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Geospatial Mapping of Early Cases in Multistate Foodborne Disease Outbreaks: A Strategy To Expedite Identification of Contaminated Imported Produce, United States, 2006 to 2013

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Abstract

From 1998 to 2008, produce-related illness outbreaks accounted for roughly one-half of reported foodborne outbreaks in the United States. In 2013, Mexico accounted for approximately 50 and 30% of the monetary value of all vegetables and fruits, respectively, imported into the United States. We used historical import data to examine the correlation between the port of entry for five implicated produce vehicles from five multistate outbreaks and the geospatial and temporal distribution of illnesses in the corresponding outbreaks in the United States. For comparison, we analyzed the geospatial and temporal distribution of cases from two U.S. multistate outbreaks associated with domestically grown produce. The geospatial distribution of illnesses in the two outbreaks linked to domestic produce differed from that of the import-related produce outbreaks. The results of our pilot study suggest that geospatial distribution of early-onset cases may be used to identify ports of entry for produce likely to be responsible for causing multistate outbreaks in the United States and that targeted sampling of produce items from these ports of entry may expedite identification of an outbreak vehicle.

Keywords

Geospatial; Import; Multistate; Outbreaks; Produce

Produce-related illness outbreaks account for a significant proportion of reported outbreaks of foodborne disease in the United States. From 1998 to 2008, 46% of foodborne illnesses were estimated to be attributable to produce (7). In recent decades, increasing quantities of produce have been imported into the United States; in 1999, 13 million metric tons of fruits and vegetables were imported, and by 2013 this number had grown to 21 million metric tons, accounting for about 22% of all imported food products (10). In 2013, Mexico was the largest exporter of vegetables to the United States, accounting for approximately half of the value of all vegetables imported into the United States. That same year, Mexico accounted

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for approximately 30% of the monetary value of all fruits imported into the United States (10).

Following an investigation of a multistate outbreak of salmonellosis linked to hot peppers (6), a detailed analysis of import data revealed that early-onset cases of illness were clustered in states in the southwestern and central regions of the United States, after the peppers had entered the country through Hidalgo, TX. These findings prompted us to conduct the present study of five multistate outbreaks linked to produce imported from Mexico or Central America to determine whether mapping locations of infections with different time frames, i.e., geospatial distributions, might reveal distinct patterns for early-onset illnesses that would point to port(s) of entry of implicated products.

During the course of multistate outbreaks due to foodborne pathogens, a delay invariably occurs between onset of the earliest illnesses and accumulation of enough evidence to identify the vehicle(s) responsible for causing the illnesses. Epidemiologic findings often used to identify responsible vehicles include those from descriptive epidemiology and responses from case patient interviews conducted to ascertain food histories preceding onset of illness. The results of these interviews drive hypothesis generation and, in some situations, the conduct of analytic epidemiologic studies (e.g., case-control studies). Microbiologic testing of targeted food products often takes place after the results of analytic studies identify one or more products associated with infection. When epidemiologic evidence identifies a particular food or ingredient as a likely vehicle of transmission of illness, a traceback investigation may be conducted to track a suspect food vehicle through the distribution and production chain back to its source(s) in the hopes of controlling the outbreak and preventing future illnesses. In some instances, during the hypothesis generation phase of outbreak investigations, tracebacks are conducted on suspect foods before any particular food has been implicated to identify convergence to a single source. Our rationale for conducting this analysis was to determine whether geospatial distribution of early outbreak-related illnesses may be used to identify ports of entry most likely to have received contaminated produce. Determination of a link between geospatial distribution of early cases and specific ports of entry could enhance hypothesis generation efforts and serve as a basis for targeted sampling of suspect imported foods, which ultimately could shorten the time between initial onset of illnesses in an outbreak and identification of implicated product(s).

We analyzed epidemiologic data pertaining to select import-related produce outbreaks along with U.S. Food and Drug Administration (FDA) import data for foods implicated as the causes of these outbreaks. For all foods imported into the United States, the FDA routinely collects information on ports of entry and first-line consignees, among other data. To our knowledge, with the exception of laborious, time-consuming, and expensive product traceback efforts undertaken to elucidate domestic food distribution chains involved in the setting of select outbreaks, no readily available data collection system exists in the United States to document the complete pathways that foods travel from production to points of retail sale. In contrast, FDA import data systems systematically and routinely track foods from production sites abroad to U.S. ports of entry and then to first-line consignees, which in most instances are distinct from retail points of sale that are often several steps further along the food distribution chain. Given the present lack of comprehensive and accessible databases to document food distribution channels within the United States, we conducted a pilot study using FDA import data to assess whether geospatial patterns of human illnesses linked to contaminated produce imported from Mexico or Central America could be discerned. The rationale for conducting the study was to determine the feasibility of employing such geospatial analyses of early-onset outbreak-related cases of foodborne illness to identify select ports of entry for targeted sampling of suspect foods as a means of implicating contaminated foods early in outbreak investigations.

MATERIALS AND METHODS

Epidemiologic data.

We analyzed the geospatial distribution of laboratory-confirmed cases from five multistate outbreaks in the United States associated with produce items grown in Mexico or Guatemala (import-related outbreaks) and for comparison purposes two multistate outbreaks linked to produce items grown in the United States (Table 1). Laboratory-confirmed cases of enteric infections in these outbreaks were identified through PulseNet, the national molecular subtyping network for enteric disease surveillance, coordinated by the Centers for Disease Control and Prevention. In each outbreak, pulsed-field gel electrophoresis (PFGE) was performed on clinical and, where available, food isolates. For a 2006 outbreak of *Escherichia coli* O157:H7 infections associated with domestic fresh spinach, multiple-locus variable-number tandem repeat analysis was also used to characterize isolates from the outbreak. Table 2 presents the case definitions of outbreak strains for each outbreak. Our primary analysis involved mapping the locations of infections at different times for each outbreak to determine whether particular geospatial distribution patterns emerged. Table 1 summarizes the epidemiologic features of these outbreaks. Epidemiologic details for case patients, including age, sex, and illness onset date, were obtained from PulseNet.

We chose for analysis the five outbreaks associated with produce imported from Mexico or Guatemala for several reasons: firm epidemiologic associations had been established between infections and implicated food items, public health officials had conducted product tracebacks to determine where the implicated foods had been grown, and import data were available to document the daily quantity (in kilograms) of each implicated product imported into the United States leading up to and during the outbreaks. For two of these outbreaks, the outbreak pathogen strain was recovered from samples of jalapeño or serrano peppers (*Salmonella* Saintpaul, 2008 outbreak) and papayas (*Salmonella* Agona, 2011 outbreak). For comparison, we chose for analysis two multistate outbreaks linked to domestically grown produce items (domestic-related outbreaks), one involving spinach from California that was contaminated with *E. coli* O157:H7 (2006 outbreak) and another involving cantaloupe from Indiana that was contaminated with *Salmonella* (2012 outbreak). For each comparison outbreak, the outbreak strain was recovered from food samples (i.e., spinach and cantaloupe).

To determine whether geospatial distribution of illnesses in multistate outbreaks linked to produce imported from Mexico or Guatemala could be used to identify likely ports of entry of contaminated produce, we conducted two separate analyses. The first used illness onset dates to create maps of geospatial distribution of cases, and the second used the dates that information was uploaded to the PulseNet database. For the first analysis, we used actual or estimated onset-of-illness dates specified in PulseNet for case patients. When neither the actual nor the estimated illness onset date was provided, we estimated the date by subtracting 3 days from the isolation date. When the isolation date was not specified, we calculated the mean lag for each outbreak between the illness onset date and the PulseNet upload date, if available, and then subtracted the mean lag, in days, from the PulseNet upload date to estimate the illness onset date for each case patient for whom no other dates were available. In situations where no dates were provided for case patients, we were unable to estimate the illness onset date; thus, we excluded these cases from the mapping analysis. The second analysis used the PulseNet upload date for each case patient to analyze the geospatial distribution of cases; when PulseNet upload dates were not provided for case patients, these cases were excluded from the analysis.

Product production data.

For the five outbreaks associated with produce imported from Mexico or Guatemala, we determined the weight (in kilograms) of implicated product that entered U.S. ports of entry each day from 2 months before the first reported illness onset date through 2 months after the last illness onset date. The basis for selecting this time period for analysis was an assumption that imported fresh produce has a short shelf life. These data were collected from the FDA Operational and Administrative System for Import Support, an automated system for processing and making admissibility determinations for shipments of foreign-origin FDA-regulated products seeking to enter domestic commerce. Filers (usually import brokers) input data for all prospective entries of FDA-regulated products, including produce. A filing must include a description of the product with the FDA product code and the business information of the filer, importer of record, and product manufacturer or distributor. Although data regarding cantaloupe production in Indiana were available for the 2012 multistate outbreak of *Salmonella* Typhimurium and *Salmonella* Newport infections, we were not able to collect data pertaining to spinach production in California for the 2006 outbreak of *E. coli* O157:H7 infections.

RESULTS

The geospatial distributions of illnesses are depicted in Figures 1 through 5 for the five import-related outbreaks and in Figures 6 and 7 for the domestic-related outbreaks. Because illness onset data identified ports of entry of contaminated produce more consistently and from 2 to 5 weeks earlier than did PulseNet upload data, we present here the geospatial distribution of cases using illness onset data only. For three import-related outbreaks, the contaminated produce items entered the United States from Mexico through a single port of entry: either Hidalgo, TX or Laredo, TX (Figs. 1 through 3). For the remaining two import-related outbreaks, the implicated produce items entered through multiple ports of entry: Hidalgo, TX, and Nogales, AZ (Fig. 4); and Los Angeles, CA, Dallas, TX, and Philadelphia, PA (Fig. 5).

For import-related outbreaks, we observed patterns of geospatial distribution for case patients with early onset of illness. Evaluation of the two outbreaks for which imported produce entered solely through Hidalgo, TX (Figs. 1 and 2) revealed cases with earliest onset of illness clustered in states located primarily in the southwestern and central regions of the United States. For example, for the 2008 hot pepper–associated outbreak of *Salmonella* Saintpaul infections (Fig. 1), when restricting analysis to the 5% of cases with the earliest illness onset dates (78 cases), 51 cases (65%) occurred in four southwestern states (Texas, New Mexico, Arizona, and Oklahoma), and 11 additional cases (14%) were located in two central states (Illinois and Missouri). Thus, 79% of early-onset cases resided in six states clustered in two distinct regions in an outbreak that eventually caused illnesses in 43 states and the District of Columbia. Similarly, for the 2011 papaya-associated outbreak of *Salmonella* Agona infections (Fig. 2), among the 10 reported cases with the earliest onset of illness, three (30%) occurred in three central states (Missouri, Illinois, and Minnesota), whereas six (60%) were located in southwestern and western states (Texas, New Mexico, California, and Nevada). Traceback of a prepackaged mixed salad product implicated as the cause of a 2013 outbreak of cyclosporiasis in Iowa and Nebraska revealed the product entered the United States from Mexico through Laredo, TX (Fig. 3).

For the 2013 cucumber-associated outbreak of *Salmonella* Saintpaul infections (Fig. 4), contaminated produce entered the United States through two ports of entry: Nogales, AZ (94% of product) and Hidalgo, TX (6% of product). All nine reported cases with earliest onset of illness occurred in states where contaminated product entered the United States (e.g., Texas) or in states contiguous with a state where a port of entry was located (e.g., Louisiana or California). Two first-line consignees received 94% of contaminated cucumbers that entered Nogales, AZ; these first-line consignees were located in Rio Rico, AZ, and Nogales, AZ.

With regard to the 2011 outbreak of *Salmonella* Panama infections associated with cantaloupe grown in Guatemala (Fig. 5), the earliest cases occurred in Washington and Oregon following importation of contaminated product through three ports of entry, one of which was Los Angeles, CA. The FDA import data indicated that all first-line consignees for product that entered through Texas were located in Miami, FL. First-line consignees for product that entered through Pennsylvania were located in Gloucester, NJ. Although 92% of the implicated cantaloupes entered the United States through ports of entry in Texas and Pennsylvania, only two illnesses were reported in the eastern section of the country (one each in Maryland and Pennsylvania), whereas no cases were reported in the southern section (including Florida) and midwestern section.

In contrast to import-related outbreaks, the distribution of cases with earliest onset of illness in a 2006 outbreak of *E. coli* O157:H7 infections associated with spinach grown in California exhibited a diffuse national pattern (Fig. 6). The 18 cases that constituted the initial 10% of cases were spread across 10 states from California to New York. The index case occurred in Utah, with an onset date of 22 August; three additional cases with onset of illness on the following day, 23 August, resided in New York (two cases) and California. For the 2012 outbreak of *Salmonella* Typhimurium and *Salmonella* Newport infections associated with cantaloupe grown in Indiana (Fig. 7), the geospatial distribution of cases with earliest onset of illness dates did not resemble the patterns observed for import-related outbreaks. Two-thirds of the 30 cases with earliest onset of illness in this outbreak were reported from Indiana or states contiguous with Indiana.

For all five import-related outbreaks analyzed in the present study, import data (Figs. 1 through 5) indicated that produce items ultimately implicated as the cause of illness were still in transit when the earliest outbreak-related cases (i.e., 5 to 25% of total cases) had onset of illness. Likewise, in all five import-related outbreaks analyzed here, implicated produce items were still in transit when approximately 50% of outbreak-related cases had onset of illness.

DISCUSSION

In settings of multistate outbreaks for which a food is suspected as the vehicle of transmission, various investigative methods are employed to identify the contaminated ingredient or food item. Among these are case patient interviews using hypothesis generation questionnaires and analytic epidemiologic studies, such as case-control or historical cohort studies. In instances when hypothesis generation interviews fail to identify a strong hypothesis for the outbreak source, open-ended interviews, which are unstructured and conversational in nature, may identify uncommon exposures. With increased use of molecular techniques, such as PFGE and whole genome sequencing, previously unrecognized outbreaks may be detected when bacterial isolates with indistinguishable molecular profiles are recovered from foods and clinical specimens. However, lags invariably occur between onset of initial illnesses and identification of implicated food vehicles. During these lags, case counts may increase with attendant morbidity and mortality, and secondary infections may occur. For some outbreaks, the implicated vehicle may not be identified until the outbreak has nearly ended (e.g., Fig. 1).

In the present pilot study of selected multistate outbreaks of foodborne disease attributed to produce, we present results that suggest that geospatial distribution of early-onset cases may help investigators identify U.S. ports through which contaminated product likely entered the country. A common pattern we observed was the occurrence of early-onset cases in the southwestern, western, and midwestern regions of the United States when contaminated produce traveled through a port of entry in Texas, Arizona, or California. This pattern was highlighted during the 2008 outbreak of *Salmonella* Saintpaul infections (Fig. 1) when contaminated jalapeño and serrano peppers entered the United States through Hidalgo, TX. Over three-quarters of early-onset cases occurred in six states clustered in two regions (Texas, New Mexico, Arizona, and Oklahoma; and Illinois and Missouri) despite the fact that nearly 1,500 cases were eventually reported from 43 states and the District of Columbia (1). A similar clustering of early cases in the southwestern and central regions of the United States and some cases in the western region was observed during a 2011 outbreak of *Salmonella* Agona infections associated with fresh papayas that entered the United States through Hidalgo, TX (Fig. 2). A clustering of early cases in Texas and California occurred during a 2013 outbreak of *Salmonella* Saintpaul infections associated with cucumbers shipped from Mexico through Hidalgo, TX, and Nogales, AZ (Fig. 4).

Our findings also revealed that for outbreaks involving products that entered the United States through multiple ports of entry, it was more difficult to use geospatial distributions of early-onset cases to identify a single port at which to conduct targeted sampling. For example, in the 2011 outbreak of *Salmonella* Panama infections linked to cantaloupes imported from Guatemala (Fig. 5), early-onset cases in Oregon and Washington likely resulted from ingestion of cantaloupe that entered the United States through the port of Los Angeles, but 92% of the total shipment from the implicated firm in Guatemala entered the United States through ports in Pennsylvania and Texas. Further complicating efforts to identify ports of entry based on geospatial distribution of early-onset cases may be the uneven contamination of harvested produce shipped to the United States, a situation that may lead to contaminated portions entering some ports but not others, contaminated produce going to some first-line consignees but not others, or contaminated product going to a given first-line consignee at some times but not others. For the 2011 outbreak linked to cantaloupes, we surmise that the bulk of contaminated cantaloupes entered the United States through Los Angeles, whereas a smaller amount of contaminated fruit may have entered through Pennsylvania (accounting for the single illnesses reported from that state and from Maryland). Similarly, for the 2013 outbreak of *Salmonella* Saintpaul infections associated with cucumbers, contaminated product, which went to retail points in Arizona, may have entered through Nogales at a later stage in the outbreak period.

An additional factor that challenges the effort to identify likely ports of entry of contaminated produce based on geospatial distribution of early-onset cases is the lack of rapid laboratory methods to molecularly type protozoan foodborne parasites such as *Cyclospora cayatenensis,* which may be involved in simultaneous outbreaks linked to multiple food items. For example, during summer 2013 in the United States multiple outbreaks of cyclosporiasis were thought to have occurred as a result of contamination of produce items such as prewashed mixed salad greens and cilantro. In total, more than 600 cases of cyclosporiasis were reported from 25 states and New York City (3, 5). We focused on the outbreak of cyclosporiasis in Iowa and Nebraska because public health officials in both states determined that exposure of case patients to *C. cayatenensis* at one of two chain restaurants was linked to a salad mix produced in Mexico and imported through Laredo, TX (Fig. 3) (3). In Figure 8, we present a geospatial summary of the patterns we observed with this particular outbreak and with other import-related and domestic-related outbreaks.

From a practical standpoint, the success with which targeted sampling of produce items at select ports of entry during early outbreak investigations can identify one or more products contaminated with the outbreak strain depends on clear signals emerging from hypothesis generating interviews or open-ended interviews. The stronger the signal for one or more food items, the more targeted the sampling can be. In contrast, vague or equivocal signals obtained from such interviews regarding suspect vehicles will likely compromise efforts to identify outbreak strains in sampled items. Traceback results documenting clear, consistent, and verified pathways of one or more suspect products from a single source of production may aid investigators in targeted sampling of produce items at ports of entry.

Geospatial distribution of outbreak-related foodborne illnesses ultimately reflects the availability of implicated food vehicles in each location. For imported products, availability in specific geographic markets likely depends on multiple factors, such as food preferences, availability of local substitutes, and costs of transporting foods to markets. Currently, approximately 350 ports of entry serve as portals through which imported foods enter the United States, and 21 of these entry ports are located along the U.S.-Mexico border. Ongoing produce sampling programs at ports of entry conducted by the FDA test only a small fraction of produce entering the United States and are based on results of previous sampling assignments, recent foodborne illness cases, and other essential data. For example, in fiscal year 2016, the FDA collected a total of 1,969 samples of produce items for microbiological testing at ports of entry. In the setting of outbreaks linked to produce imported from Mexico and Central America, we believe a combination of product demand and efficiency of market distribution explains why earliest onset cases were located principally in the southwestern, western, and central regions of the United States. Thus, during early stages of investigations of outbreaks with epidemiologic features consistent with produce as a likely vehicle (e.g., preponderance of cases in young and middle-aged women (8)) it may be prudent for public health authorities to sample select produce items (2) for microbiologic culture analysis at targeted ports of entry based on the geospatial distribution of earliest illnesses. Such early targeted sampling at ports of entry may be particularly relevant when illnesses occur during out-of-season growing periods in the United States for produce items suspected of causing an outbreak. In two of the outbreaks we included in the present analysis (2011 *Salmonella* Panama infections associated with cantaloupes from Guatemala and the 2013 *Salmonella* Saintpaul infections associated with cucumbers from Mexico), onset of illness occurred during a time of year (winter and spring) when the implicated vehicles were not likely to have been grown in the United States (9). We believe that early targeted sampling of select products at ports of entry is not a stand-alone strategy but, rather, one best used to complement other investigative methods, the most important being the collection of rigorous epidemiologic data. Targeted sampling at ports of entry is feasible only when sufficient epidemiologic data exist to point to produce as a likely vehicle of infection; lacking such data, sampling of produce at select ports of entry is likely to be ineffective, to divert scarce resources, and potentially to delay ongoing investigations.

The potential for analysis of the geospatial distribution of illnesses during outbreaks to identify Mexico or Central America as a possible source of contaminated produce was demonstrated in 2010 and 2011. The *Salmonella* Agona strain from the 2011 papaya-associated outbreak presented in this study was composed of four closely related PFGE patterns (Table 2) that had been rarely identified before in PulseNet (4). Three of these four PFGE patterns were first identified in 2010 when a total of 119 illness cases from 14 states were reported from May to September. Distribution of age, sex, ethnicity, and state of residence among ill persons was similar to the distribution seen in the 2011 outbreak. Despite an intensive investigation during summer 2010 by local, state, and federal public health agencies focusing on fresh fruit, including papaya, the source of the outbreak was not determined. In 2010, the FDA did not sample papayas at ports of entry to the United States, whereas such sampling conducted in 2011 identified the outbreak strain of *Salmonella* Agona from papayas shipped from Mexico.

Analyses utilizing geospatial distribution of early-onset illnesses may be useful for outbreaks that involve foods other than produce imported from nations other than Mexico or Central America. The data that the FDA routinely collects on the foreign origin of FDA-regulated foods seeking to enter domestic commerce includes information such as description of each product, name and address of manufacturers, countries of production, and the port of entry into the United States. The methods and results presented here serve as a pilot study and are not intended to be applicable for all foods imported from Mexico and Central America. Further efforts are needed to determine whether the methods described here could be useful for identifying ports of entry for targeted product sampling in the setting of outbreaks due to produce or other food items imported from countries other than Mexico or Central America.

Our study has several limitations. First, underdiagnosis and/or underreporting of foodborne illnesses may have skewed the true geospatial distribution patterns of illnesses in the outbreaks we selected for study. If this were true, states with more aggressive investigative, diagnostic, and reporting practices would be more likely to register outbreak-related illnesses than would states with less robust practices. Second, for outbreaks in which a single PFGE pattern was used to define laboratory-confirmed outbreak-related cases (such as the one in 2008 involving *Salmonella* Saintpaul infections associated with hot peppers; Fig. 1), some cases defined as outbreak related may not actually have been related to the outbreak. With increased reliance on dual PFGE patterns and whole genome sequencing, such misclassifications are less likely to occur in future outbreaks. Third, the present lack of rapid laboratory methods to molecularly type protozoan foodborne parasites such as *C. cayatenensis* makes it difficult to identify outbreak strains in a timely manner, as is possible for bacterial pathogens. Fourth, the inherent time lag between dates of onset of illness and dates of upload in PulseNet can affect analysis based on these data. Although a retrospective analysis such as that described here revealed general patterns of geospatial distribution of early onset cases in select import-related outbreaks, lags between onset of illnesses, PulseNet upload dates, and hypothesis generating interviews (or open-ended interviews) may hinder accurate recall of foods consumed, thereby complicating efforts to identify outbreak vehicles. In some instances, contaminated produce responsible for causing illnesses may have already passed through ports of entry by the time targeted sampling is undertaken. Fifth, whereas databases maintained by the FDA routinely track ports of entry and locations of first-line consignees for imported foods, to our knowledge no publicly available databases routinely track the distribution of food products through domestic market channels within the United States. As a result, in outbreak settings investigators must complete laborious and resource-consuming traceback procedures beginning with retail points of purchase to ascertain the source of the implicated product. The accuracy of such traceback investigations depends in part upon the validity of invoices at multiple market distribution points.

In conclusion, we believe further research is merited to determine whether assessments of geospatial distributions of early-onset illness cases in the setting of ongoing foodborne disease outbreaks may be used to identify likely ports of entry for potential targeted sampling of suspect produce items. It is particularly important to determine whether this strategy can be used economically, practically, and effectively to speed the rate at which currently employed epidemiologic measures identify foodborne vehicles responsible for causing import-related outbreaks.

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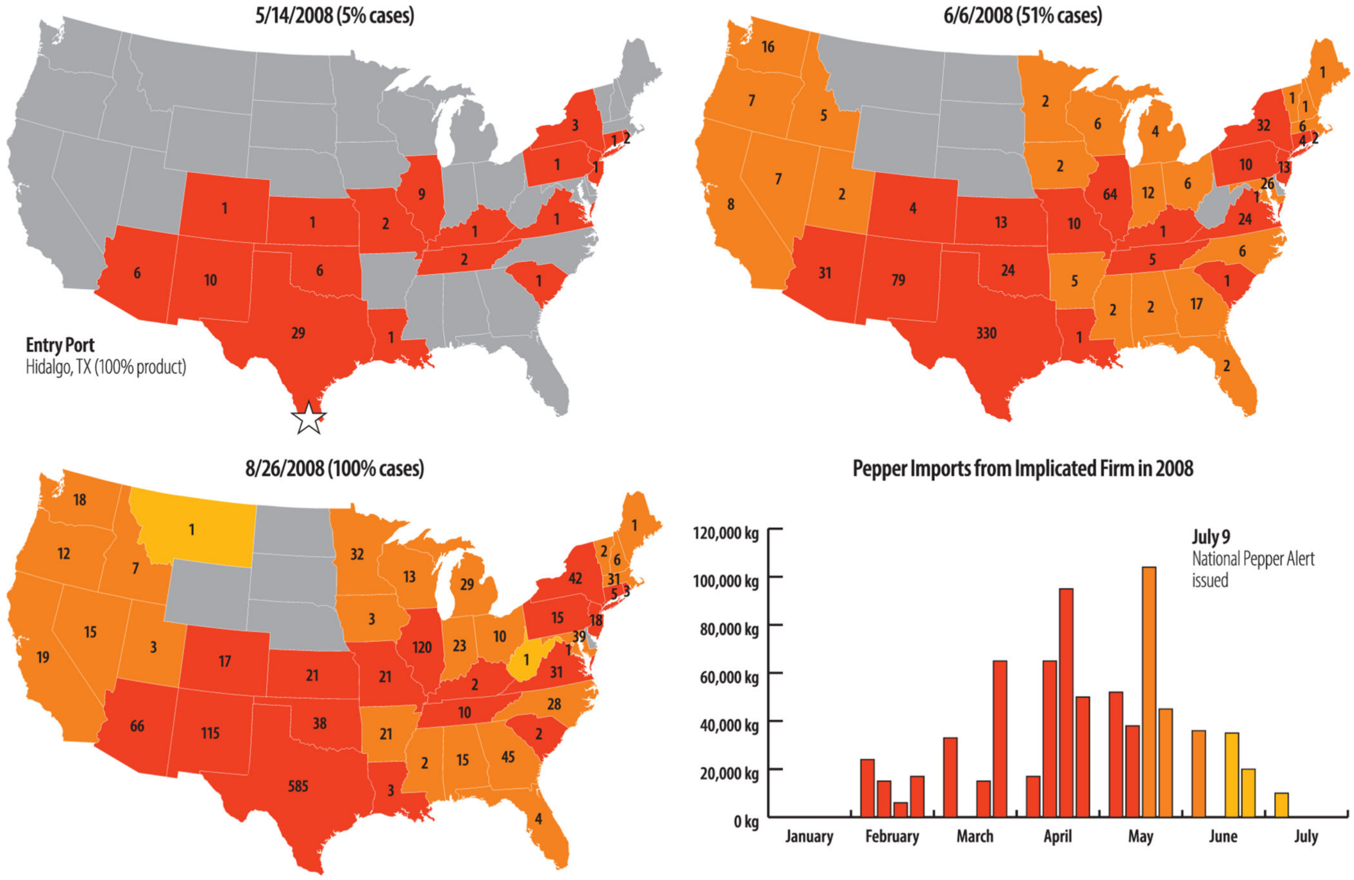
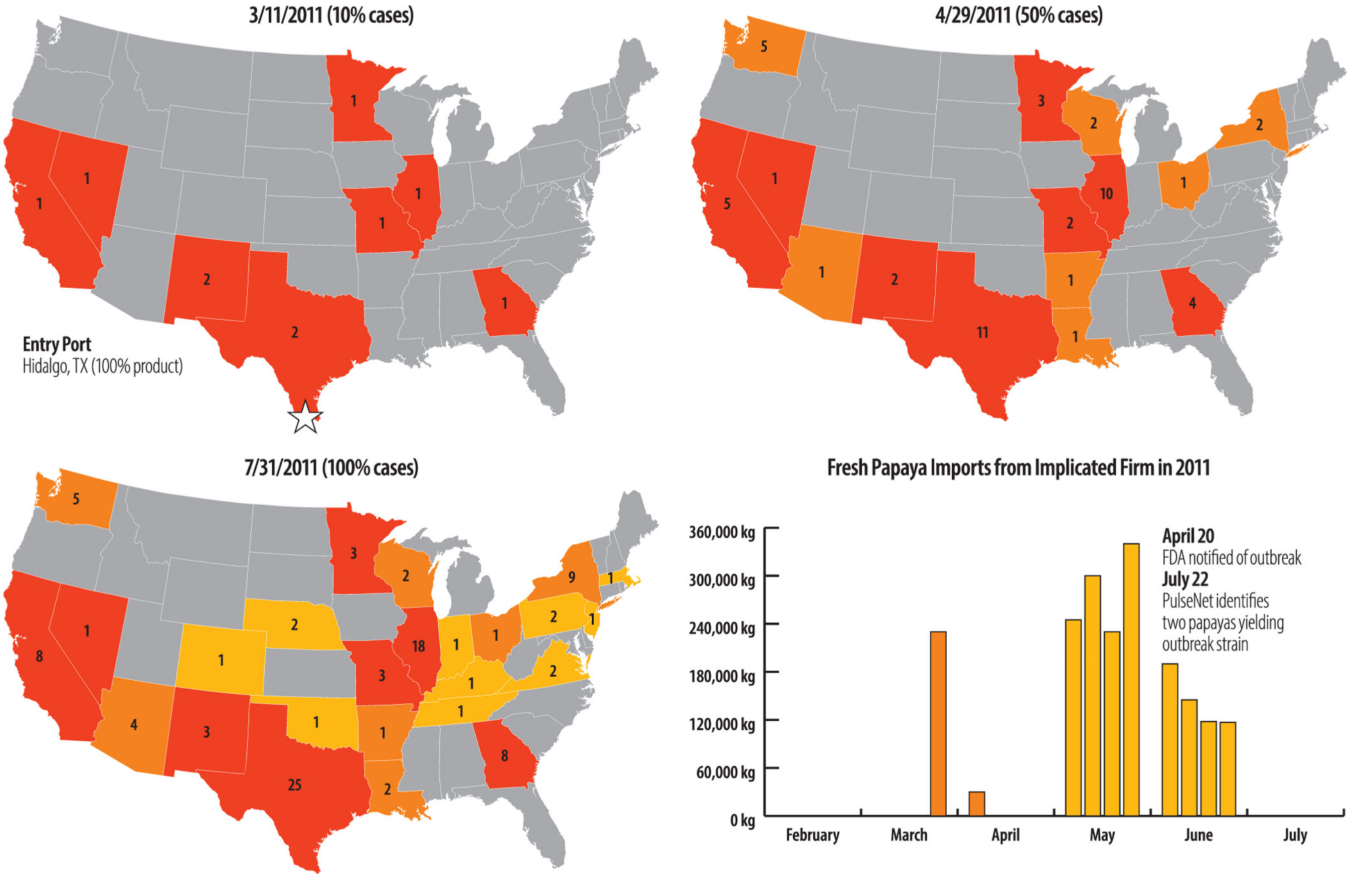


FIGURE 1.

Cumulative number of cases of Salmonella *Saintpaul infection (*n *= 1,495) associated with jalapeño and serrano peppers, by state, by date of onset of illness, 2008 (16 April to 26 August). Peppers were imported from Mexico. States with outbreak-related cases with onset of illness during one of three time periods in 2008: red, 16 April to 14 May; orange, 15 May to 6 June; yellow, 7 June to 26 August. Gray, states reporting no cases.*



3/11/2011 (10% cases)

Entry Port
Hidalgo, TX (100% product)

4/29/2011 (50% cases)

7/31/2011 (100% cases)

Fresh Papaya Imports from Implicated Firm in 2011

April 20
FDA notified of outbreak
July 22
PulseNet identifies two papayas yielding outbreak strain

FIGURE 2.

Cumulative number of cases of Salmonella *Agona infection (*n *= 102) associated with fresh papayas, by state, by date of onset of illness, 2011 (17 January to 31 July). Papayas were imported from Mexico. States with outbreak-related cases with onset of illness during one of three time periods in 2011: red, 17 January to 11 March; orange, 12 March to 29 April; yellow, 30 April to 31 July. Gray, states reporting no cases.*

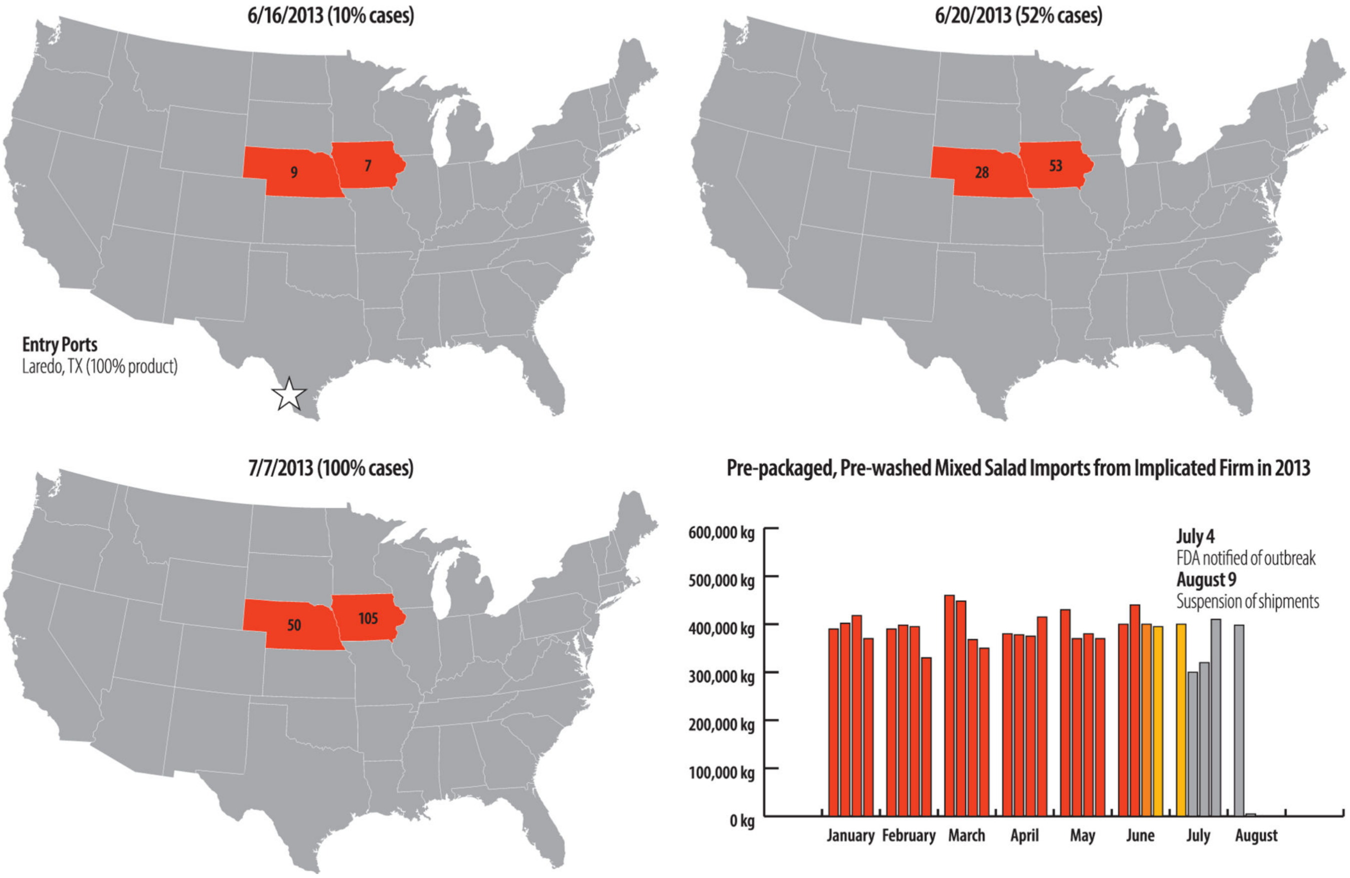


FIGURE 3.

*Cumulative number of cases (*n = *162) of cyclosporiasis associated with prepackaged prewashed mixed salad, by state, by date of onset of illness, 2013 (4 June to 7 July). The mixed salad was imported from Mexico. States with outbreak-related cases with onset of illness during one of three time periods in 2013: red, 4 to 16 June; orange, 17 to 20 June; yellow, 21 June to 7 July. Gray, states reporting no cases.*

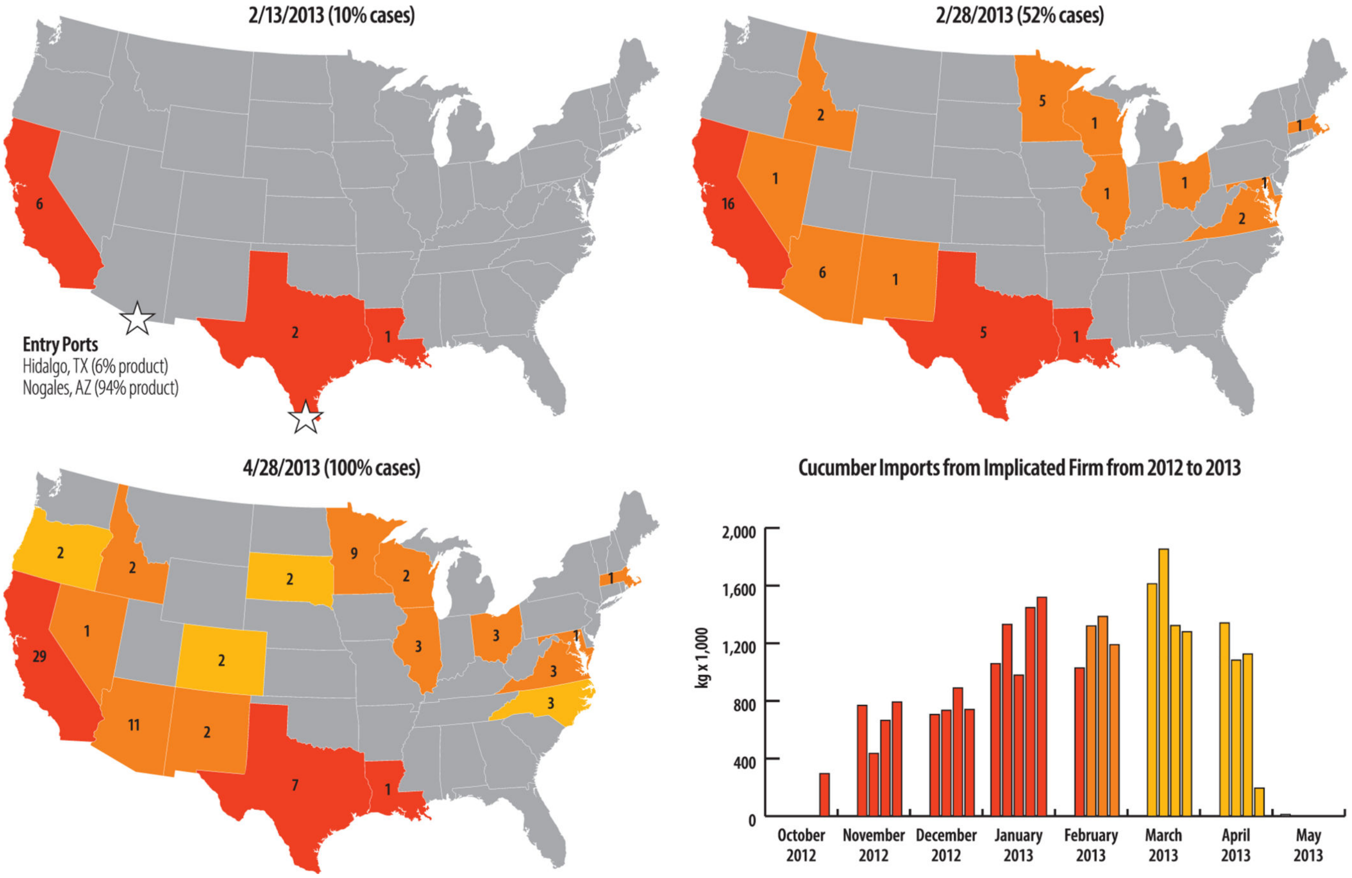


FIGURE 4.

Cumulative number of cases of Salmonella *Saintpaul infection (*n *= 84) associated with fresh cucumbers, by state, by date of onset of illness, 2013 (12 January to 28 April). Cucumbers were imported from Mexico. States with outbreak-related cases with onset of illness during one of three time periods in 2013: red, 12 January to 13 February; orange, 14 to 28 February; yellow, 1 March to 28 April. Gray, states reporting no cases.*

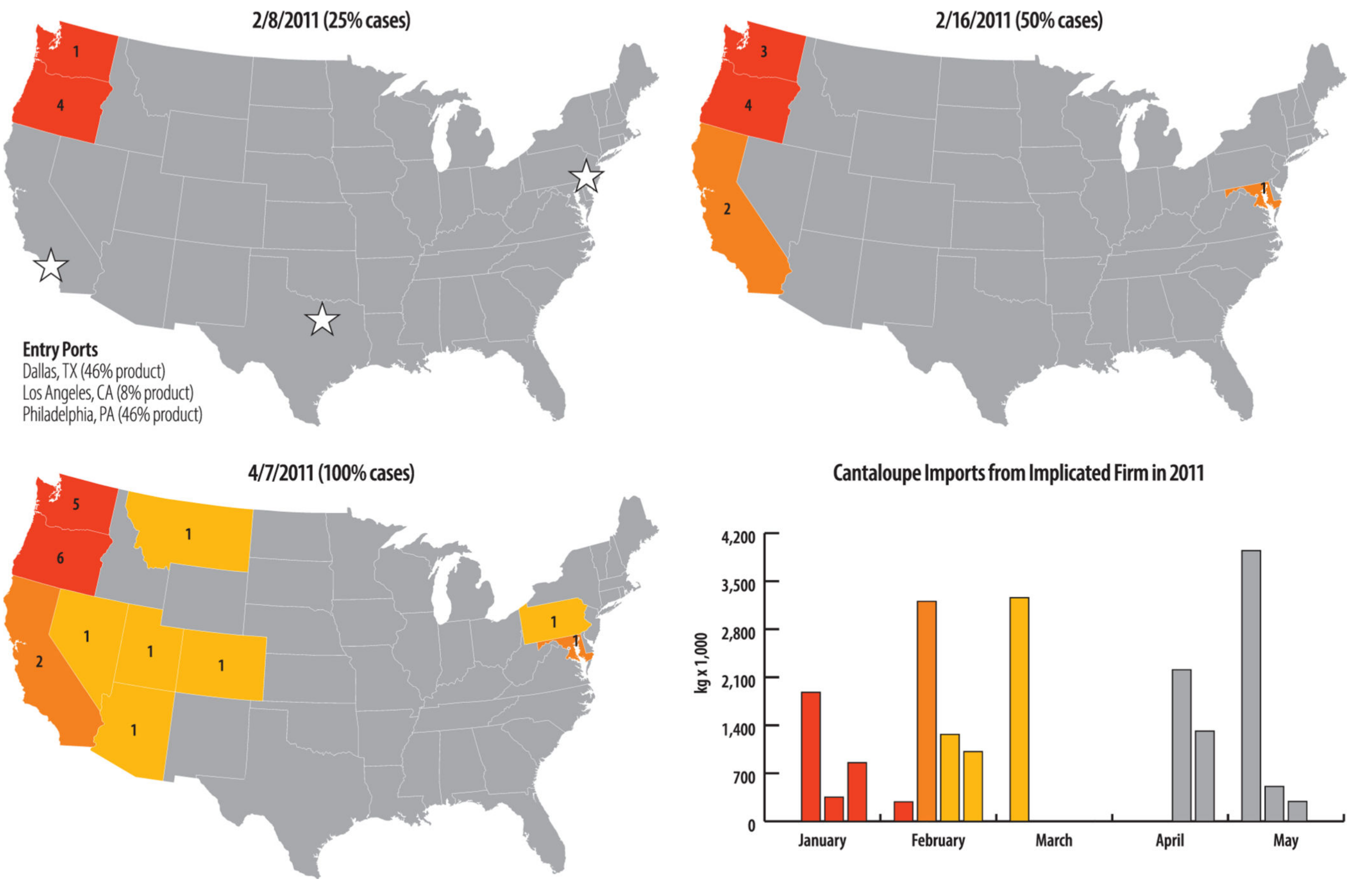


FIGURE 5.

*Cumulative number of cases (*n = *20) of* Salmonella *Panama infection associated with fresh cantaloupes, by state, by date of onset of illness, 2011 (5 February to 7 April). Cantaloupes were imported from Guatemala. States with outbreak-related cases with onset of illness during one of three time periods in 2011: red, 5 to 8 February; orange, 9 to 16 February; yellow, 17 February to 7 April. Gray, states reporting no cases.*

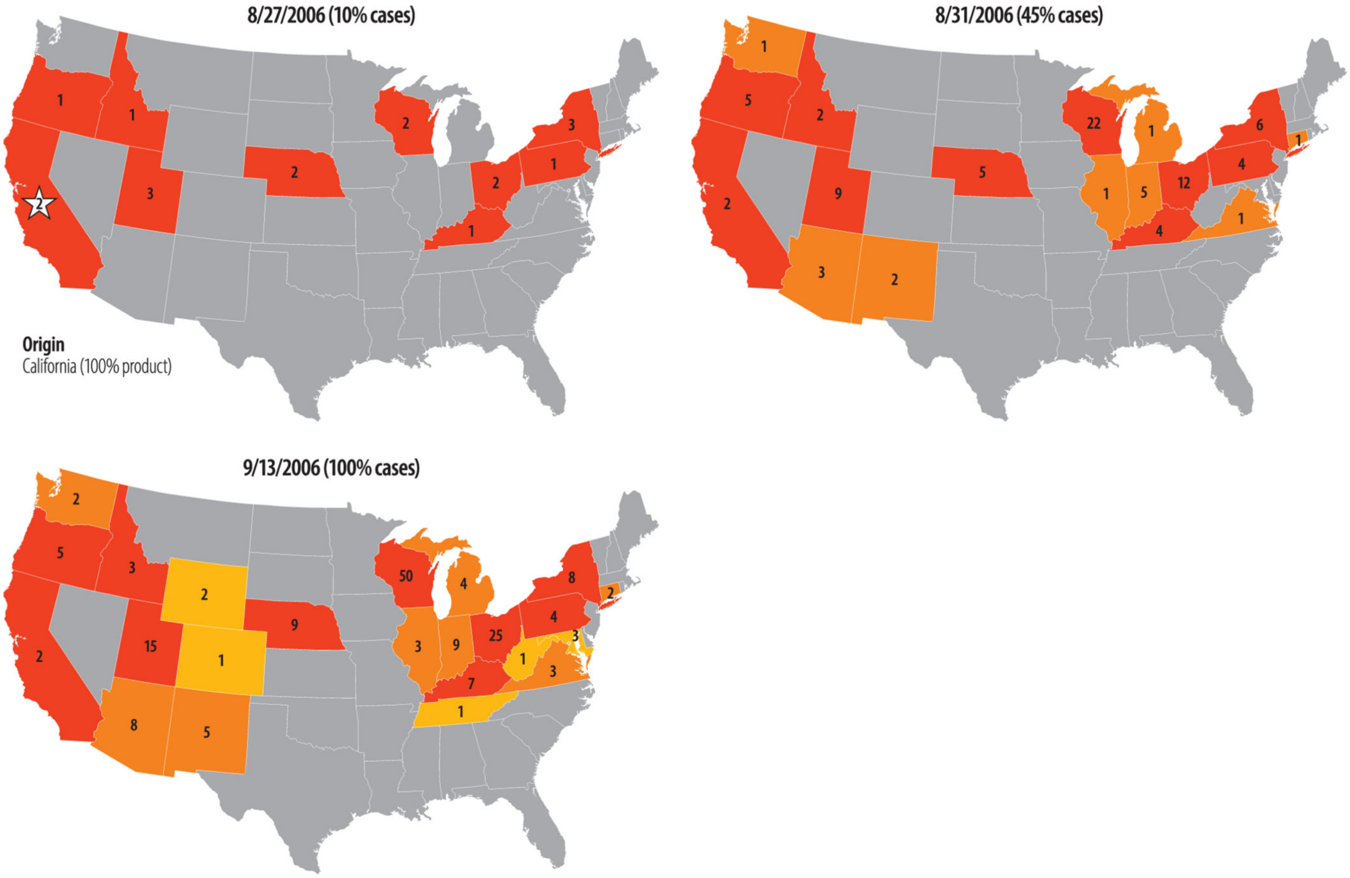


FIGURE 6.

Cumulative number of cases of E. coli *O157:H7 infection (*n *= 191) associated with fresh spinach, by state, by date of onset of illness, 2006 (22 August to 13 September). Spinach was grown in California. No onset date was given for 20 cases (not included in the maps). States with outbreak-related cases with onset of illness during one of three time periods in 2006: red, 22 to 27 August; orange, 28 to 31 August; yellow, 1 to 13 September. Gray, states reporting no cases.*

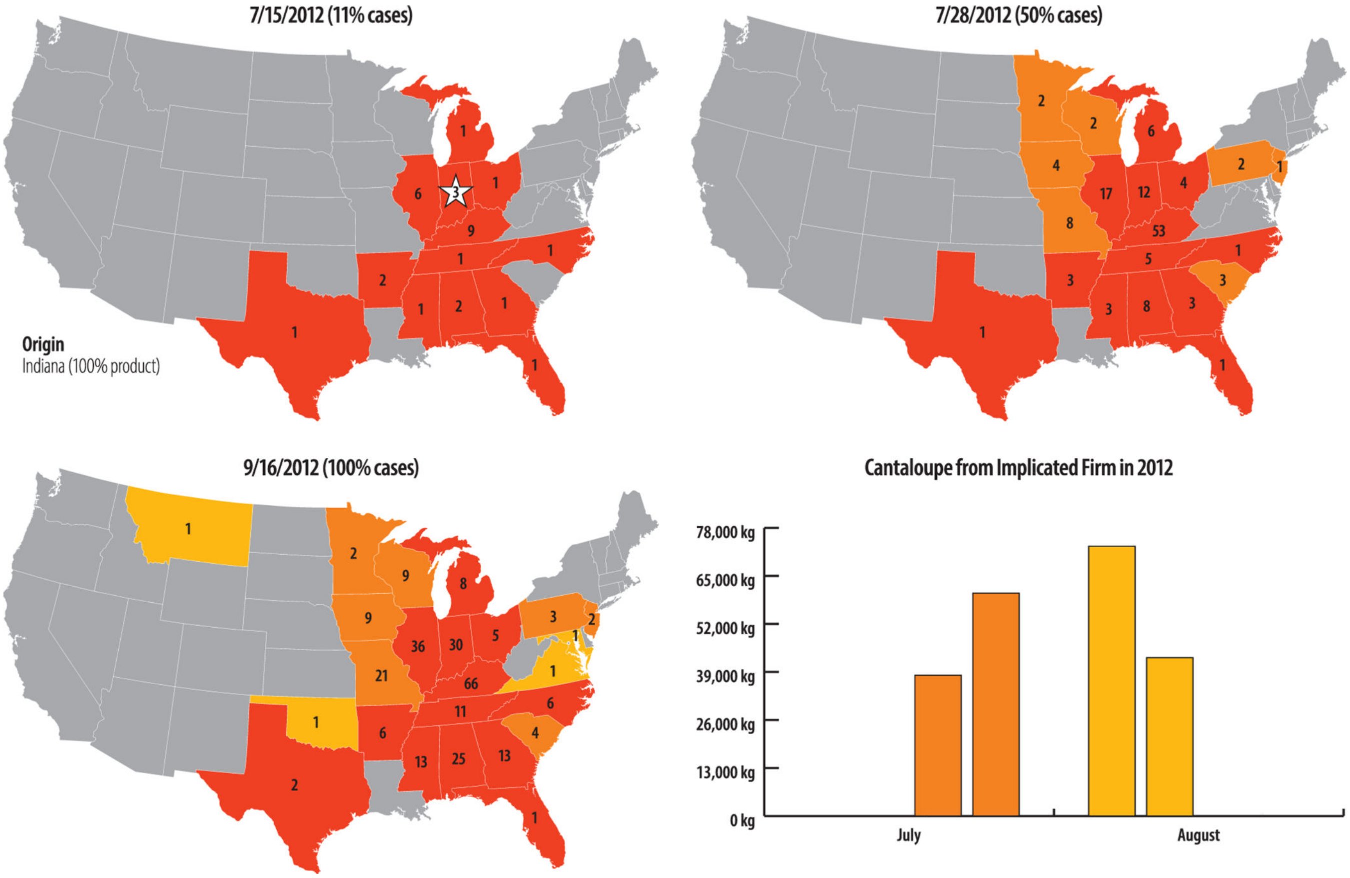


FIGURE 7.

Cumulative number of cases of Salmonella *Typhimurium and* Salmonella *Newport infections (*n *= 272) associated with fresh cantaloupe, by state, by date of onset of illness, 2012 (6 July to 16 September). Cantaloupe was grown in Indiana. States with outbreak-related cases with onset of illness during one of three time periods in 2012: red, 6 to 15 July; orange, 16 to 28 July; yellow, 29 July to 16 September. Gray, states reporting no cases.*

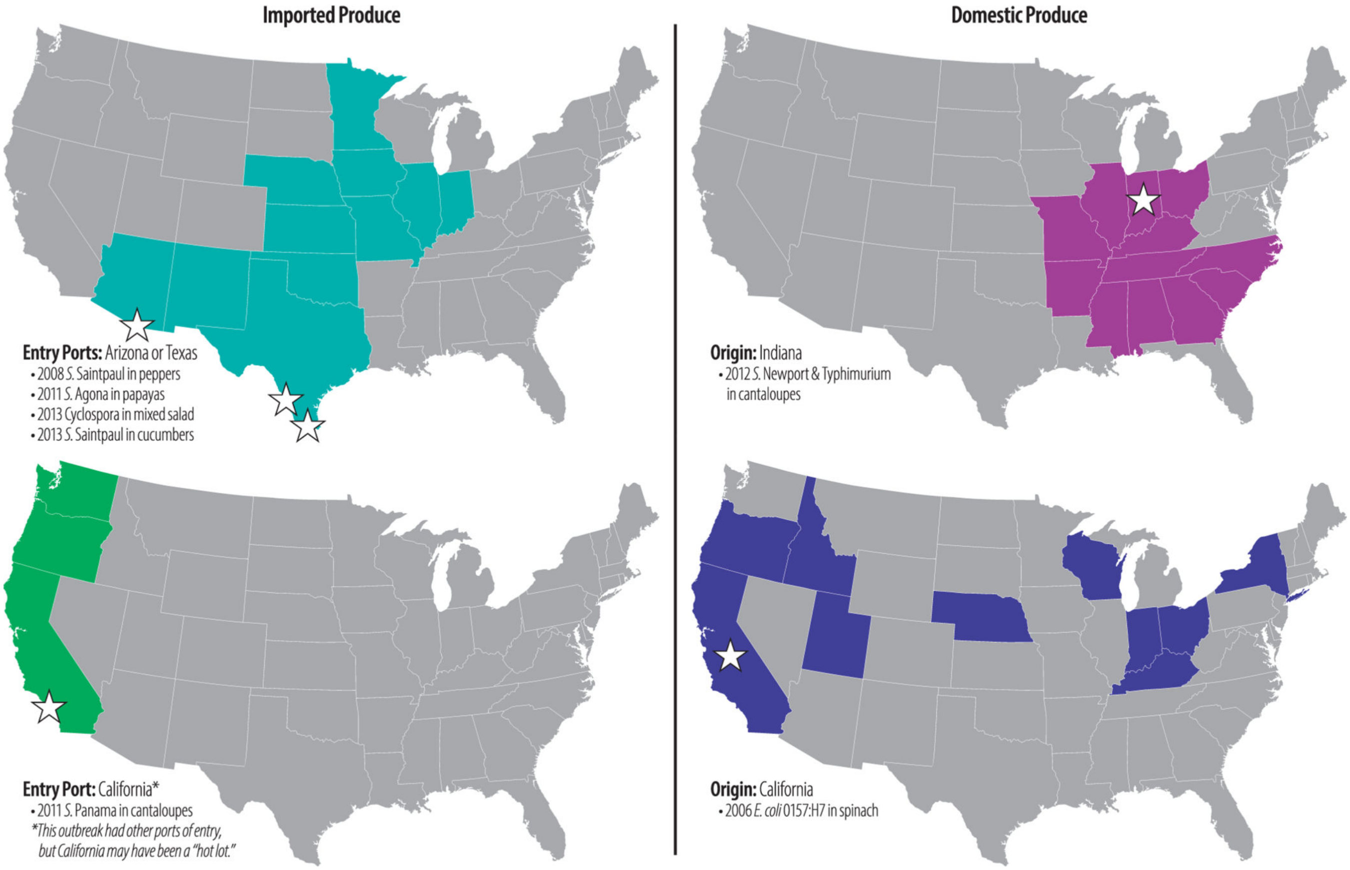


FIGURE 8.

Geospatial summary of distributions of early-onset cases in five import-related multistate foodborne outbreaks with ports of entry and two domestic-related multistate foodborne outbreaks with origin or source of produce. Turquoise, states with reported cases associated with produce from ports of entry in Arizona or Texas; green, states with reported cases associated with produce from ports of entry in California; purple, states with reported cases associated with cantaloupe from Indiana; blue, states with reported cases associated with spinach from California.

TABLE 1.

Epidemiologic features of illnesses involved in multistate outbreaks associated with produce from Mexico or Central America (import related) or the United States (domestic)

Outbreak	Food vehicle	Source	Outbreak dates[a]	No. of states	No. of illnesses	Median age (yr)	% female individuals
Import related							
2008 *Salmonella* Saintpaul	Jalapeño and serrano peppers	Mexico	16 Apr.–26 Aug. 2008	43 + District of Columbia	1,495	31	50
2011 *Salmonella* Agona	Papaya	Mexico	17 Jan.–24 June 2011	25	102	29	56
2011 *Salmonella* Panama	Cantaloupe	Guatemala	5 Feb.–7 Apr. 2011	10	20	12.5	37
2013 *Salmonella* Saintpaul	Cucumber	Mexico	12 Jan.–28 Apr. 2013	17	84	27	62
2013 *Cyclospora cayatenensis*	Prepackaged mixed salad	Mexico	4 June–7 July 2013	2	162	57	61
Domestic							
2006 *Escherichia coli* O157:H7	Spinach	California	22 Aug.–13 Sep. 2006	23	191	27	73
2012 *Salmonella* Typhimurium and *Salmonella* Newport	Cantaloupe	Indiana	6 July–16 Sep. 2012	23	272	47	55

[a] Range of onset of illnesses.

TABLE 2.

Molecular profiles specified in case definitions for laboratory confirmation of outbreak strains linked to produce from Mexico or Central America (import related) or the United States (domestic)

	Outbreak strain PFGE profile	
Outbreak	***Xba*I**	***Bln*I**
Import related		
2008 *Salmonella* Saintpaul	JN6X01.0048	
2011 *Salmonella* Agona	JABX01.0653	JABA26.0047
	JABX01.0122	
	JABX01.0701	
2011 *Salmonella* Panama	JKGX01.0367	JKGA26.0003
2013 *Salmonella* Saintpaul	JN6X01.0161	JN6A26.0020
		JN6A26.0025
		JN6A26.0213
2013 *Cyclospora cayatenensis*	None	
Domestic		
2006 *Escherichia coli* O157:H7	EXHX01.0124 MLVA pattern A[a]	EXHA26.0015
2012 *Salmonella* Typhimurium and *Salmonella* Newport	JPXX01.0324 JJPX01.0807	JPXA26.0363 JJPA26.029

[a] This *E. coli* outbreak strain had multiple-locus variable-number tandem repeat analysis (MLVA) pattern A in addition to the PFGE profiles.