract Title	Using Whole Genome Sequencing to Uncover a Prolonged Multistate <i>Shigella Sonnei</i> Cluster, United States, 2017 — 2018

Abstract

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

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

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

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

Submission Complete?	Yes
Committee	Infectious Disease
Topic	Enteric Diseases
Keywords	Enteric Infectious Diseases; Surveillance
Consider for Different Presentation?	Yes
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Submission Type	Roundtable
ID	10731
Abstract Type	Roundtable
Abstract Title	Best Practices for Identifying, Communicating with, and Surveying Clinical Laboratories

Abstract

Key Objectives:

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

Brief Summary:

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Surveillance; Foodborne Disease
Consider for Different Presentation?	No
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Institution Affiliation	Centers for Disease Control and Prevention CDC

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

Abstract

Key Objectives:

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

Brief Summary:

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

Submission Complete?	Yes
Committee Topic	Infectious Disease Enteric Diseases
Keywords	Enteric Infectious Diseases; Outbreaks; Behavioral Health
Consider for Different Presentation?	No
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