
Attribution of Foodborne Illnesses, Hospitalizations, and Deaths to Food Commodities by using Outbreak Data, United States, 1998–2008

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Each year, >9 million foodborne illnesses are estimated to be caused by major pathogens acquired in the United States. Preventing these illnesses is challenging because resources are limited and linking individual illnesses to a particular food is rarely possible except during an outbreak. We developed a method of attributing illnesses to food commodities that uses data from outbreaks associated with both simple and complex foods. Using data from outbreak-associated illnesses for 1998–2008, we estimated annual US foodborne illnesses, hospitalizations, and deaths attributable to each of 17 food commodities. We attributed 46% of illnesses to produce and found that more deaths were attributed to poultry than to any other commodity. To the extent that these estimates reflect the commodities causing all foodborne illness, they indicate that efforts are particularly needed to prevent contamination of produce and poultry. Methods to incorporate data from other sources are needed to improve attribution estimates for some commodities and agents.

Despite advances in food safety, foodborne illness remains common in the United States; >9 million persons each year have a foodborne illness caused by a major pathogen (1). One challenge in preventing foodborne illness is determining how to prioritize limited food safety resources across a large number of foods (2). Furthermore, attributing all illnesses to specific foods is challenging because most agents are transmitted through a variety of foods, and linking an illness to a particular food is rarely possible except during an outbreak.

To help determine priorities for food safety efforts, we organized the large number of foods implicated in outbreaks in the United States into 17 mutually exclusive food

commodities. Here, we provide estimates of the number of domestically acquired foodborne illnesses, hospitalizations, and deaths attributable to these commodities.

Methods

Data Sources

State and local health departments report foodborne disease outbreaks to the Centers for Disease Control and Prevention (CDC) through the Foodborne Disease Outbreak Surveillance System (3). Reports include, when available, number of persons ill, outbreak etiology, description of the implicated food vehicle(s), lists of ingredients, and identification of the contaminated ingredient(s). We reviewed all outbreaks from 1998, the first year with detailed information on ingredients, through 2008 that were reported to the CDC by October 2010. For this analysis, we included all outbreaks with an implicated food vehicle and a single etiologic agent.

Health officials may report whether an etiologic agent was confirmed or suspected on the basis of published criteria (4,5) and the method of confirmation. Reports may include ≥ 1 of 5 reasons for implicating a food vehicle: 1) statistical evidence from an epidemiologic investigation; 2) laboratory evidence identifying the etiologic agent in the implicated food; 3) compelling or other supportive data; 4) previous experience suggesting that the food vehicle is the source; and 5) other data, such as identification of the same etiologic subtype on the farm that supplied the implicated food. We considered an implicated food confirmed when 1 of the first 2 reasons was reported. Other implicated food vehicles were considered suspect.

To determine whether to analyze outbreaks with suspect foods, we reviewed a convenience sample of 117 outbreak reports for which the reason for implication was not reported. Supporting evidence implicated the food vehicle

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for 65% of these reports. Some of these outbreaks involved too few persons to conduct an epidemiologic investigation; in most, no food was tested. Outbreaks with suspect vehicles constituted a large proportion of the dataset, but it was not possible to locate and review the documentation for all investigations. However, because a large percentage of documentation reviewed had reasonable evidence to implicate the reported food, we included all outbreaks with suspect foods in the analysis.

During 1998–2008, a total of 13,352 foodborne disease outbreaks, causing 271,974 illnesses, were reported in the United States (online Technical Appendix 1 Table 1, wwwnc.cdc.gov/EID/article/19/3/11-1866-Techapp1.pdf). Of those outbreaks, 4,887 (37%), causing 128,269 (47%) illnesses, had an implicated food vehicle and a single etiology; 298 of those outbreaks were excluded because information about the vehicle was insufficient to categorize the ingredients. We also did not include the 3% of outbreaks that had multiple etiologies reported.

To assess possible bias when including outbreaks with a suspected vehicle or etiology in our estimates, we compared the rank order of each of the 17 food commodities in our model based on the total number of associated illnesses with the rank order when including only those illnesses with a confirmed etiology and vehicle. The order of the top 8 commodities associated with the highest number of illnesses changed only slightly (ranks 5 and 6 switched); therefore, we included all outbreaks to maximize the data available for the lower-ranking commodities.

The estimated number of domestically acquired illnesses, hospitalizations, and deaths for each etiology was obtained from published estimates (1) or, when not available, by extrapolating from available data. To highlight differences in sources for nontyphoidal *Salmonella* spp. serotypes, we made estimates for those most frequently isolated from humans (i.e., Enteritidis, Heidelberg, Javiana, Newport, Typhimurium) and, separately, for all others. We estimated the number of illnesses, hospitalization, and deaths by multiplying the numbers for nontyphoidal *Salmonella* spp. (1) by the proportion of all serotyped human *Salmonella* isolates reported during 1998–2008 (6).

The outbreak dataset included outbreaks with chemical etiologies and those caused by *Anisakis simplex*, for which published illness estimates were not available. For these, the number of illnesses was estimated as the product of the mean annual number of illnesses reported to CDC through outbreak surveillance during 1998–2008 by using the same multipliers for underdiagnosis ($\times 25$), underreporting ($\times 30$), case-hospitalization rate ($\times 0.006$), and case-fatality rate ($\times 0.0004$) as for infection with *Clostridium perfringens*, a short-duration illness (1).

We attempted to attribute food commodities for an estimated 9,638,301 illnesses, 57,462 hospitalizations, and 1,451 deaths caused by known agents (online Technical Appendix 1 Table 2). We did not attribute illnesses to commodities for illnesses caused by astrovirus, *Mycobacterium bovis*, *Toxoplasma gondii*, and *Vibrio vulnificus* because no outbreaks were reported for these pathogens. These pathogens caused an estimated 1.1% of illnesses, 8.1% of hospitalizations, and 25.2% of deaths (a high number of deaths were estimated to be caused by toxoplasmosis [1]).

Food Categorization

We defined 3 commodities for aquatic animals (fish, crustaceans, and mollusks), 6 for land animals (dairy, eggs, beef, game, pork, and poultry), and 8 for plants (grains-beans; oils-sugars [refined plant foods]; fruits-nuts; fungi; and leafy, root, sprout, and vine-stalk vegetables) (7). Foods were categorized into ≥ 1 of 17 mutually exclusive commodities according to ingredients listed in outbreak reports, or, when ingredients were not listed, in recipes found on the Internet (7). In some analyses, we grouped commodities (Figure 1).

We defined as simple an implicated food vehicle that contained ingredients from 1 commodity, such as apple juice (fruits-nuts commodity). This category included foods such as fruit salad that were composed of several ingredients from the same commodity. We defined as complex an implicated food vehicle that contained ingredients from ≥ 1 commodity, such as apple pie (made of ingredients from several commodities: fruits-nuts [apples],

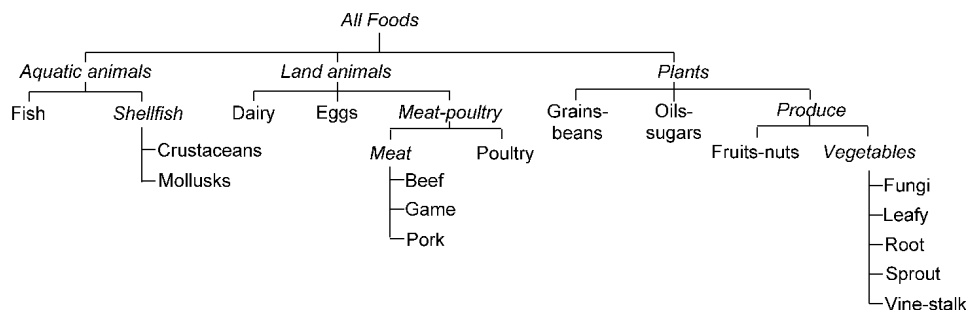


Figure 1. Hierarchy of food commodities. *Italics* indicate commodity groups.

grains-beans [flour], oils-sugars [sugar], and dairy [butter]). We excluded water as an ingredient.

Estimation Method

We calculated for each etiology the proportion of outbreak-associated illnesses transmitted by each commodity. We allocated illnesses from simple food outbreaks of a given etiology to their single implicated commodities. For each complex food outbreak, we partitioned the associated illnesses to the multiple implicated commodities in proportion to the relative numbers of illnesses in all simple food outbreaks that implicated those specific commodities; we then added the results from all outbreaks to obtain commodity illness percentages. We then applied the commodity-specific percentage of ill persons to the total estimated proportion of domestically acquired illnesses, hospitalizations, and deaths for each etiology (1). Last, we added the total proportions of commodity-specific illnesses, hospitalizations, and deaths for simple and complex foods for all etiologies. We considered these the most probable estimates for each commodity (online Technical Appendix 2, wwwnc.cdc.gov/EID/article/19/3/11-1866-Techapp2.pdf).

To provide a range for the most probable estimates, we determined a minimum estimate by attributing illnesses to commodities implicated only in outbreaks where illness was transmitted by simple foods and a maximum estimate by including complex food outbreaks and attributing the outbreak illnesses to each ingredient in the implicated food (online Technical Appendix 1 Table 3). Thus, all illnesses in a complex food outbreak with 3 ingredient commodities were included 3 times, once for each commodity. The numbers provided in the Results section are the most probable estimate, unless stated otherwise. Calculations were performed in SAS version 9.3 (SAS Institute, Cary, NC, USA).

Results

The final dataset consisted of 4,589 outbreaks with an implicated food vehicle and a single etiologic agent (online Technical Appendix 3, wwwnc.cdc.gov/EID/article/19/3/11-1866-Techapp3.xlsx; online Technical Appendix 1 Table 1); a total of 120,321 outbreak-associated illnesses were caused by 36 agents (online Technical Appendix 1 Table 2). Norovirus caused the most outbreaks (1,419) and outbreak-associated illnesses (41,257), far above the median for all agents (29 outbreaks, 1,208 illnesses). No outbreaks were caused by *Mycobacterium bovis*, *Vibrio vulnificus*, astrovirus, or *Toxoplasma gondii*. The implicated food vehicle was complex for 2,239 (49%) outbreaks (online Technical Appendix 1 Table 2); the median number of commodities for complex food vehicles was 4 (range 2–13).

We applied percentages derived from outbreak-associated illnesses for each etiology to the 9.6 million

estimated annual illnesses assessed and attributed \approx 4.9 million (\approx 51%) to plant commodities, \approx 4.0 million (\approx 42%) to land animal commodities, and \approx 600,000 (\approx 6%) to aquatic animal commodities (Table 1). Produce commodities (fruits-nuts and the 5 vegetable commodities) accounted for 46% of illnesses; meat-poultry commodities (beef, game, pork, and poultry) accounted for 22%. Among the 17 commodities, more illnesses were associated with leafy vegetables (2.2 million [22%]) than any other commodity. The high estimate for illnesses attributable to leafy vegetables was many times higher than the low estimate (Figure 2, panel A), which indicates that leafy vegetables were frequently found in complex foods. After leafy vegetables, the commodities linked to the most illnesses were dairy (1.3 million [14%]), fruits-nuts (1.1 million [12%]), and poultry (900,000 [10%]). Norovirus comprised 57% of all illnesses.

An estimated 26,000 (46%) annual hospitalizations were attributed to land animal commodities, 24,000 (41%) to plant commodities, and 3,000 (6%) to aquatic animal commodities (Table 2). Produce commodities accounted for 38% of hospitalizations and meat-poultry commodities for 22%. Dairy accounted for the most hospitalizations (16%), followed by leafy vegetables (14%), poultry (12%), and vine-stalk vegetables (10%) (Figure 2, panel B). Among the estimated 57,000 hospitalizations, 8% were not attributed to a pathogen, mainly because the dataset did not include data for *Toxoplasma* spp.

An estimated 629 (43%) deaths each year were attributed to land animal, 363 (25%) to plant, and 94 (6%) to aquatic commodities (Table 3). Meat-poultry commodities accounted for 29% of deaths and produce 23%. Among the 17 commodities, poultry accounted for the most deaths (19%), followed by dairy (10%), vine-stalk vegetables (7%), fruits-nuts (6%), and leafy vegetables (6%) (Figure 2, panel C). Of the 278 deaths attributed to poultry, most were attributed to *Listeria monocytogenes* (63%) or *Salmonella* spp. (26%). Among the 1,451 estimated deaths, 25% were not attributed to a pathogen, mainly because the dataset did not include data for *Toxoplasma* spp.

Most bacterial illnesses were attributed to dairy (18%), poultry (18%), and beef (13%) commodities (Table 1). Most chemical illnesses were attributed to fish (60%, most caused by the marine biotoxin ciguatoxin). Most parasitic illnesses were attributed to mollusks (33%) and fruits-nuts (26%); this reflects the fact that 1 simple food outbreak was caused by *Giardia intestinalis* (mollusks) and 1 by *Cryptosporidium* spp. (fruits-nuts). Most viral illnesses were attributed to leafy vegetables (35%), fruits-nuts (15%), and dairy (12%). Of the 20 outbreaks associated with simple foods and caused by norovirus transmitted by dairy, 14 (70%) were transmitted by cheese products.

The plant commodity group accounted for 66% of viral, 32% of bacterial, 25% of chemical, and 30% of

Table 1. Estimates of annual domestically acquired foodborne illnesses attributed to specific food commodities and commodity groups, by pathogen type, United States, 1998–2008*

Commodity or commodity group	No. (%) illnesses				
	All agents	Bacterial	Chemical	Parasitic	Viral
Aquatic animals†	589,310 (6.1)	142,415 (3.9)	153,488 (61.6)	77,795 (33.3)	215,613 (3.9)
Fish	258,314 (2.7)	15,362 (0.4)	148,958 (59.8)	955 (0.4)	93,040 (1.7)
Shellfish†	330,997 (3.4)	127,053 (3.5)	4,531 (1.8)	76,840 (32.9)	122,573 (2.2)
Crustaceans	46,528 (0.5)	32,626 (0.9)	1,247 (0.5)		12,654 (0.2)
Mollusks	284,469 (3.0)	94,427 (2.6)	3,283 (1.3)	76,840 (32.9)	109,919 (2.0)
Land animals†	4,021,839 (41.7)	2,334,000 (64.0)	33,031 (13.3)	156 (0.1)	1,654,651 (30.0)
Dairy	1,330,098 (13.8)	656,951 (18.0)	3,773 (1.5)		669,374 (12.1)
Eggs	574,298 (6.0)	179,421 (4.9)	6,995 (2.8)		387,882 (7.0)
Meat-poultry†	2,117,442 (22.0)	1,497,628 (41.1)	22,263 (8.9)	156 (0.1)	597,394 (10.8)
Meat†	1,174,257 (12.2)	844,006 (23.2)	2,437 (1.0)	156 (0.1)	327,658 (5.9)
Beef	639,640 (6.6)	482,199 (13.2)	661 (0.3)		156,780 (2.8)
Game	9,934 (0.1)	5,111 (0.1)	1,568 (0.6)	156 (0.1)	3,100 (0.1)
Pork	524,684 (5.4)	356,697 (9.8)	209 (0.1)		167,778 (3.0)
Poultry	943,185 (9.8)	653,622 (17.9)	19,826 (8.0)		269,737 (4.9)
Plants†	4,924,877 (51.1)	1,169,202 (32.1)	62,753 (25.2)	69,023 (29.5)	3,623,899 (65.8)
Grains-beans	435,936 (4.5)	183,394 (5.0)	12,995 (5.2)		239,547 (4.3)
Oils-sugars	65,631 (0.7)		2,344 (0.9)		63,287 (1.1)
Produce†	4,423,310 (45.9)	985,807 (27.0)	47,414 (19.0)	69,023 (29.5)	3,321,066 (60.3)
Fruits-nuts	1,123,808 (11.7)	230,636 (6.3)	29,483 (11.8)	60,573 (25.9)	803,116 (14.6)
Vegetables†	3,299,501 (34.2)	755,171 (20.7)	17,931 (7.2)	8,450 (3.6)	2,517,949 (45.7)
Fungi	4,542 (0.0)	686 (0.0)	3,857 (1.5)		
Leafy	2,152,652 (22.3)	188,327 (5.2)	9,113 (3.7)	7,256 (3.1)	1,947,955 (35.4)
Root	349,715 (3.6)	96,910 (2.7)	1,240 (0.5)		251,566 (4.6)
Sprout	32,703 (0.3)	32,703 (0.9)			
Vine-stalk	759,889 (7.9)	436,546 (12.0)	3,721 (1.5)	1,194 (0.5)	318,428 (5.8)
Undetermined	102,275 (1.1)	156 (0.0)		86,686 (37.1)	15,433 (0.3)
Total	9,638,301 (100.0)	3,645,773 (100.0)	249,273 (100.0)	233,660 (100.0)	5,509,596 (100.0)

*Most estimates from (1); some were made as described in Methods. Numbers of illnesses are the most probable estimate, as described in Methods.

Estimates are rounded; some row and column sums may differ from their totals. Blank cells indicate no data.

†Indicates commodity group.

parasitic illnesses (Table 1). This group accounted for a greater proportion of illnesses than the land or aquatic animal commodity groups for *Bacillus cereus*; *Clostridium botulinum*; enterotoxigenic *Escherichia coli*; Shiga toxin-producing *Escherichia coli* (STEC) O157; non-O157 STEC; *Salmonella enterica* serotypes Javiana, Newport, and other (e.g., serotypes other than Javiana, Newport, Enteritidis, Heidelberg, Typhimurium, and Typhi); *Shigella* spp.; mycotoxins; other chemicals; *Cryptosporidium* spp.; *Cyclospora cayentansensis*; hepatitis A; norovirus; and sapovirus (Table 4, Appendix, wwwnc.cdc.gov/EID/article/19/3/11-1866-T4.htm). The land animal group accounted for the highest proportion of illnesses for *Campylobacter* spp., *Clostridium perfringens*, *Listeria* spp., *Salmonella* serotypes Enteritidis and Heidelberg, *Streptococcus* spp. group A, *Yersinia enterocolitica*, and *Trichinella* spp.

Discussion

We developed a method to attribute domestically acquired foodborne illnesses, hospitalizations, and deaths in the United States to specific commodities by using outbreak data. We found most illnesses were attributed to plant commodities and most deaths to land animal commodities. We attributed 46% of illnesses to produce; the large number of

norovirus illnesses was a major driver of this result. More deaths were attributed to poultry than to any other commodity. To the extent that these outbreak-based estimates reflect the commodities associated with all foodborne illness, they indicate that efforts are particularly needed to prevent contamination of produce and poultry.

More illnesses were attributed to leafy vegetables (22%) than to any other commodity; illnesses associated with leafy vegetables were the second most frequent cause of hospitalizations (14%) and the fifth most frequent cause of death (6%). Previous studies have shown that produce-containing foods were the food source for approximately half of norovirus outbreaks with an identified simple food vehicle during 2001–2008 (8) and the second most frequent food source for *E. coli* O157 outbreaks during 1982–2002 (9). Outbreaks of *E. coli* O157 infections transmitted by spinach (10) and lettuce (11) and *Salmonella* spp. infections transmitted by tomatoes (12,13), juice (14,15), mangoes (16), sprouts (17,18), and peppers (19,20) underline concerns about contamination of produce consumed raw.

More deaths were attributed to poultry (19%) than to any other commodity, and most poultry-associated deaths were caused by *Listeria* or *Salmonella* spp. From 1998 through 2002, three large listeriosis outbreaks were linked to turkey delicatessen meat contaminated in the processing

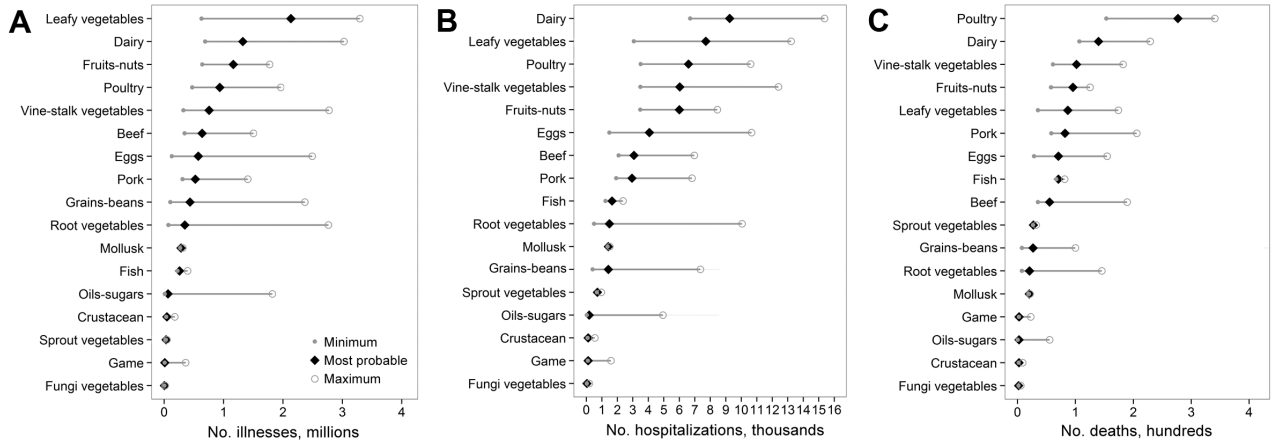


Figure 2. Minimum, most probable, and maximum estimates of the annual number of foodborne illnesses, hospitalizations, and deaths from all etiologies attributed to food commodities, United States, 1998–2008. A) Foodborne illnesses; 102,275 (1.1%) illnesses were not attributed to a commodity and are not shown. B) Foodborne illness–associated hospitalizations; 4,639 (8.1%) hospitalizations were not attributed to a commodity and are not shown. C) Foodborne illness–associated deaths; 366 (25.2%) deaths were not attributed to a commodity and are not shown. Minimum and maximum values represent extreme boundaries for the most probable estimate; they are not the SE of the most probable estimate. For commodities with outbreaks associated with only simple food vehicles, the minimum, maximum, and most probable estimate are the same. For commodities with outbreaks associated with both simple and complex foods, the minimum and maximum estimates reflect the different weighting given to outbreaks associated with complex foods relative to simple. When the most probable estimate for a commodity is close to the minimum estimate, most illnesses from outbreaks associated with complex foods were attributed to another commodity in the food implicated in the outbreak; when the most probable estimate for a commodity is close to the maximum estimate, most illnesses from outbreaks associated with complex foods were attributed to that commodity.

plant after cooking (21–23). A risk-ranking model for listeriosis among ready-to-eat foods identified delicatessen meat as the highest risk food (24).

The dairy commodity was the second most frequent food source for infections causing illnesses (14%) and deaths (10%). Foods in this commodity are typically consumed after pasteurization, which eliminates pathogens, but improper pasteurization and incidents of contamination after pasteurization occur (25). In our dataset, norovirus outbreaks associated with cheese illustrate the role of contamination of dairy products after pasteurization by food handlers. Because of the large volume of dairy products consumed, even infrequent contamination of commercially distributed products can result in many illnesses (26). The prominence of dairy in our model reflects a relatively high number of reported outbreaks associated with raw milk compared with the quantity of raw milk consumed (27) and issues related to *Campylobacter* spp. infection (discussed below); these factors likely resulted in an overestimation of illnesses attributed to dairy. Models that partition raw versus pasteurized milk and that incorporate other data sources for *Campylobacter* spp. infection could improve estimates of illnesses related to dairy.

Our method of attributing illnesses incorporated data from outbreaks associated with complex foods and attributed most of the estimated number of illnesses caused by known pathogens to specific food sources. Other methods for attributing illnesses to food sources may be applied to

various stages of the food distribution chain and therefore may yield different but complementary estimates (2). A method for *Salmonella* spp. attribution used in Denmark compared isolates from food animal reservoirs with human isolates to attribute infections to the reservoirs, the live animals (28). A similar method in a US study attributed *Salmonella* spp.–associated foodborne illnesses to the point of processing (29). Risk assessment models have focused primarily on the point of processing; case studies of sporadic illness, expert elicitation, and analysis of outbreak data represent attribution at the point of consumption. Outbreak investigations have been reported for most foodborne etiologies and food commodities and provide the most comprehensive data for attribution.

We made several assumptions. We assumed that using the number of outbreak-associated illnesses rather than number of outbreaks would enable better assignment of illnesses to commodities. Our choice had the potential to bias the results toward large outbreaks. However, large outbreaks often represent system failures that have resulted in smaller, undetected outbreaks; investigation may determine the source for illnesses that otherwise might have been considered sporadic. Small outbreaks may better represent sources of sporadic illnesses, but because many small outbreaks are not detected or investigated, their sources would not be well represented by any method. Similar studies have used outbreak counts (30,31); either choice (number of outbreak-associated illnesses or number of outbreaks)

Table 2. Estimates of annual hospitalizations for domestically acquired foodborne illnesses attributed to specific food commodities and commodity groups, by pathogen type, United States, 1998–2008*

Commodity or commodity group	No. (%) hospitalizations				
	All agents	Bacterial	Chemical	Parasitic	Viral
Aquatic animals†	3,199 (5.6)	1,158 (3.2)	921 (61.6)	231 (4.7)	889 (5.8)
Fish	1,661 (2.9)	210 (0.6)	894 (59.8)	6 (0.1)	551 (3.6)
Shellfish†	1,538 (2.7)	948 (2.6)	27 (1.8)	225 (4.6)	338 (2.2)
Crustaceans	117 (0.2)	75 (0.2)	7 (0.5)		34 (0.2)
Mollusks	1,421 (2.5)	873 (2.4)	20 (1.3)	225 (4.6)	303 (2.0)
Land animals†	26,118 (45.5)	21,471 (60.0)	198 (13.3)	6 (0.1)	4,443 (29.1)
Dairy	9,284 (16.2)	7,464 (20.9)	23 (1.5)		1,798 (11.8)
Eggs	4,062 (7.1)	2,979 (8.3)	42 (2.8)		1,041 (6.8)
Meat-poultry†	12,772 (22.2)	11,029 (30.8)	134 (8.9)	6 (0.1)	1,604 (10.5)
Meat†	6,138 (10.7)	5,238 (14.6)	15 (1.0)	6 (0.1)	880 (5.8)
Beef	3,075 (5.4)	2,650 (7.4)	4 (0.3)		421 (2.8)
Game	117 (0.2)	94 (0.3)	9 (0.6)	6 (0.1)	8 (0.1)
Pork	2,946 (5.1)	2,494 (7.0)	1 (0.1)		450 (2.9)
Poultry	6,634 (11.5)	5,791 (16.2)	119 (8.0)		724 (4.7)
Plants†	23,506 (40.9)	13,043 (36.4)	377 (25.2)	221 (4.5)	9,865 (64.5)
Grains-beans	1,437 (2.5)	695 (1.9)	78 (5.2)		664 (4.3)
Oils-sugars	184 (0.3)		14 (0.9)		170 (1.1)
Produce†	21,885 (38.1)	12,349 (34.5)	284 (19.0)	221 (4.5)	9,031 (59.1)
Fruits-nuts	5,829 (10.1)	3,279 (9.2)	177 (11.8)	213 (4.4)	2,160 (14.1)
Vegetables†	16,057 (27.9)	9,070 (25.3)	108 (7.2)	8 (0.2)	6,871 (45.0)
Fungi	37 (0.1)	14 (0.0)	23 (1.5)		
Leafy	7,769 (13.5)	2,393 (6.7)	55 (3.7)	7 (0.1)	5,314 (34.8)
Root	1,501 (2.6)	793 (2.2)	7 (0.5)		700 (4.6)
Sprout	713 (1.2)	713 (2.0)			
Vine-stalk	6,038 (10.5)	5,157 (14.4)	22 (1.5)	1 (0.0)	857 (5.6)
Undetermined	4,639 (8.1)	124 (0.3)		4,428 (90.6)	87 (0.6)
Total	57,462 (100.0)	35,797 (100.0)	1,496 (100.0)	4,886 (100.0)	15,284 (100.0)

*Most estimates from (1); some were made as described in Methods. Numbers of hospitalizations are the most probable estimate, as described in Methods. Estimates are rounded; some row and column sums may differ from their totals. Blank cells indicate no data.

†Indicates commodity group.

results in biases (32). Because of other methodological differences, direct comparison of the results for these studies is difficult. To assess the effect of outbreak size on our estimates, we adjusted our model to give no weight to outbreak size (online Technical Appendix 1 Tables 4, 5); the rank order of commodities by number of attributed illnesses changed by no more than 1 for most commodities. The largest outbreak in our study was 1,644 *Campylobacter* spp.-associated illnesses resulting from the consumption of pasteurized milk; even so, counting outbreaks instead of illnesses resulted in a relatively small (2.6%) reduction in the percentage of illnesses attributed to dairy.

We further assumed outbreak illnesses represented all illnesses and weighted the results for each agent by number of all foodborne illnesses attributed to each agent (1). Unweighted outbreak data may be biased toward seafood outbreaks caused by marine biotoxins (e.g., scombroid) that are frequently reported but cause relatively few illnesses. For some agents, foods implicated in outbreaks might not well represent foods responsible for sporadic illnesses. For example, outbreak data underrepresent poultry (8%) and overrepresent dairy (67%) as sources of *Campylobacter* spp. infection; studies of sporadic infections implicate consumption of poultry but not dairy as a major risk factor (33). *Campylobacter* spp. are estimated to be the third most

common bacterial cause of foodborne illness, but relatively few outbreaks are detected (1). For pathogens for which outbreaks are uncommon or do not reflect major modes of transmission, methods that incorporate data from nonoutbreak sources are needed.

We also assumed that, for a given agent, when an outbreak was associated with a complex food, the likelihood that any commodity was the source was proportional to the frequency of illnesses for outbreaks associated with simple foods associated with that commodity. However, when the number of outbreaks associated with simple foods for an etiology is small compared with the number associated with complex foods, the result may be biased toward commodities for which simple foods were vehicles for outbreaks. Other attribution estimates that used outbreak surveillance data have excluded complex foods or have not partitioned them into component commodities (9,34). Were complex food outbreaks excluded, the result for each commodity would be the same as our minimum estimate. However, inclusion of outbreaks associated with complex foods provides important information. For example, in a review of egg-associated *S. enterica* serotype Enteritidis outbreaks (35), eggs were implicated as simple food vehicles in 20% of the outbreaks, but complex foods containing eggs were implicated in an additional 57% of the outbreaks.

Table 3. Estimates of annual deaths resulting from domestically acquired foodborne illnesses attributed to specific food commodities and commodity groups, by pathogen type, United States, 1998–2008*

Commodity or commodity group	No. (%) deaths				
	All agents	Bacterial	Chemical	Parasitic	Viral
Aquatic animals†	94 (6.4)	24 (2.8)	61 (61.6)	2 (0.7)	6 (3.7)
Fish	71 (4.9)	8 (1.0)	60 (59.8)	0 (0.1)	2 (1.4)
Shellfish†	23 (1.6)	16 (1.8)	2 (1.8)	2 (0.6)	4 (2.3)
Crustaceans	3 (0.2)	2 (0.2)	0 (0.5)		0 (0.2)
Mollusks	20 (1.4)	14 (1.6)	1 (1.3)	2 (0.6)	3 (2.1)
Land animals†	629 (43.3)	570 (66.2)	13 (13.3)	0	45 (29.0)
Dairy	140 (9.7)	121 (14.0)	2 (1.5)		18 (11.8)
Eggs	71 (4.9)	57 (6.6)	3 (2.8)		11 (6.8)
Meat-poultry†	418 (28.8)	393 (45.5)	9 (8.9)	0	16 (10.4)
Meat†	140 (9.7)	130 (15.1)	1 (1.0)	0	9 (5.7)
Beef	55 (3.8)	51 (5.9)	0 (0.3)		4 (2.7)
Game	3 (0.2)	2 (0.2)	1 (0.6)	0	0 (0.1)
Pork	82 (5.7)	77 (9.0)	0 (0.1)		5 (2.9)
Poultry	278 (19.1)	262 (30.4)	8 (8.0)		7 (4.7)
Plants†	363 (25.0)	229 (26.5)	25 (25.2)	4 (1.2)	105 (67.4)
Grains-beans	27 (1.9)	16 (1.8)	5 (5.2)		6 (4.1)
Oils-sugars	3 (0.2)		1 (0.9)		2 (1.1)
Produce†	333 (22.9)	213 (24.7)	19 (19.0)	4 (1.2)	97 (62.2)
Fruits-nuts	93 (6.4)	55 (6.4)	12 (11.8)	4 (1.2)	22 (14.2)
Vegetables†	240 (16.5)	158 (18.3)	7 (7.2)	0	75 (48.0)
Fungi	2 (0.1)	0	2 (1.5)		
Leafy	88 (6.0)	27 (3.1)	4 (3.7)	0	57 (36.7)
Root	21 (1.4)	12 (1.4)	0 (0.5)		9 (5.6)
Sprout	27 (1.9)	27 (3.2)			
Vine-stalk	102 (7.0)	92 (10.6)	1 (1.5)	0	9 (5.7)
Undetermined	366 (25.2)	39 (4.5)		327 (98.1)	0
Total	1,451 (100.0)	862 (100.0)	100 (100.0)	333 (100.0)	156 (100.0)

*Most estimates from (1); some were made as described in Methods. Numbers of deaths are the most probable estimate, as described in Methods. Estimates are rounded; some row and column sums may differ from their totals. Blank cells indicate no data.

†Indicates commodity group.

A limitation of our study is the absence of outbreaks caused by some agents. None caused by *Toxoplasma* spp. or *Vibrio vulnificus* were reported. The attributable risk for *Toxoplasma* infection is highest for meat (49%) and mollusks (16%) (36); most foodborne *V. vulnificus* infections are linked to oysters (37). The effect of this absence of data for agents that are uncommon but often cause fatal illnesses is reflected mostly in the number of deaths in our study, 25% of which were not attributed. Attributing an additional 49% of *Toxoplasma* spp.–associated deaths to meats would make meats a more frequent source of foodborne illness–associated deaths than poultry. Attributing all foodborne deaths caused by *V. vulnificus* and 16% of those caused by *Toxoplasma* spp. to mollusks would move this commodity from the thirteenth to the fourth most frequent source of foodborne illness–associated deaths.

Other limitations of our study included the choice not to use the credible interval for the estimated number of illnesses, hospitalization, and deaths (1); the lack of published estimates for the number of illnesses caused by chemical etiologies; and the fact that the quality of outbreak data is dependent on the quality and quantity of investigations reported. We maximized the amount of data we compiled by including outbreaks with suspect etiologies or vehicles and developing a method to incorporate

data from outbreaks attributed to both simple and complex foods; even so, our study yielded a paucity of data for some agents. Among the agents associated with <10 outbreaks in the dataset, only 1 (non-O157 STEC) is estimated to cause >1% of foodborne illnesses caused by known agents (1). Our estimates should be considered an approximation, to be refined by further research and analyses. To improve the quality and accuracy of outbreak attribution, models can be developed that include other types of data (e.g., studies of sporadic cases, isolates from foods and animals, agent subtypes). Measurements that indicate the substantial uncertainty of many of the estimates are particularly critical for agents causing few outbreaks and those for which the major sources for outbreaks are dissimilar to those for sporadic cases. Ultimately, the best data sources and methods for estimating the number of illnesses, hospitalizations, and deaths attributable to each food commodity may vary by etiologic agent, commodity, point of food chain analyzed, and other factors.

For consistency and to obtain sufficient data, we chose to use all years of data for all pathogens, but a shorter, more recent period is desirable when major implicated commodities have changed. For example, outbreaks of *Listeria* spp. infection caused by contamination of ready-to-eat meats markedly decreased after 2002

(38). However, using data from only the few listeriosis outbreaks that occurred after 2002 would result in a few commodities having a large effect on results. Developing methods to examine trends should be a high priority. When combined with updated estimates of the number of illnesses, attribution analyses performed at appropriate intervals could help determine the results of prevention efforts. Longer intervals would increase data for agents with few outbreaks, but if the frequency of illness attributed to a commodity changes substantially, results might not reflect the current situation.

In summary, our outbreak-based method attributed most foodborne illnesses to food commodities that constitute a major portion of the US diet. When food commodities are consumed frequently, even those with a low risk for pathogen transmission per serving may result in a high number of illnesses. The attribution of foodborne-associated illnesses and deaths to specific commodities is useful for prioritizing public health activities; however, additional data on the specific food consumed is needed to assess per-serving risk. The risk for foodborne illness is just one part of the risk–benefit equation for foods; other factors, such as the health benefits of consuming a diet high in fruits and vegetables, must also be considered (39).

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Dr Painter is an epidemiologist with the Centers for Disease Control and Prevention who worked for the Division of Foodborne, Waterborne, and Environmental Diseases while most of the work for this study was completed. Currently, he is the epidemiology team lead for the Immigrant, Refugee, and Migrant Health Branch of the Division of Global Migration and Quarantine. His research interests include outbreak investigations and the epidemiology of tuberculosis among foreign-born persons.

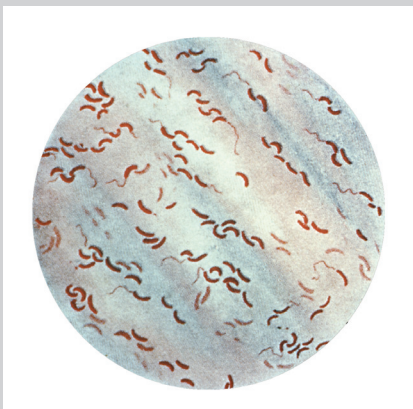
References

- Scallan E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, et al. Foodborne illness acquired in the United States—major pathogens. *Emerg Infect Dis*. 2011;17:7–15.
- Batz MB, Doyle MP, Morris G Jr, Painter J, Singh R, Tauxe RV, et al. Attributing illness to food. *Emerg Infect Dis*. 2005;11:993–9. <http://dx.doi.org/10.3201/eid1107.040634>
- Centers for Disease Control and Prevention. Outbreak surveillance data. 2010 [cited 2012 Jun 22]. http://www.cdc.gov/outbreaknet/surveillance_data.html
- Lynch M, Painter J, Woodruff R, Braden C. Surveillance for foodborne-disease outbreaks—United States, 1998–2002. *MMWR Surveill Summ*. 2006;55:1–42.
- Olsen SJ, MacKinnon LC, Goulding JS, Bean NH, Slutsker L. Surveillance for foodborne-disease outbreaks—United States, 1993–1997. *MMWR CDC Surveill Summ*. 2000;49:1–62.
- Centers for Disease Control and Prevention. *Salmonella* surveillance: annual summary. 2008 [cited 2012 Jun 22]. <http://www.cdc.gov/ncidod/dbmd/phlisdata/salmonella.htm>
- Painter JA, Ayers T, Woodruff R, Blanton E, Perez N, Hoekstra RM, et al. Recipes for foodborne outbreaks: a scheme for categorizing and grouping implicated foods. *Foodborne Pathog Dis*. 2009;6:1259–64. <http://dx.doi.org/10.1089/fpd.2009.0350>
- Hall AJ, Eisenbart VG, Etingue AL, Gould LH, Lopman BA, Parashar UD. Epidemiology of foodborne norovirus outbreaks, United States, 2001–2008. *Emerg Infect Dis*. 2012;18:1566–73. <http://dx.doi.org/10.3201/eid1810.120833>
- Rangel JM, Sparling PH, Crowe C, Griffin PM, Swerdlow DL. Epidemiology of *Escherichia coli* O157:H7 outbreaks, United States, 1982–2002. *Emerg Infect Dis*. 2005;11:603–9. <http://dx.doi.org/10.3201/eid1104.040739>
- Centers for Disease Control and Prevention. Ongoing multistate outbreak of *Escherichia coli* serotype O157:H7 infections associated with consumption of fresh spinach—United States, September 2006. *MMWR Morb Mortal Wkly Rep*. 2006;55:1045–6.
- Hilborn ED, Mermin JH, Mshar PA, Hadler JL, Voetsch A, Wojtkunski C, et al. A multistate outbreak of *Escherichia coli* O157:H7 infections associated with consumption of mesclun lettuce. *Arch Intern Med*. 1999;159:1758–64. <http://dx.doi.org/10.1001/archinte.159.15.1758>
- Centers for Disease Control and Prevention. Multistate outbreaks of *Salmonella* infections associated with raw tomatoes eaten in restaurants—United States, 2005–2006. *MMWR Morb Mortal Wkly Rep*. 2007;56:909–11.
- Greene SK, Daly ER, Talbot EA, Demma LJ, Holzbauer S, Patel NJ, et al. Recurrent multistate outbreak of *Salmonella* Newport associated with tomatoes from contaminated fields, 2005. *Epidemiol Infect*. 2008;136:157–65. <http://dx.doi.org/10.1017/S095026880700859X>
- Jain S, Bidol SA, Austin JL, Berl E, Elson F, Lemaile-Williams M, et al. Multistate outbreak of *Salmonella* Typhimurium and Saintpaul infections associated with unpasteurized orange juice—United States, 2005. *Clin Infect Dis*. 2009;48:1065–71. <http://dx.doi.org/10.1086/597397>
- Vojdani JD, Beuchat LR, Tauxe RV. Juice-associated outbreaks of human illness in the United States, 1995 through 2005. *J Food Prot*. 2008;71:356–64.
- Sivapalasingam S, Barrett E, Kimura A, Van Duyn S, De Witt W, Ying M, et al. A multistate outbreak of *Salmonella enterica* Serotype Newport infection linked to mango consumption: impact of water-dip disinfection technology. *Clin Infect Dis*. 2003;37:1585–90. <http://dx.doi.org/10.1086/379710>
- Brooks JT, Rowe SY, Shillam P, Heltzel DM, Hunter SB, Slutsker L, et al. *Salmonella* Typhimurium infections transmitted by chlorine-pretreated clover sprout seeds. *Am J Epidemiol*. 2001;154:1020–8. <http://dx.doi.org/10.1093/aje/154.11.1020>
- Winthrop KL, Palumbo MS, Farrar JA, Mohle-Boetani JC, Abbott S, Beatty ME, et al. Alfalfa sprouts and *Salmonella* Kottbus infection: a multistate outbreak following inadequate seed disinfection with heat and chlorine. *J Food Prot*. 2003;66:13–7.
- Barton Behravesh C, Mody RK, Jungk J, Gaul L, Redd JT, Chen S, et al. 2008 outbreak of *Salmonella* Saintpaul infections associated with raw produce. *N Engl J Med*. 2011;364:918–27. <http://dx.doi.org/10.1056/NEJMoa1005741>
- Mody RK, Greene SA, Gaul L, Sever A, Pichette S, Zambrana I, et al. National outbreak of *Salmonella* serotype Saintpaul infections: importance of Texas restaurant investigations in implicating jalapeño peppers. *PLoS ONE*. 2011;6:e16579. <http://dx.doi.org/10.1371/journal.pone.0016579>

21. Gottlieb SL, Newbern EC, Griffin PM, Graves LM, Hoekstra RM, Baker NL, et al. Multistate outbreak of listeriosis linked to turkey deli meat and subsequent changes in US regulatory policy. *Clin Infect Dis*. 2006;42:29–36. <http://dx.doi.org/10.1086/498113>
22. Mead PS, Dunne F, Graves L, Wiedmann M, Patrick M, Hunter S, et al. Nationwide outbreak of listeriosis due to contaminated meat. *Epidemiol Infect*. 2006;134:744–51. <http://dx.doi.org/10.1017/S0950268805005376>
23. Olsen SJ, Patrick M, Hunter SB, Reddy V, Kornstein L, MacKenzie WR, et al. Multistate outbreak of *Listeria monocytogenes* infection linked to delicatessen turkey meat. *Clin Infect Dis*. 2005;40:962–7. <http://dx.doi.org/10.1086/428575>
24. Food and Drug Administration. Quantitative assessment of relative risk to public health from foodborne *Listeria monocytogenes* among selected categories of ready-to-eat foods. 2003 Sep [cited 2012 Dec 20]. <http://www.fda.gov/downloads/food/scienceresearch/researchareas/riskassessmentsafetyassessment/ucm197330.pdf>
25. Olsen SJ, Ying M, Davis MF, Deasy M, Holland B, Iampietro L, et al. Multidrug-resistant *Salmonella* Typhimurium infection from milk contaminated after pasteurization. *Emerg Infect Dis*. 2004;10:932–5. <http://dx.doi.org/10.3201/eid1005.030484>
26. Ryan CA, Nickels MK, Hargrett-Bean NT, Potter ME, Endo T, Mayer L, et al. Massive outbreak of antimicrobial-resistant salmonellosis traced to pasteurized milk. *JAMA*. 1987;258:3269–74. <http://dx.doi.org/10.1001/jama.1987.03400220069039>
27. Langer AJ, Ayers T, Grass J, Lynch M, Angulo FJ, Mahon BE. Non-pasteurized dairy products, disease outbreaks, and state laws—United States, 1993–2006. *Emerg Infect Dis*. 2012;18:385–91. <http://dx.doi.org/10.3201/eid1803.111370>
28. Hald T, Vose D, Wegener HC, Koupeev T. A Bayesian approach to quantify the contribution of animal-food sources to human salmonellosis. *Risk Anal*. 2004;24:255–69. <http://dx.doi.org/10.1111/j.0272-4332.2004.00427.x>
29. Guo C, Hoekstra RM, Schroeder CM, Pires SM, Ong KL, Hartnett E, et al. Application of Bayesian techniques to model the burden of human salmonellosis attributable to U.S. Food commodities at the point of processing: adaptation of a Danish model. *Foodborne Pathog Dis*. 2011;8:509–16. <http://dx.doi.org/10.1089/fpd.2010.0714>
30. Batz MB, Hoffmann S, Morris JG. Ranking the disease burden of 14 pathogens in food sources in the United States using attribution data from outbreak investigations and expert elicitation. *J Food Prot*. 2012;75:1278–91. <http://dx.doi.org/10.4315/0362-028X.JFP-11-418>
31. Dewall CS, Hicks G, Barlow K, Alderton L, Vegosen L. Foods associated with foodborne illness outbreaks from 1990 through 2003. *Food Prot Trends*. 2006;26:466–73.
32. Pires SM, Vieira AR, Perez E, Lo Fo Wong D, Hald T. Attributing human foodborne illness to food sources and water in Latin America and the Caribbean using data from outbreak investigations. *Int J Food Microbiol*. 2012;152:129–38. <http://dx.doi.org/10.1016/j.ijfoodmicro.2011.04.018>
33. Friedman CR, Hoekstra RM, Samuel M, Marcus R, Bender J, Shiferaw B, et al. Risk factors for sporadic *Campylobacter* infection in the United States: a case-control study in FoodNet sites. *Clin Infect Dis*. 2004;38(Suppl 3):S285–96. <http://dx.doi.org/10.1086/381598>
34. Adak GK, Meakins SM, Yip H, Lopman BA, O'Brien SJ. Disease risks from foods, England and Wales, 1996–2000. *Emerg Infect Dis*. 2005;11:365–72.
35. St Louis ME, Morse DL, Potter ME, DeMelfi TM, Guzewish JJ, Tauxe RV, et al. The emergence of grade A eggs as a major source of *Salmonella* Enteritidis infections. New implications for the control of salmonellosis. *JAMA*. 1988;259:2103–7. <http://dx.doi.org/10.1001/jama.259.14.2103>
36. Jones JL, Dargelas V, Roberts J, Press C, Remington JS, Montoya JG. Risk factors for *Toxoplasma gondii* infection in the United States. *Clin Infect Dis*. 2009;49:878–84. <http://dx.doi.org/10.1086/605433>
37. Altekruse SF, Bishop RD, Baldy LM, Thompson SG, Wilson SA, Ray BJ, et al. *Vibrio* gastroenteritis in the US Gulf of Mexico region: the role of raw oysters. *Epidemiol Infect*. 2000;124:489–95. <http://dx.doi.org/10.1017/S0950268899003714>
38. Cartwright EJ, Jackson KA, Johnson SD, Graves LM, Silk BJ, Mahon BE. Listeriosis outbreaks and associated food vehicles, United States, 1998–2008. *Emerg Infect Dis*. 2013;19:1–9. <http://dx.doi.org/10.3201/eid1901.120393>
39. US Department of Agriculture; US Department of Health and Human Services. Dietary guidelines for Americans, 2010. 7th ed. 2010 Dec [cited 2012 Dec 20]. <http://www.health.gov/dietaryguidelines/dga2010/dietaryguidelines2010.pdf>

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Attribution of Foodborne Illnesses, Hospitalizations, and Deaths to Food Commodities Using Outbreak Data, United States, 1998–2008

Technical Appendix 1

Technical Appendix 1 Table 1. Foodborne disease outbreaks reported to CDC, 1998–2008. Shaded area indicates the categories of outbreaks (N=4,887) included in this analysis. Of these, 298 outbreaks were not included in analysis because information about the vehicle was insufficient to categorize the ingredient commodities.

Etiologic Agent	Confirmed		Suspected		Food vehicle		Unidentified		TOTAL							
	Outbreaks		Illnesses		Outbreaks		Illnesses		Outbreaks		Illnesses					
	No.	(%)	No.	(%)	No.	(%)	No.	(%)	No.	(%)	No.	(%)				
Single, confirmed	1,811	(57)	73,103	(68)	1,285	(28)	27,145	(49)	1,908	(34)	54,869	(50)	5,004	(37)	155,117	(57)
Single, suspected	560	(18)	14,914	(14)	1,231	(27)	13,107	(24)	962	(17)	16,247	(15)	2,753	(21)	44,268	(16)
Multiple	120	(4)	4,998	(5)	121	(3)	1,805	(3)	126	(2)	1,490	(1)	367	(3)	8,293	(3)
Unidentified	698	(22)	14,676	(14)	1,884	(42)	13,251	(24)	2,646	(47)	36,369	(33)	5,228	(39)	64,296	(24)
TOTAL	3,189	(100)	107,691	(100)	4,521	(100)	55,308	(100)	5,642	(100)	108,975	(100)	13,352	(100)	271,974	(100)

Technical Appendix 1 Table 2. The number of foodborne disease outbreaks, with simple or complex implicated food vehicles, 1998–2008, and the estimated annual number of illnesses, hospitalizations, and deaths, by etiology

Etiologic Agent	Reported Outbreaks			Reported outbreak-associated Illnesses			Estimated Annual Numbers*		
	Total	Simple food	Complex food	Total	Simple food	Complex food	Illnesses	Hosp. †	Deaths
Bacterial	2,469	1,301	1,168	72,890	40,107	32,783	3,645,773	35,797	862
<i>Bacillus cereus</i>	197	74	123	1,647	699	948	63,400	20	0
<i>Brucella</i> spp.	4	4	.	14	14	.	839	55	1
<i>Campylobacter</i> spp.	138	105	33	4,395	3,911	484	845,024	8,463	76
<i>Clostridium botulinum</i>	30	20	10	111	62	49	55	42	9
<i>Clostridium perfringens</i>	461	234	227	18,710	9,470	9,240	965,958	438	26
<i>Escherichia</i>	206	138	68	6,778	4,382	2,396	205,781	2,429	21
<i>E. coli</i> , ETEC†	11	3	8	1,878	466	1,412	17,894	12	0
<i>E. coli</i> , O157 STEC†	186	128	58	4,844	3,867	977	63,153	2,138	20
<i>E. coli</i> , non-O157 STEC†	6	6	.	37	37	.	112,752	271	1
<i>E. coli</i> , other†	3	1	2	19	12	7	11,982	8	0
<i>Listeria monocytogenes</i>	21	15	6	336	217	119	1,591	1,455	255
<i>Mycobacterium bovis</i>	60	31	3
<i>Salmonella enterica</i>	877	482	395	29,685	16,000	13,685	1,029,382	19,533	378
Ser. Enteritidis	284	149	135	8,627	4,629	3,998	168,041	3,162	62
Ser. Heidelberg	66	23	43	3,151	456	2,695	49,478	931	18
Ser. Javiana	17	11	6	1,279	916	363	40,337	759	15
Ser. Newport	58	40	18	2,280	1,903	377	95,119	1,790	35
Ser. Typhimurium	106	59	47	4,113	1,767	2,346	202,497	3,810	74
S. spp., other non-typhoidal	344	199	145	10,213	6,323	3,890	472,089	8,883	174
Ser. Typhi	2	1	1	22	6	16	1,821	197	0
<i>Shigella</i> spp.	63	25	38	3,875	1,808	2,067	131,254	1,456	10
<i>Staphylococcus aureus</i>	384	135	249	6,032	2,356	3,676	241,148	1,063	6
<i>Streptococcus</i> spp. group A	1	1	.	4	4	.	11,217	1	0
<i>Vibrio</i>	80	62	18	1,238	1,128	110	52,408	278	48
<i>V. cholerae</i> , toxigenic	3	3	.	12	12	.	84	2	0
<i>V. parahaemolyticus</i>	68	51	17	1,208	1,100	108	34,664	100	4
<i>V. vulnificus</i>	96	93	36
<i>V. spp.</i> , other	9	8	1	18	16	2	17,564	83	8
<i>Yersinia enterocolitica</i>	7	6	1	65	56	9	97,656	533	29
Chemical	632	573	59	3,235	2,746	489	249,273	1,496	100
Marine biotoxins	527	513	14	2,170	2,129	41	147,955	888	59
Mycotoxins	16	15	1	128	121	7	8,727	52	3
Other chemicals	89	45	44	937	496	441	92,591	556	37
Parasitic	33	22	11	1,449	1,156	293	233,660	4,886	333
<i>Anisakis simplex</i>	1	1	.	14	14	.	955	6	0
<i>Cryptosporidium</i> spp.	3	1	2	157	144	13	57,616	210	4
<i>Cyclospora cayetanensis</i>	16	12	4	1,164	965	199	11,407	11	0
<i>Giardia intestinalis</i>	4	1	3	74	3	71	76,840	225	2
<i>Toxoplasma gondii</i>	86,686	4,428	327
<i>Trichinella</i> spp.	9	7	2	40	30	10	156	6	0
Viral	1,455	448	1,007	42,747	13,113	29,634	5,509,596	15,284	156
Astrovirus	15,433	87	0
Hepatitis A virus	29	13	16	1,303	1,145	158	1,566	99	7

Etiologic Agent	Reported Outbreaks			Reported outbreak-associated Illnesses						Estimated Annual Numbers*					
	Total	Simple food	Complex food	Total	Simple food	Complex food	Illnesses	Hosp. †	Deaths						
Norovirus	1,419	431	988	41,257	11,922	29,335	5,461,731	14,663	149						
Rotavirus	5	2	3	148	7	141	15,433	348	0						
Sapovirus	2	2	.	39	39	.	15,433	87	0						
Total	4,589	2,344	2,245	120,321	57,122	63,199	9,638,301	57,462	1,451						

*The values not previously published¹ were estimated as described in methods.

†Hosp.=Hospitalizations, STEC=Shiga toxin-producing *Escherichia coli*, ETEC=Enterotoxigenic *Escherichia coli*, other= diarrheagenic other than STEC and ETEC

Technical Appendix 1 Table 3. Minimum and maximum percentages of annual U.S. foodborne illnesses caused by each agent that were attributed to each food commodity, by etiologic agent, using outbreak data from 1998 through 2008

Etiologic Agent	Fish		Crust.		Mollusks		Dairy		Eggs		Beef		Game		Pork		Poultry		Grains-Beans		Oils-Sugars		Fruits-Nuts		Fungi		Leafy		Root		Sprout		Vine-Stalk				
	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max					
Bacterial	0.0	0.2	0.1	0.3	0.4	0.4	2.3	4.1	0.3	1.6	1.1	2.6	0.0	0.2	1.0	2.3	1.5	3.4	0.2	1.9	.	.	0.7	1.3	0.0	0.0	0.5	1.8	0.1	2.2	0.1	0.2	1.0	2.7			
<i>Bacillus cereus</i>	0.5	5.6	7.2	10.0	.	.	0.2	12.8	.	.	5.4	13.9	.	.	5.7	13.4	7.9	29.1	10.7	53.0	.	.	0.4	5.0	.	.	4.2	42.9	.	.	0.2	14.5					
<i>Brucella</i> spp.	100	100			
<i>Campylobacter</i> spp.	0.1	0.2	.	.	6.2	6.3	61.8	65.2	0.0	0.6	0.6	6.3	5.3	10.3	0.7	5.4	.	.	8.4	10.4	3.1	9.1	.	.	2.8	6.2			
<i>Clostridium botulinum</i>	35.1	40.5	3.6	7.2	1.8	12.6	1.8	1.8	.	.	5.4	35.1	.	.	8.1	29.7			
<i>Clostridium perfringens</i>	.	.	0.3	2.5	.	.	0.1	22.0	0.5	8.0	16.3	41.1	.	.	5.1	17.2	18.9	38.7	3.9	27.7	0.4	10.9	.	.	0.0	25.8	.	.	5.1	23.1	
<i>Escherichia coli</i>	.	.	4.1	5.8	.	.	2.1	3.0	.	.	26.4	29.0	0.2	0.2	0.2	1.2	0.2	0.8	0.0	3.2	.	.	40.5	42.4	.	.	11.0	18.8	.	.	0.4	0.5	2.7	3.4			
<i>Escherichia coli</i> , ETEC	10.4	16.8	.	.	6.9	53.3	31.2	38.7			
<i>Escherichia coli</i> , O157 STEC	6.7	9.8	.	.	33.0	41.3	0.5	0.8	0.7	4.0	0.8	2.5	0.1	10.4	.	.	18.0	22.5	.	.	19.3	31.5	.	.	1.1	1.7	
<i>Escherichia coli</i> , non-O157 STEC	29.7	29.7	62.2	62.2	.	.	8.1	8.1	
<i>Escherichia coli</i> , other	.	.	70.6	100		
<i>Listeria monocytogenes</i>	15.7	16.3	.	.	1.2	35.6	.	.	4.2	38.1	38.4	72.8	6.0	6.0
<i>Mycobacterium bovis</i>	
<i>Salmonella enterica</i>	0.6	3.6	0.1	0.7	0.3	0.3	6.0	18.6	11.6	29.0	3.5	14.9	0.3	2.5	3.6	11.4	10.1	29.2	6.0	11.5	0.1	1.4	1.9	18.5	0.8	14.8	1.8	2.1	9.6	22.9			
Ser [†] . Enteritidis	0.2	9.1	0.3	2.2	.	.	0.5	16.7	35.2	61.8	0.8	11.1	.	.	0.5	7.3	10.6	20.9	2.6	8.1	.	.	0.2	25.2	.	.	1.3	1.9	1.7	19.9			
Ser [†] . Heidelberg	6.7	48.6	0.6	19.6	7.5	34.3	0.1	29.8		
Ser [†] . Javiana	6.9	10.3	0.5	22.1	48.1	48.5	.	.	3.1	22.2	0.3	24.9	.	.	12.7	32.9			
Ser [†] . Newport	7.4	12.8	.	.	9.6	15.4	.	.	5.7	8.0	8.1	13.0	10.0	17.1	.	.	4.8	13.9	4.2	13.4	.	.	33.6	40.8			
Ser [†] . Typhi	100	100		
Ser [†] . Typhimurium	1.5	2.3	12.5	31.4	1.0	16.6	4.2	19.8	0.7	6.8	5.5	19.4	13.3	44.2	0.3	3.9	2.2	18.9	0.2	29.6	4.0	4.2	6.6	20.8			
Other non-typhoidal	0.6	1.8	0.1	1.1	.	.	0.9	14.7	1.4	15.5	6.7	13.2	0.4	3.9	5.9	11.5	10.3	19.6	2.5	12.7	.	.	9.3	21.5	.	.	0.7	13.7	0.2	14.8	4.2	7.0	18.9	29.9			
<i>Shigella</i> spp.	1.4	1.4	.	.	0.2	0.2	0.2	22.6	0.1	16.6	2.1	7.4	.	.	0.1	1.8	1.4	12.2	0.3	23.5	.	.	1.7	11.2	.	.	16.0	44.6	23.2	57.5			
<i>Staphylococcus aureus</i>	0.2	1.9	0.5	2.6	0.3	1.7	0.9	24.9	0.3	29.9	3.9	18.9	0.0	4.9	22.9	51.5	9.4	40.6	0.1	28.3	0.6	23.9	0.0	12.9			
<i>Streptococcus</i> spp. group A	100	100		
<i>Vibrio</i>	3.7	7.5	13.5	18.9	70.8	73.6	2.6	2.8		
<i>V. cholerae</i> , toxigenic	.	.	50.0	50.0	50.0	50.0	
<i>V. parahaemolyticus</i>	.	.	20.3	28.4	67.4	71.6	3.9	4.2		
<i>V. spp.</i> , other	11.1	22.2	.	.	77.8	77.8	
<i>V. vulnificus</i>	

Etiologic Agent	Fish		Crust.		Mollusks		Dairy		Eggs		Beef		Game		Pork		Poultry		Grains-Beans		Oils-Sugars		Fruits-Nuts		Fungi		Leafy		Root		Sprout		Vine-Stalk			
	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max	min	max				
<i>Yersinia enterocolitica</i>	0	0	86.2	100		
Chemical	8.4	8.5	0.1	0.1	0.2	0.2	0.0	1.1	0.1	0.9	0.0	0.1	0.1	0.1	0.0	0.1	0.6	1.4	0.2	1.8	0.0	0.9	1.5	1.7	0.2	0.4	0.1	1.4	0.0	1.4	.	.	0.1	0.8		
Marine biotoxins	95.4	97.3	0.5	0.9	2.2	2.5		
Mycotoxins	58.6	58.6	35.9	41.4		
Other chemicals	5.4	5.4	0.5	0.5	.	.	0.7	20.8	2.8	17.0	0.6	2.8	1.6	2.8	0.2	1.4	12.2	25.5	2.9	33.5	0.4	16.6	22.0	27.4	0.2	3.0	2.1	26.8	0.2	26.4	.	.	1.0	14.9		
Parasitic	0.1	0.1	.	.	9.4	9.4	0.0	0.0	7.8	8.3	.	.	0.0	0.1	0.0	0.2		
<i>Anisakis simplex</i>	100	100	
<i>Cryptosporidium</i> spp.	94.7	100	
<i>Cyclospora cayetanensis</i>	82.9	88.9	.	.	0.7	5.6	0.3	15.3		
<i>Giardia intestinalis</i>	100	100	
<i>Toxoplasma gondii</i>
<i>Trichinella</i> spp.	90.9	100
Viral	0.2	0.5	0.0	0.3	0.3	0.4	0.3	5.1	0.1	5.4	0.2	2.2	0.0	0.8	0.2	2.2	0.2	2.8	0.1	4.9	0.0	4.7	1.0	3.5	.	.	1.3	7.3	0.1	5.7	.	.	0.2	5.4		
Astrovirus
Hepatitis A virus	.	.	0.5	1.0	3.1	3.1	0.6	6.0	2.9	8.2	.	.	57.7	65.6	23.3	31.5	.	.	1.8	7.9		
Norovirus	1.2	3.4	0.2	2.0	1.8	2.5	2.2	36.0	0.9	37.9	1.2	15.3	0.0	5.7	1.2	15.3	1.6	19.7	0.7	34.1	0.2	33.1	7.0	24.9	.	.	8.9	51.3	0.7	39.8	.	.	1.3	38.3		
Rotavirus	4.3	98.3	.	.	1.7	1.7	
Sapovirus	46.2	46.2	53.8	53.8	
TOTAL	2.3	4.1	0.4	1.9	2.8	3.3	7.2	31.7	1.3	26.1	3.6	15.8	0.1	3.8	3.2	14.8	5.0	20.6	1.1	24.8	0.1	19.1	6.7	18.6	0.0	0.2	6.6	34.5	0.8	29.0	0.3	0.5	3.4	29.1		

*STEC=Shiga toxin-producing *Escherichia coli*; ETEC=Enterotoxigenic *Escherichia coli*; other= diarrheagenic *E. coli* other than STEC and ETEC; ser.=serotype.

Technical Appendix 1 Table 4. Number of foodborne disease outbreaks that were attributed to each food commodity, by etiologic agent, using outbreak data from 1998 through 2008

Etiologic agent	TOTAL	Aquatic animals			Land animals						Plants							
		Fish	Crustacean	Mollusk	Dairy	Eggs	Meat-Poultry			Poultry	Grains-Beans	Oils-Sugars	Produce					
							Meat	Game	Pork				Fruits-Nuts	Fungi	Leafy	Root	Sprout	Vine-Stalk
Bacterial	2,469	81	97	85	596	586	593	120	413	713	742	361	207	29	501	554	45	492
<i>Bacillus cereus</i>	197	5	8	3	35	59	27	8	21	52	131	64	17	5	54	80	3	37
<i>Brucella</i> spp.	4	.	.	.	4
<i>Campylobacter</i> spp.	138	2	1	4	78	11	10	3	10	37	12	8	8	1	20	14	1	17
<i>Clostridium botulinum</i>	30	15	2	2	.	1	3	2	1	2	3	1	1	1	4	8	.	6
<i>Clostridium perfringens</i>	461	6	9	4	93	44	199	22	98	173	157	55	21	6	64	111	1	102
<i>Escherichia</i>	206	2	3	1	28	23	109	7	12	11	43	15	22	1	67	26	8	39
<i>E. coli</i> , ETEC	11	1	.	.	4	5	2	.	1	2	5	3	2	.	7	5	.	4
<i>E. coli</i> , O157 STEC	186	1	1	1	23	17	103	6	10	8	36	11	18	1	59	20	8	34
<i>E. coli</i> , non-O157 STEC	6	3	2	.	1	.	.	.
<i>E. coli</i> , other	3	.	2	.	1	1	1	1	1	1	2	1	.	.	.	1	.	1
<i>Listeria monocytogenes</i>	21	1	.	.	7	1	6	.	6	10	1	.	.	.	2	1	1	1
<i>Salmonella</i>	877	28	26	9	210	324	128	38	115	271	211	114	103	11	160	169	29	160
Ser [†] . Enteritidis	284	12	13	4	78	192	32	7	24	61	81	45	23	2	50	51	7	42
Ser [†] . Heidelberg	66	1	.	.	29	36	9	4	7	22	25	21	10	1	8	9	.	10

Etiologic agent	TOTAL	Aquatic animals			Land animals						Plants								
		Shellfish			Dairy	Eggs	Meat-Poultry				Grains-Beans	Oils-Sugars		Produce					
		Fish	Crustacean	Mollusk			Beef	Game	Pork	Poultry		Fruits-Nuts	Vegetables						
													Meat	Fungi	Leafy	Root	Sprout	Vine-Stalk	
<i>Ser.</i> [†] Javiana	17	.	.	.	3	1	1	.	3	4	4	1	4	.	4	5	.	6	
<i>Ser.</i> [†] Newport	58	.	.	.	11	4	12	3	6	15	9	3	13	.	11	10	.	15	
<i>Ser.</i> [†] Typhimurium	106	3	2	1	29	21	15	5	15	39	28	18	14	4	22	25	3	20	
<i>Ser.</i> [†] spp., other non-typhoidal	344	12	11	3	59	70	59	19	60	130	64	26	38	4	65	69	19	67	
<i>Ser.</i> [†] Typhi	2	.	.	1	1	1	
<i>Shigella</i> spp.	63	2	2	2	17	20	11	2	5	12	16	12	8	1	27	25	3	20	
<i>Staphylococcus aureus</i>	384	14	15	10	118	97	98	37	137	141	161	87	24	3	98	117	1	107	
<i>Streptococcus</i> spp. group A	1	1	
<i>Vibrio</i>	80	6	31	50	5	6	1	1	1	2	7	5	.	.	6	3	.	1	
<i>V. cholerae</i> , toxigenic	3	.	1	2	
<i>V. parahaemolyticus</i>	68	4	30	41	5	6	1	1	1	2	6	5	.	.	5	3	.	1	
<i>V. spp.</i> , other	9	2	.	7	1	.	.	.	1	.	.	.	
<i>Yersinia enterocolitica</i>	7	.	.	.	1	.	1	.	7	1	
Chemical	632	526	8	14	32	21	7	5	5	10	32	29	22	18	31	34	3	19	
Marine biotoxins	527	514	6	14	7	6	5	2	.	.	9	12	.	1	
Mycotoxins	16	.	.	.	1	3	13	1	1	.	.	
Other chemicals	89	12	2	.	24	15	7	5	5	10	27	27	19	5	21	21	3	18	
Parasitic	33	2	.	1	.	4	2	8	3	4	6	6	11	1	9	8	1	7	
<i>Anisakis simplex</i>	1	1	
<i>Cryptosporidium</i> spp.	3	1	1	1	1	.	1	2	.	1	
<i>Cyclospora cayetanensis</i>	16	1	.	.	.	2	1	.	1	1	4	4	9	.	5	3	.	4	
<i>Giardia intestinalis</i>	4	.	.	1	.	1	.	.	.	2	1	1	.	1	3	3	1	2	
<i>Trichinella</i> spp.	9	1	8	2	1	.	.	1	
Viral	1,455	49	43	69	552	518	250	104	221	326	527	491	286	83	741	540	69	536	
Hepatitis A virus	29	1	2	1	7	6	2	.	1	2	2	6	8	5	16	11	5	9	
Norovirus	1419	46	41	67	545	510	247	104	219	321	522	483	278	78	722	528	64	525	
Rotavirus	5	2	.	1	.	2	1	.	1	3	2	2	.	.	2	1	.	2	
Sapovirus	2	1	.	.	.	1	.	.	.	
Total	4,589	658	148	169	1,180	1,129	852	237	642	1,053	1,309	889	477	131	1,286	1,138	118	1,057	

[†]STEC=Shiga toxin-producing *Escherichia coli*; ETEC=Enterotoxigenic *Escherichia coli*; other= diarrheagenic *E. coli* other than STEC and ETEC; ser.=serotype.

Technical Appendix 1 Table 5. Comparison of rank order of illnesses, hospitalizations, and deaths attributed to food commodities when adjusting the attribution algorithm to account for variation among the number of outbreak illnesses.

A) Comparison of rank order and percentage of **illnesses** attributed to food commodities when adjusting the attribution algorithm to account for variation among the number of outbreak illnesses.

Commodity	Attributed Illnesses As a Function of Outbreak-associated Illnesses Included in Model									
	All Outbreaks, all illnesses [*]		Small Outbreaks, 2–19 Illnesses per outbreak [†]		Medium Outbreaks, 10–100 Illnesses per outbreak [‡]		Large Outbreaks, ≥20 illnesses per outbreak [§]		All Outbreaks, 1 illness per outbreak [¶]	
	Rank	%	Rank	%	Rank	%	Rank	%	Rank	%
Leafy	1	22.3	1	20.5	1	23.4	1	22.7	1	22.3
Dairy	2	13.8	3	11.5	4	9.4	2	14.2	3	11.2
Fruits-Nuts	3	11.7	6	7.0	2	12.3	3	11.9	4	8.6
Poultry	4	9.8	2	14.4	3	11.1	4	9.1	2	13.3
Vine	5	7.9	9	5.3	8	6.2	5	8.1	10	4.9
Beef	6	6.6	4	8.3	5	7.2	7	6.0	5	8.5
Eggs	7	6.0	8	5.5	6	6.9	6	6.1	8	5.3
Pork	8	5.4	7	6.6	7	6.7	8	5.5	7	6.3
Grains-Beans	9	4.5	5	7.9	9	4.7	11	3.6	6	6.6
Root	10	3.6	11	3.2	10	4.5	10	3.6	11	3.4
Mollusk	11	3.0	10	3.5	13	1.3	13	1.9	9	4.0
Fish	12	2.7	12	2.3	12	1.9	12	2.5	12	2.5
Undetermined	13	1.1	13	1.8	11	2.4	9	3.7	13	1.1
Oils-Sugars	14	0.7	14	0.8	14	0.9	14	0.6	15	0.7
Crustacean	15	0.5	15	0.7	15	0.6	16	0.4	14	0.7
Sprout	16	0.3	17	0.2	16	0.5	15	0.4	16	0.3
Game	17	0.1	16	0.5	17	0.1	17	0.0	17	0.3
Fungi	18	0.1	18	0.2	18	0.0	18	0.0	18	0.1

*4,589 Outbreaks; 120,321 illnesses

†3,126 Outbreaks; 21,701 illnesses

‡2,244 Outbreaks; 80,368 illnesses

§1,463 Outbreaks; 98,620 illnesses

¶4,589 Outbreaks

#Each outbreak adjusted to count only one illness per outbreak, which is equivalent to modeling attribution based on outbreak counts. Further discussion of attribution models based on outbreak counts versus outbreak illnesses can be found in Technical Appendix 2 (wwwnc.cdc.gov/EID/article/19/3/11-1866-Techapp2.pdf).

B) Comparison of rank order of **hospitalizations** attributed to food commodities when adjusting the attribution algorithm to account for variation among the number of outbreak illnesses.

Commodity	Attributed Hospitalizations As a Function of Outbreak Illnesses Included in Model									
	All Outbreaks, all illnesses		Small Outbreaks, 2–19 Illnesses per outbreak [†]		Medium Outbreaks, 10–100 Illnesses per outbreak [‡]		Large Outbreaks, ≥20 illnesses per outbreak [§]		All Outbreaks, 1 illness per outbreak [¶]	
	Rank	%	Rank	%	Rank	%	Rank	%	Rank	%
Dairy	1	16.2	2	15.3	3	13.0	1	16.1	2	14.6
Leafy	2	13.5	3	13.0	1	14.2	2	13.7	3	13.4
Poultry	3	11.5	1	17.8	2	13.5	3	11.4	1	17.0
Vine	4	10.5	8	5.3	5	7.5	5	11.2	7	4.8
Fruits-Nuts	5	10.1	9	5.3	9	8.6	4	10.3	9	6.4
Undetermined	6	8.1	5	8.5	4	9.7	6	10.2	5	8.1
Eggs	7	7.1	4	8.5	6	7.9	7	7.0	4	8.3
Beef	8	5.4	6	6.6	7	6.9	9	4.8	6	7.1
Pork	9	5.1	7	6.1	8	6.9	8	5.0	8	6.2
Fish	10	2.9	11	2.7	12	2.0	11	2.2	11	3.0
Root	11	2.6	12	2.5	10	4.0	10	2.5	12	2.7
Grains-Beans	12	2.5	10	3.4	11	2.6	12	2.1	10	3.0
Mollusk	13	2.5	13	2.3	14	0.6	13	1.7	13	2.8
Sprout	14	1.2	15	0.7	13	1.7	14	1.4	14	1.2
Oils-Sugars	15	0.3	17	0.4	15	0.4	15	0.3	17	0.4
Crustacean	16	0.2	14	0.5	16	0.2	17	0.1	15	0.5
Game	17	0.2	16	0.9	17	0.2	16	0.1	16	0.6
Fungi	18	0.1	18	0.3	18	0.0	18	0.0	18	0.2

*4,589 Outbreaks; 120,321 illnesses

†3,126 Outbreaks; 21,701 illnesses

‡2,244 Outbreaks; 80,368 illnesses

§1,463 Outbreaks; 98,620 illnesses

¶4,589 Outbreaks

#Each outbreak adjusted to count only one illness per outbreak, which is equivalent to modeling attribution based on outbreak counts. Further discussion of attribution models based on outbreak counts versus outbreak illnesses can be found in Technical Appendix 2 (wwwnc.cdc.gov/EID/article/19/3/11-1866-Techapp2.pdf).

C) Comparison of rank order of **deaths** attributed to food commodities when adjusting the attribution algorithm to account for variation among the number of outbreak illnesses.

Commodity	Attributed Deaths As a Function of Outbreak Illnesses Included in Model									
	All Outbreaks, all illnesses		Small Outbreaks, 2–19 Illnesses per outbreak [†]		Medium Outbreaks, 10–100 Illnesses per outbreak [‡]		Large Outbreaks, ≥20 illnesses per outbreak [§]		All Outbreaks, 1 illness per outbreak [¶]	
	Rank	%	Rank	%	Rank	%	Rank	%	Rank	%
Undetermined	1	25.2	1	25.5	1	26.6	1	27	1	25.2
Poultry	2	19.1	3	14.6	2	21.3	2	24	2	17.2
Dairy	3	9.7	2	15.9	3	8.0	5	7	3	11.9
Vine	4	7.0	10	3.2	10	4.6	4	7	10	3.0
Fruits-Nuts	5	6.4	9	3.0	7	5.2	3	7	9	3.9
Leafy	6	6.0	5	6.3	4	6.6	6	6	5	6.1
Pork	7	5.7	4	8.4	5	6.7	9	4	4	7.8
Fish	8	4.9	7	5.0	9	4.4	8	4	8	5.2
Eggs	9	4.9	6	6.1	6	5.5	7	5	6	6.0
Beef	10	3.8	8	4.9	8	4.5	10	3	7	5.6
Sprout	11	1.9	15	0.5	11	2.4	11	2	13	1.7
Grains-Beans	12	1.9	11	2.0	12	1.8	12	1	11	1.9
Root	13	1.4	12	1.6	13	1.7	13	1	12	1.7
Mollusk	14	1.4	13	1.3	14	0.5	14	1	14	1.4
Game	15	0.2	14	0.7	15	0.2	17	0	16	0.4
Oils-Sugars	16	0.2	18	0.3	17	0.2	15	0	17	0.4
Crustacean	17	0.2	16	0.4	16	0.2	16	0	15	0.4
Fungi	18	0.1	17	0.4	18	0.0	18	0	18	0.3

[†] Scallan E, Hoekstra RM, Angulo FJ, Tauxe RV, Widdowson MA, Roy SL, et al. Foodborne illness acquired in the United States--major pathogens. Emerg Infect Dis. 2011 Jan;17(1):7-15.

*4,589 Outbreaks; 120,321 illnesses

[†]3,126 Outbreaks; 21,701 illnesses

[‡]2,244 Outbreaks; 80,368 illnesses

[§]1,463 Outbreaks; 98,620 illnesses

[¶]4,589 Outbreaks

#Each outbreak adjusted to count only one illness per outbreak, which is equivalent to modeling attribution based on outbreak counts. Further discussion of attribution models based on outbreak counts versus outbreak illnesses can be found in Technical Appendix 2 (wwwnc.cdc.gov/EID/article/19/3/11-1866-Techapp2.pdf).

Attribution of Foodborne Illnesses, Hospitalizations, and Deaths to Food Commodities Using Outbreak Data, United States, 1998–2008

Technical Appendix 2

In this appendix, we reframe the problem of attributing human illness to food commodities in a more mathematical fashion to provide additional documentation and insight into our method.

The population of interest is defined as the set of all instances of symptomatic human illness caused by consuming contaminated food in the United States during some time period. We observe a set of reports describing outbreaks linked to particular etiologic agents and food exposures. The outbreaks analyzed are restricted to those for which there is a single etiologic agent and the ingredients of the contaminated food(s) can be characterized. We then map the information in those reports to create a set of outbreak-specific multivariate observations containing the specific etiologic agent, the contaminated food(s), and the number of illnesses for each outbreak. Next, each food is mapped to a set of ingredients among a specific 17-category food commodity classification scheme (1). At this point, each outbreak is identified with an etiologic agent, a number of human illnesses, and a 17-vector of 0/1 indicator variables recording whether or not the implicated food(s) included ingredients from a given commodity.

If the implicated foods contain ingredients from only one commodity, or if the contaminated ingredient is known, then that outbreak is classified as simple, whereas if the ingredients are from multiple commodities, and the contaminated ingredient is not known, then that outbreak is classified as complex.

Estimated total number of illnesses (\hat{T}) attributed to each of the 17 commodities by using the three estimators described in the methods section of the manuscript, minimum, most probable (MP) and maximum, are given by the following equations:

$$\begin{aligned}
\hat{\mathbf{T}} &= (\hat{\mathbf{T}}_1, \hat{\mathbf{T}}_2, \dots, \hat{\mathbf{T}}_j, \dots, \hat{\mathbf{T}}_{17})' \\
\hat{\mathbf{T}}(\text{minimum}) &= \sum_{i=1}^K b_i \times \left[\frac{\mathbf{n}'_i \mathbf{S}_i}{\left(\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\text{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \text{diag}(\mathbf{q}_i) \right) \mathbf{1}_{17}} \right]' \\
&= \text{where } \mathbf{q}_i = \frac{\mathbf{n}'_i \mathbf{S}_i}{(\mathbf{n}'_i \mathbf{S}_i) \mathbf{1}_{17}} \\
\hat{\mathbf{T}}(\text{MP}) &= \sum_{i=1}^K b_i \times \left[\frac{\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\text{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \text{diag}(\mathbf{q}_i)}{\left(\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\text{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \text{diag}(\mathbf{q}_i) \right) \mathbf{1}_{17}} \right]' \\
\hat{\mathbf{T}}(\text{maximum}) &= \sum_{i=1}^K b_i \times \left[\frac{\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i \mathbf{C}_i}{\left(\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\text{diag}(\mathbf{q} \mathbf{C}_i)]^{-1} \mathbf{C}_i \text{diag}(\mathbf{q}_i) \right) \mathbf{1}_{17}} \right]'
\end{aligned}$$

where i indexes the etiologic agents, b_i are the public health burdens (e.g., numbers of illnesses, hospitalizations, or deaths), \mathbf{n}_i and \mathbf{m}_i are column vectors with elements equal to the numbers of reported cases in simple and complex outbreaks respectively, \mathbf{S}_i and \mathbf{C}_i are 0/1 matrices corresponding to simple and complex outbreaks of etiology i with rows indexing outbreaks and columns corresponding to whether or not a given commodity was represented by ingredients of the contaminated food or foods from the outbreak. In some instances, one or both of \mathbf{S}_i and \mathbf{C}_i will be null matrices because no outbreaks of a given etiology were reported in that category. In addition, when \mathbf{S}_i is null, \mathbf{C}_i is defined to be null and the term in the summation is defined to be 0. When a column of \mathbf{S}_i is null then the corresponding column of \mathbf{C}_i is null. This follows from the general rule that no illnesses from complex food outbreaks due to a given etiologic agent will be allocated to commodities that are not represented among the simple food outbreaks due to that agent. The vector $\mathbf{1}_{17}$ is a column vector of 1's with dimension 17.

Estimated proportions ($\hat{\mathbf{p}}$) of all illnesses attributed to the 17 defined commodity groups are given by related equations:

$$\begin{aligned}\hat{\mathbf{p}} &= (\hat{\mathbf{p}}_1, \hat{\mathbf{p}}_2, \dots, \hat{\mathbf{p}}_j, \dots, \hat{\mathbf{p}}_{17})' \\ \hat{\mathbf{p}}(\mathit{minimum}) &= \sum_{i=1}^K \frac{b_i}{\sum b_i} \times \left[\frac{\mathbf{n}'_i \mathbf{S}_i}{(\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\mathit{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \mathit{diag}(\mathbf{q}_i)) \mathbf{1}_{17}} \right]' \\ &\quad \text{where } \mathbf{q}_i = \frac{\mathbf{n}'_i \mathbf{S}_i}{(\mathbf{n}'_i \mathbf{S}_i) \mathbf{1}_{17}} \\ \hat{\mathbf{p}}(\mathit{MP}) &= \sum_{i=1}^K \frac{b_i}{\sum b_i} \times \left[\frac{\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\mathit{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \mathit{diag}(\mathbf{q}_i)}{(\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\mathit{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \mathit{diag}(\mathbf{q}_i)) \mathbf{1}_{17}} \right]' \\ \hat{\mathbf{p}}(\mathit{maximum}) &= \sum_{i=1}^K \frac{b_i}{\sum b_i} \times \left[\frac{\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i \mathbf{C}_i}{(\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\mathit{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \mathit{diag}(\mathbf{q}_i)) \mathbf{1}_{17}} \right]'\end{aligned}$$

Note that the minimum estimated totals sum to less than the total estimated number of illnesses, $\sum b_i$, and the maximum estimated totals sum to more than $\sum b_i$, when there are attributable illnesses due to complex foods. The same is true of the minimum estimated proportions and maximum estimated proportions; they sum to less than and more than 1, respectively. Thus the minimum and maximum estimates cannot be interpreted as estimators of the set of commodity attribution fractions by themselves. Only the most probable estimates perform that function. With these limitations in mind, there are several things to note about the equations. The minimum, MP, and maximum estimates reflect the different allocations of observed illnesses from complex outbreaks that are added to illnesses observed from simple outbreaks. The minimum estimates, $\hat{\mathbf{T}}(\mathit{minimum})$, evaluate the minimal level of individual commodity attribution, before adding the contribution from complex outbreak data. They do not represent what might be called simple outbreak attribution, because while the numerators are based on allocating simple food outbreak illnesses, the denominators reflect both simple and complex illnesses. The MP estimates, $\hat{\mathbf{T}}(\mathit{MP})$, add in the information from complex outbreaks in a weighted fashion, and the maximum estimates, $\hat{\mathbf{T}}(\mathit{maximum})$, evaluate the maximal level of individual commodity attribution derived from the addition of all complex food illnesses allocated to single commodities.

The MP equation in its proportional formulation, $\hat{\mathbf{p}}(\mathit{MP})$, allows comparison of commodity attributions between models with different burdens. Also, by varying the set of

etiologies being summed from the complete set to subsets, comparisons of commodity attributions can be made between, for example, bacterial etiologies and viral etiologies. As mentioned, the minimum and maximum equations are set up to provide bounds on attributions to individual commodities. The vectors of proportions, $\hat{\mathbf{p}}(\mathbf{minimum})$ and $\hat{\mathbf{p}}(\mathbf{maximum})$, do not provide comparisons of attributions across the 17 commodities. Note that the vector, \mathbf{q}_i , is composed of a set of proportions that sum to 1, and does correspond to the attribution of illnesses from only simple food outbreaks due to a specific etiologic agent.

The dimensions of the vectors and matrices in the equations vary with etiologic agent; for each etiology and each set of simple and complex outbreaks, the number of rows is defined by the number of reported outbreaks satisfying the requirements for estimation. This embeds a hidden level of uncertainty in the output of the equations in that for some etiologic agents the number of reported outbreaks is small. This is a different type of uncertainty from that captured by the range of values described by the three estimators. This model does not incorporate uncertainties associated with the accuracy of reported etiologies, food exposures, or numbers of ill persons.

Mathematically, the equations are quite general. For example, the MP equation in its proportional form can be looked at as

$$\begin{aligned} \hat{\mathbf{p}}(\mathbf{MP}) &= \sum_{i=1}^K \frac{b_i}{\sum b_i} \times \left[\frac{\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\mathbf{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \mathbf{diag}(\mathbf{q}_i)}{(\mathbf{n}'_i \mathbf{S}_i + \mathbf{m}'_i [\mathbf{diag}(\mathbf{C}_i \mathbf{q}_i)]^{-1} \mathbf{C}_i \mathbf{diag}(\mathbf{q}_i)) \mathbf{1}_{17}} \right] \\ &= \sum_{etiologies} \mathbf{P}(etiology) \times \mathbf{P}(comm1, comm2, \dots, comm17 | etiology) \end{aligned}$$

where $\mathbf{P}(etiology)$ are weights in proportional form given to each etiology and $\mathbf{P}(comm1, comm2, \dots, comm17 | etiology)$ are commodity proportions derived from reported numbers of illnesses for each etiology. We have made specific choices for these quantities; other possible choices have been reported in the literature. For example costs have been used to weight the etiologies(2) and outbreak counts have been used as the basis for computing the commodity proportions.(3) It is useful to note that using outbreak counts as the basis for computing commodity proportions is equivalent to using reported numbers of illnesses

if all outbreaks are the same size. For example, the two calculations applied to poultry compare as follows

$$\textit{Poultry attribution proportion} = \frac{\text{sum of reported illnesses from poultry outbreaks}}{\text{sum of all reported illnesses}}$$

which can also be written as

$$\begin{aligned} \textit{Poultry attribution proportion} \\ = \frac{\text{number of poultry outbreaks} \times \text{average of reported illnesses from poultry outbreaks}}{\text{total number of outbreaks} \times \text{average of reported illnesses from all outbreaks}} \end{aligned}$$

versus

$$\textit{Poultry attribution proportion} = \frac{\text{number of poultry outbreaks}}{\text{total number of outbreaks}}$$

When all outbreaks are the same size, the averages of the numerator and denominator of the middle equation equal that constant size, and they cancel, making illness-based and outbreak-based proportions the same. The equations show that the equivalence holds more generally; if the average outbreak size for a commodity equals the overall average, then the numerator and denominator averages cancel. If each commodity average outbreak size equals the overall average, then all commodity attribution proportions will be the same, and illness-based and outbreak-based attributions are the same. Although this discussion focuses on source attribution for simple foods, the same concepts apply to source attribution for complex foods. Differences between outbreak-associated illness-based and outbreak-based attribution proportions reflect differences in outbreak sizes among commodities. The degree to which one or the other measure, outbreak-associated illnesses or outbreaks, reflect illnesses as they are caused by commodities in overall domestic foodborne illness is a subject for future research.

Expanded Methods

In this appendix, as a complement to the technical appendix, we provide a narrative description and examples of key elements of our method. To estimate illnesses attributable to specific commodities from reports of outbreaks of foodborne illnesses, we 1) attribute illnesses to specific commodities for each etiologic agent, and 2) sum the etiology-specific estimates, weighted by estimates of the number of illnesses (i.e., illnesses, hospitalizations, or deaths) for each etiology.

Attributing illnesses to specific commodities for each etiologic agent

To determine etiologic agent-specific attribution, we wanted to sum the number of illnesses attributed to specific commodities implicated in foodborne disease outbreaks caused by each agent. For outbreaks in which the implicated food(s) contained ingredients from a single commodity, this can be done easily because each outbreak contributes illnesses to a single commodity. For outbreaks in which the implicated food(s) contained ingredients from more than one commodity this cannot be done until illnesses are allocated to the multiple commodities in some fashion. To use data from commodities in both simple and complex foods, we calculated an estimate that sums the number of illnesses from simple food outbreaks attributed to specific commodities and adds to those sums partitioned numbers of illnesses from complex food outbreaks. The partitioning is based on proportions observed in simple food outbreaks. We refer to this estimate as the most probable estimate (MP).

To indicate a range of possible values for the number of illnesses caused by a commodity we calculated two additional estimates based on alternate partitions of the illnesses from complex food outbreaks. The minimum estimate derives from not allocating any complex food outbreak illnesses to any commodity. The maximum estimate derives from allocating all illnesses from a complex food outbreak to each commodity associated with the outbreak, as long as that commodity was also implicated in a simple food outbreak caused by that agent (which establishes the commodity as a possible causal exposure). This last allocation counts illnesses multiple times, but that is consistent with the maximum estimate as providing an upper bound for the number of illnesses attributed to individual commodities.

In Table A, we illustrate the attribution of illnesses in a dataset of four hypothetical outbreaks of illnesses caused by Etiologic Agent X. Illnesses in simple food

outbreaks in which ground beef, lettuce, and apple juice were implicated were attributed to the commodities beef, leafy vegetables, and fruits-nuts, respectively, for all three estimates—minimum, MP, and maximum. Outbreak D was due to a complex food so no illnesses from this outbreak were included in the minimum estimate. For the maximum estimate, all six illnesses were attributed to the beef commodity (because the vehicle contained ground beef) and all six were also attributed to the leafy vegetables commodity (because the vehicle contained lettuce), but no illnesses were attributed to the vine-stalk vegetables commodity (although the vehicle contained tomato) or the grain-beans commodity (the vehicle contained bread). This is because the dataset contained at least one simple Etiologic Agent X outbreak attributed to the commodity beef, and at least one simple Etiologic Agent X outbreak attributed to the commodity leafy vegetables, but no simple Etiologic Agent X outbreak was attributed to either vine-stalk vegetables or grains-beans.

In this example, to partition the illnesses in Outbreak D into the most probable number of illnesses for each commodity, we determined the proportion of illnesses in simple food outbreaks caused by that agent that were attributed to any commodity included in the hamburger sandwich: of the illnesses in the simple food outbreaks due to these commodities, 69% were attributed to beef and 31% to leafy vegetables. We applied these proportions to the six illnesses in Outbreak D, which yielded 4 illnesses attributed to beef and 2 attributed to leafy vegetables. The crude percentage of Etiologic Agent X illnesses attributed to each commodity was calculated by summing the number of attributed illnesses and dividing by the total number of actual illnesses in all Etiologic Agent X outbreaks. Note that although the actual number of illnesses was 46, only 40 illnesses were attributed to commodities for the minimum estimate and 52 were attributed for the maximum estimate; only the MP estimate counted each illness once and only once.

Summing the etiology-specific estimates, weighted by estimated number of domestically-acquired foodborne illnesses for each etiology

To calculate the total number of illnesses attributed to each commodity, we summed the etiologic agent-specific estimates obtained by applying the proportion of illnesses for each commodity to the estimated number of domestically acquired foodborne illnesses. In Tables B1-B3, we illustrate the calculations for the number of illnesses and deaths in a dataset of two hypothetical etiologies (X and Y). In Table B1, the minimum, MP, and maximum estimates of

illnesses attributed to each commodity were calculated as above, and shown as a percentage of the total for each etiology. In Table B2, a hypothetical estimated number of US illnesses each year, by etiology, is shown in the second column. (In the manuscript these estimates are from Scallan et al.) The far-right column shows the total numbers of illnesses allocated for the minimum, MP, and maximum attribution estimates. The number of illnesses attributed to each commodity is calculated as the product of the percentage of illnesses attributed to each commodity and the estimated actual number of illnesses for each etiology. To calculate the total number of illnesses attributed to each commodity for Etiologies X and Y, we summed the number of illnesses attributed to each commodity. A similar table is shown to illustrate the method for calculating the number of deaths (Table B3). In both tables the commodity percentages are reported for the most probable estimates. Note that for a specific etiology, the percentage attributed to each commodity was the same for illnesses, hospitalizations, and deaths. However, the percentage of total illnesses and deaths attributed to each commodity is different for the summed etiologies because the estimated number of illnesses, hospitalizations, and deaths is different for each etiology. Calculations for the estimated number of hospitalizations are identical in form and are not shown.

Technical Appendix 2 Table A. Attribution of illnesses to commodities in a hypothetical dataset of Etiology X outbreaks to illustrate the method for calculating minimum, most probable (MP), and maximum estimates

Ob*	Illnesses	Implicated food	Type of food†	Estimate	No. Illnesses Attributed to Commodity				
					Commodity				Total
					Beef	Grains-beans	Fruits-nuts	Leafy vegetables	
A	22	Ground beef	Simple	Minimum	22	0	0	0	22
				MP	22	0	0	0	22
				Maximum	22	0	0	0	22
B	10	Lettuce	Simple	Minimum	0	0	0	10	10
				MP	0	0	0	10	10
				Maximum	0	0	0	10	10
C	8	Apple juice	Simple	Minimum	0	0	8	0	8
				MP	0	0	8	0	8
				Maximum	0	0	8	0	8
D	6	Hamburger sandwich‡	Complex	Minimum	0	0	0	0	0
				MP**	4	0	0	2	6
				Maximum	6	0	0	6	12
Total	46			Minimum	22	0	8	10	40
				MP	26	0	8	12	46
				Maximum	28	0	8	16	52
				(% of 46)	(48%)		(17%)	(22%)	(87%)
				(% of 46)	(57%)		(17%)	(26%)	(100%)
				(% of 46)	(61%)		(17%)	(35%)	(113%)

*Ob, Outbreak; Minimum, minimum estimate of the number of illnesses attributed to a commodity; MP, most probable estimate of the number of illnesses attributed to a commodity; Maximum, maximum estimate of the number of illnesses attributed to a commodity.

†Illnesses in outbreaks in which the implicated food was simple were included in the minimum, maximum, and most probable estimates; illnesses in outbreaks in which the implicated foods were complex were included only in the most probable and maximum estimates.

‡Hamburger sandwich ingredients: ground beef, lettuce, tomato, bread.

** For Outbreak D, the MP estimate of illnesses due to each commodity relies on information from the simple food outbreaks due to those commodities in the dataset. The total number of outbreak-associated illnesses caused by Etiology X and due to simple foods contained in the hamburger sandwich was 32, with 22 (69%) due to beef and 10 (31%) due to leafy vegetables. Rounding to the nearest integer, the MP estimate of illnesses in outbreak D attributed to beef was 4 (69% of 6) and the MP estimate of illnesses attributed to leafy vegetables was 2 (31% of 6).

Technical Appendix 2 Table B1. Percentages of illnesses attributed to specific commodities, by etiology

Etiology	Estimate	Percentage Attributed to Commodity				
		Commodity				Total
		Beef	Grains-beans	Fruits-nuts	Leafy vegetable	
X	Minimum	48%	0%	17%	22%	87%
	MP	57%	0%	17%	26%	100%
	Maximum	61%	0%	17%	35%	113%
Y	Minimum	14%	17%	18%	23%	72%
	MP	19%	24%	25%	32%	100%
	Maximum	41%	45%	46%	51%	183%

Technical Appendix 2 Table B2. Number of illnesses attributed to specific commodities by etiology and for total

Etiology	Hypothetical actual number of illnesses	Estimate	No. Illnesses Attributed to Commodity				Total
			Commodity				
			Beef	Grains-beans	Fruits-nuts	Leafy vegetable	
X	300,000	Minimum	143,000	0	52,000	65,000	261,000
		MP	170,000	0	52,000	77,000	300,000
		Maximum	183,000	0	52,000	104,000	339,000
Y	1,000,000	Minimum	138,000	172,000	184,000	230,000	724,000
		MP	190,000	238,000	254,000	317,000	1,000,000
		Maximum	414,000	448,000	460,000	506,000	1,828,000
Total X and Y	1,300,000	Minimum	281,000	172,000	236,000	295,000	985,000
		MP (% of total)	361,000 (28%)	238,000 (18%)	306,000 (24%)	395,000 (30%)	1,300,000 (100%)
		Maximum	596,000	448,000	512,000	610,000	2,167,000

Technical Appendix 2 Table B3. Number of deaths attributed to specific commodities by etiology and for total

Etiology	Hypothetical actual number of deaths	Estimate	No. Deaths Attributed to Commodities				Total
			Commodity				
			Beef	Grains-beans	Fruits-nuts	Leafy vegetable	
X	200	Minimum	96	0	35	43	174
		MP	114	0	35	52	200
		Maximum	122	0	35	70	226
Y	50	Minimum	7	9	9	11	36
		MP	10	12	13	16	50
		Maximum	21	22	23	25	91
Total X and Y	250	Minimum	103	9	44	55	210
		MP (% of total)	123 (49%)	12 (5%)	47 (19%)	68 (27%)	250 (100%)
		Maximum	142	22	58	95	317

References

1. Painter JA, Ayers T, Woodruff R, Blanton E, Perez N, Hoekstra RM, et al. Recipes for foodborne outbreaks: a scheme for categorizing and grouping implicated foods. *Foodborne Pathog Dis.* 2009 Dec;6(10):1259-64.

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DOI: 10.3201/eid1903.111866; TOC Head: Research

2. Batz MB, Hoffmann S, Morris JG. Ranking the Disease Burden of 14 Pathogens in Food Sources in the United States Using Attribution Data from Outbreak Investigations and Expert Elicitation. *J Food Protect.* 2012 Jul;75(7):1278-91.
3. Pires SM, Vieira AR, Perez E, Lo Fo Wong D, Hald T. Attributing human foodborne illness to food sources and water in Latin America and the Caribbean using data from outbreak investigations. *Int J Food Microbiol.* 2012 Jan 16;152(3):129-38.