

Ranking the Disease Burden of 14 Pathogens in Food Sources in the United States Using Attribution Data from Outbreak Investigations and Expert Elicitation[†]

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MS 11-418: Received 17 September 2011/Accepted 24 January 2012

ABSTRACT

Understanding the relative public health impact of major microbiological hazards across the food supply is critical for a risk-based national food safety system. This study was conducted to estimate the U.S. health burden of 14 major pathogens in 12 broad categories of food and to then rank the resulting 168 pathogen-food combinations. These pathogens examined were *Campylobacter*, *Clostridium perfringens*, *Escherichia coli* O157:H7, *Listeria monocytogenes*, norovirus, *Salmonella enterica*, *Toxoplasma gondii*, and all other FoodNet pathogens. The health burden associated with each pathogen was measured using new estimates of the cost of illness and loss of quality-adjusted life years (QALYs) from acute and chronic illness and mortality. A new method for attributing illness to foods was developed that relies on both outbreak data and expert elicitation. This method assumes that empirical data are generally preferable to expert judgment; thus, outbreak data were used for attribution except where evidence suggests that these data are considered not representative of food attribution. Based on evaluation of outbreak data, expert elicitation, and published scientific literature, outbreak-based attribution estimates for *Campylobacter*, *Toxoplasma*, *Cryptosporidium*, and *Yersinia* were determined not representative; therefore, expert-based attribution were included for these four pathogens. Sensitivity analyses were conducted to assess the effect of attribution data assumptions on rankings. Disease burden was concentrated among a relatively small number of pathogen-food combinations. The top 10 pairs were responsible for losses of over \$8 billion and 36,000 QALYs, or more than 50% of the total across all pairs. Across all 14 pathogens, poultry, pork, produce, and complex foods were responsible for nearly 60% of the total cost of illness and loss of QALYs.

Risk-based food safety, as called for by the FDA Food Safety Modernization Act and national and international public health bodies, relies on systematic identification and quantification of the specific pathogens in specific foods that are responsible for the greatest burden of foodborne disease in the United States (6, 13, 34, 35, 37, 50, 52–54). Such an approach requires use of integrated measures of the public health burden associated with these pathogens that allow for the comparison of diseases with very different incidence, symptoms, and severities (29, 33). Food attribution estimates, i.e., measures of how illnesses associated with a given pathogen are distributed across food sources, are also needed (2, 40).

Much like recent Centers for Disease Control and Prevention (CDC) national foodborne disease incidence estimates, this study was conducted to provide a systematic, national assessment of the relationship between the burden of disease from major foodborne pathogens and food

consumption across the entire U.S. food supply. It builds on new cost of illness and quality-adjusted life year (QALY) loss estimates for 14 major foodborne pathogens in the United States (20). These pathogens account for more than 95% of the illnesses, hospitalizations, and deaths due to identified foodborne pathogens, as estimated by Scallan et al. (48).

A growing body of scientific research has been focused on methods for attributing foodborne illness to their source (2, 40). Five basic approaches to source attribution have emerged: analysis of outbreak surveillance (1, 10, 16, 39, 42, 45), case-control and other epidemiological studies (14, 19, 25, 26, 56, 57), use of microbiological subtyping analysis to compare pathogen strains in food and in clinical cases (17, 28, 32, 41, 43), comparative exposure assessments (12, 51), and expert elicitation studies (8, 9, 18, 21–23, 44, 55). These studies typically do not use the counterfactual approach common in epidemiological studies of causation (46) but rather focus on quantifying the portion of illness due to a particular pathogen that can be attributed directly to a food source. The present study is innovative in combining information from two distinct data sources to attribute illnesses from pathogens to foods: 10 years of outbreak data (1999 through 2008) taken from publicly available line listings published by the CDC (4) and a

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† The views expressed herein are those of the authors and do not necessarily reflect the views of the Economic Research Service or the U.S. Department of Agriculture.

compatible expert elicitation conducted for this project (21–23). Although reported outbreak cases reflect a very small percentage of overall foodborne illness, these data nevertheless are the most comprehensive primary source of information to explicitly link human infections to food vehicles for a wide range of pathogens (40). Attribution estimates based on case-control studies, serotyping, or comparative exposure assessment are available for only a small subset of these 14 major pathogens and are extremely difficult to integrate across a wide range of pathogens and foods due to differences in study designs (2). Based on evidence from multiple sources, we found that for some pathogens outbreak data do not provide a reliable representation of food attribution. For these pathogens, we instead used attribution estimates from the expert elicitation study.

We estimated that the top 10 pathogen-food combinations, which reflect five pathogens (*Campylobacter*, *Listeria monocytogenes*, norovirus, *Salmonella*, and *Toxoplasma gondii*) in eight food categories (poultry, pork, deli meats, dairy, produce, beef, eggs, and complex foods), are responsible for losses of more than \$8 billion and 36,000 QALYs, or more than 50% of the total health burden from all foods due to all 14 pathogens studied. Based on exposure to all 14 pathogens, poultry, pork, produce, and complex foods are the commodities responsible for the most disease burden.

MATERIALS AND METHODS

In the following sections we discuss methodological decisions made in this study: choice of public health burden measures, development of a food categorization scheme, estimation of attribution percentages based on outbreak data, estimation of attribution percentages based on expert elicitation, and analysis supporting choice of attribution data source for each pathogen. Additional tables and figures, including outbreak data tables, expert elicitation details, and the complete list of pathogen-food rankings, may be found in the online Appendix (<http://foodrisk.org/pubs/riskranking>).

Public health burden measures. The CDC has estimated 48 million illnesses, 128,000 hospitalizations, and 3,000 deaths due to foodborne disease annually. Of these, 9.4 million cases, 56,000 hospitalizations, and 1,400 deaths are due to 31 identifiable pathogens (47, 48). Although summary incidence estimates are valuable, they cannot be directly combined to compare the total burden of disease due to specific pathogens. Integrated measures of disease burden, such as cost of illness and QALYs lost, can be built on such incidence estimates to provide a common metric for comparing diseases with different symptoms and severities, including congenital impacts and chronic conditions not reflected in summary statistics (27, 29, 33).

This study utilizes new estimates of the cost of illness and QALY loss from both acute and chronic illness due to 14 major foodborne pathogens as described in an accompanying article (20). The pathogens discussed in this article will be referred to as indicated in parentheses: *Campylobacter* spp. (*Campylobacter*), *Clostridium perfringens* (*C. perfringens*), *Cryptosporidium parvum* (*Cryptosporidium*), *Cyclospora cayatanensis* (*Cyclospora*), *Escherichia coli* O157:H7 (*E. coli* O157), Shiga toxin-producing *E. coli* non-O157 (STEC non-O157), *Listeria monocytogenes* (*Listeria*), norovirus, nontyphoidal *Salmonella enterica* (*Salmonella*), *Shigella* spp. (*Shigella*), *Toxoplasma*

gondii (*Toxoplasma*), *Vibrio vulnificus* (*V. vulnificus*), *Vibrio parahaemolyticus* and other noncholera *Vibrio* spp. (*Vibrio* other), and *Yersinia enterocolitica* (*Yersinia*). Cost of illness estimates reflect medical costs, productivity losses, and valuation of mortality, whereas QALY estimates capture loss of health-related quality of life using the EuroQol EQ5D instrument (3, 49). These 14 foodborne pathogens are estimated to cause a total loss of \$14.0 billion (\$4.4 to \$33.0 billion) and 61,000 (19,000 to 145,000) QALYs per year (Table 1), with roughly 90% of these impacts due to just five pathogens: *Salmonella*, *Campylobacter*, *Listeria*, *Toxoplasma*, and norovirus.

Food categories. No consensus exists on how to categorize foods for attribution (1, 2, 16, 39, 45). Categorization schemes used for broad evaluation of risks across the entire food supply, as in the present study, are likely to be quite different from those useful for targeted risk management. Attribution approaches also differ in their points of attribution (2). The “point of production” approaches focus on primary food production activities, such as animal reservoirs, as pathogen sources (e.g., *E. coli* O157 in cattle), whereas “point of consumption” approaches, such as the one used in the present study, focus on food vehicles that directly lead to exposure (e.g., *E. coli* O157 in hamburgers) (40).

We estimated attribution to food as close to the time of consumption as practicable because this approach provides the most direct link between human disease surveillance and exposure to pathogens in foods. Upstream points of attribution, such as attribution to on-farm contamination sources, neglect the role of downstream contamination events, such as cross-contamination during preparation, in causing disease. Consumption-oriented categories better reflect the information provided in outbreak investigations. Estimates of disease burden focused at consumption also provide a basis for quantitative risk assessments focusing on the contribution of production, processing, and food preparation to final exposure of consumers. We therefore created a scheme with a dozen primary categories (Table 2) designed to span the U.S. food supply at the point of consumption and to be compatible for primary analysis of CDC outbreak data, useful to food safety practitioners, and congruent with established guidance on categorization for risk ranking (30).

Categorization entails judgment. To better reflect foods at the point of consumption, our broad categories better reflect groupings found in grocery store aisles or restaurant menus than do ingredients of specific products (e.g., baked goods instead of grains, sugars, oils). In pretests, food safety experts also recommended that we treat deli meats (e.g., sliced turkey, ham, roast beef) as a separate category rather than categorizing them by food animal together with raw meat, principally for understanding risks due to *Listeria* (51). The “complex foods” category is included for analysis of outbreak data to capture multi-ingredient dishes for which a specific contaminated ingredient was never identified; further explanation of this category is provided in the next section.

Estimating attribution percentages from outbreak data. As in other outbreak attribution studies (1, 10, 16, 39, 42, 45), data from multiple years were averaged to address significant year-to-year variability in foodborne illness and to ensure sufficient data for analysis. We based our estimates on the most recent 10 years available (1999 through 2008) in the CDC’s online repository of foodborne outbreaks with identified etiology (4). Outbreaks with an unidentified etiology but suspected of being associated with enterohemorrhagic *E. coli* were treated as STEC non-O157.

Three methodological issues had to be addressed in developing attribution estimates from outbreak data: cleaning the data, coding each outbreak to a food category based on identified vehicle, and deciding whether to base attribution estimates on

TABLE 1. Annual burden of disease caused by 14 foodborne pathogens^a

Pathogen	Cost of illness (\$ million)	QALY loss	No. of illnesses	No. of hospitalizations	No. of deaths
<i>Campylobacter</i>	1,747 (841–4,152)	13,256 (7,993–26,021)	845,024 (337,031–1,611,083)	8,463 (4,300–15,227)	76 (0–332)
<i>C. perfringens</i>	309 (20–1,572)	876 (83–3,942)	965,958 (192,316–2,483,309)	438 (44–2,008)	26 (0–163)
<i>C. parvum</i>	47 (3–192)	341 (40–1,265)	57,616 (12,060–166,771)	210 (58–518)	4 (0–19)
<i>C. cayentensis</i>	2 (0–8)	10 (0–33)	11,407 (137–37,673)	11 (0–109)	0
<i>E. coli</i> O157:H7	255 (25–1,102)	1,660 (131–7,872)	63,153 (17,587–149,631)	2,138 (549–4,614)	20 (0–113)
STEC non-O157	24 (1–77)	149 (10–268)	112,752 (11,467–287,321)	271 (0–971)	0
<i>L. monocytogenes</i>	2,577 (204–6,952)	9,375 (1,531–23,525)	1,591 (557–3,161)	1,455 (521–3,018)	255 (0–733)
Norovirus	2,002 (1,140–3,147)	5,027 (2,897–7,832)	5,461,731 (3,227,078–8,309,480)	14,663 (8,097–23,323)	149 (84–237)
<i>S. enterica</i>	3,309 (160–8,586)	16,782 (304–44,380)	1,027,561 (644,786–1,679,667)	19,336 (8,545–37,490)	378 (0–1,011)
<i>Shigella</i>	121 (8–639)	545 (14–3,372)	131,254 (24,511–374,789)	1,456 (287–3,695)	10 (0–67)
<i>T. gondii</i>	2,973 (1,763–4,437)	10,964 (6,026–16,771)	86,686 (64,861–111,912)	4,428 (2,634–6,674)	327 (200–482)
<i>Vibrio</i> other	103 (28–298)	210 (60–595)	52,228 (29,108–84,502)	183 (101–293)	12 (3–36)
<i>V. vulnificus</i>	291 (154–460)	557 (294–882)	96 (60–139)	93 (53–139)	36 (19–57)
<i>Y. enterocolitica</i>	252 (3–1,412)	1,415 (13–8,216)	97,656 (30,388–172,734)	533 (0–1,173)	29 (0–173)
Total	14,012 (4,352–33,034)	61,166 (19,397–144,974)	8,914,713 (4,591,947–15,472,172)	53,678 (25,189–99,252)	1,322 (306–3,423)

^a Values are means with ranges or credible intervals in parentheses. Mean numbers of annual illnesses, hospitalizations, and deaths are followed by 90% credible intervals for acute disease reported by Scallan et al. (48) but do not include all cases of fetal and chronic disease included in estimates of cost of illness and quality-adjusted life year (QALY) loss. Ranges for cost of illness and QALY loss reflect estimates based on credible intervals reported by Scallan et al. and discussed in Hoffmann et al. (20). *Vibrio* other refers to noncholera *Vibrio* spp. other than *V. vulnificus*.

counts of outbreak events or on cases of illness associated with these events.

For the 14 pathogens in this study, we compiled a data set of 5,830 outbreaks associated with 172,495 cases of illness. In 2,636 outbreaks (70,568 cases), the food vehicle was listed as “unknown.” In an additional 606 outbreaks (22,485 cases), no single food was identified, so the investigation report listed multiple foods (e.g., steak, beets, and veggie-based pasta). We decided such information on food vehicle was too vague to support reliable food attribution. These multisource outbreaks were dropped from the analysis, although we explored this decision in sensitivity analyses. Thus, our outbreak data set included 2,588 attributable outbreaks with 79,442 associated cases.

Outbreak investigations do not use a standardized coding scheme for the responsible food vehicle but rather provide text descriptions that are often incomplete, colloquial, or otherwise vague. For example, an outbreak might be attributed in the data to “ethnic food.” Thus, the first step in estimating outbreak-based attribution was to develop a coding scheme to categorize these descriptions of food vehicles.

In cases in which investigators identified the cause as a single food item (e.g., tomatoes) or a specific ingredient in a multi-ingredient dish (e.g., eggs in lemon meringue pie), we coded based on the identified food. In many outbreaks, however, the investigation report listed a multi-ingredient dish but did not specify a single ingredient (e.g., cheeseburger or seafood gumbo). Multi-ingredient dishes were classified in one of three ways: (i) those in which the vast majority of ingredients fell into a single category were lumped into that category (e.g., salsa as produce); (ii) because many foodborne pathogens are recognized as zoonoses with well-understood reservoirs in animal production, outbreaks in which beef, poultry, pork, seafood, or eggs were the primary ingredient were classified by species (e.g., beef stew as beef, chicken pot pie as poultry, quiche as egg); and (iii) all remaining dishes were classified as complex foods. For example, green salads were assumed to be composed solely of vegetables and were classified as produce unless the description also included nonproduce ingredients such as eggs or cheese, in which case these salads were classified as complex foods. Deli salads, such as macaroni salad, were assumed to be composed of foods from multiple categories and were therefore classified as complex foods rather than produce, eggs, or another category. Ultimately, 776 outbreaks reflecting 24,357 cases, or about a quarter of all outbreaks with identified vehicles, were categorized as complex foods. Our approach to multi-ingredient dishes might bias results toward meat and poultry because outbreaks due to foods such as cheeseburgers are classified as beef even though other ingredients, such as tomato, lettuce, or the bun, could have been the contaminated ingredient. An alternate approach to complex foods has been described by Painter et al. (39), but this approach to disambiguation requires significant assumptions about which ingredients constitute each dish (recipes) and how risk of contamination is distributed across constituent ingredients. We examined the role of complex foods in the sensitivity analysis.

Outbreak-based attribution studies have based estimates either on the distribution of outbreak cases across foods (1, 10, 39, 42) or on the distribution of outbreak events across foods (16, 45). These attribution percentages are calculated by dividing the number of outbreaks (or outbreak cases) associated with a specific pathogen-food combination by the number of outbreaks (or outbreak cases) associated with that pathogen.

Attribution based on outbreak counts are likely more representative of sporadic cases than those based on case counts. For each outbreak case in our data set, more than 1,000 cases of

TABLE 2. Food categories used in food attribution

Food	Food subcategories ^a
Beef	Ground beef, other beef (intact), beef dishes
Pork	Ham, other pork (intact), pork dishes
Poultry	Chicken, turkey, other poultry (intact), poultry dishes
Deli and other meats	Deli meats, other meats, other meat dishes
Game	Game
Eggs	Eggs, egg dishes
Dairy	Milk, cheese, ice cream, other dairy dishes
Seafood	Finfish, shellfish, other seafood, seafood dishes
Produce	Fruits, vegetables, produce dishes
Beverages	Juices, other beverages (not including water)
Baked goods	Breads, bakery goods, cereals
Complex foods	Nonmeat multi-ingredient dishes: salads (e.g., deli), sandwiches, rice, beans, hot pasta, sauces, dressings, oils, etc.

^a Subcategories were used for coding outbreaks and were provided to participants in the expert elicitation reported by Hoffmann et al. (21) to provide a clearer understanding of the foods included in each category. The food subcategories were not used to categorize food in the present analysis.

sporadic disease are estimated, i.e., our data include 79,442 attributable outbreak cases over 10 years compared with nearly 9 million annual cases of illness estimated by Scallan et al. (48) for these same pathogens. This difference suggests that most of these 9 million foodborne illnesses occur in small, isolated events that are arguably better reflected by smaller outbreaks than large outbreaks. The larger an outbreak, the more likely it is to represent a major and unusual failure in food safety systems, the more likely it is to have been noticed and fully investigated, and the more likely it is that the vehicle will be identified. As a result, large events are likely overrepresented in the outbreak data. Outbreak size is heavily skewed to the right; the average outbreak size is about 28 cases, but the median is 12 and the mode is 2. To the extent that outbreak size varies by food category, attribution percentages based on number of cases become effectively skewed towards those foods more likely to cause large events. We found that produce outbreaks had an average of 51 cases, dairy outbreaks had 36 cases, and complex foods outbreaks had 31 cases, whereas beef, pork, and seafood outbreaks averaged 23, 24, and 15 cases, respectively. Thus, outbreak attribution estimates based on case counts attribute a greater portion of disease to produce, dairy, and complex foods than do estimates based on outbreak events. Attribution percentages based on outbreak counts are presented in Table 3. Attribution based on case counts was examined in the sensitivity analysis.

Attribution percentages from expert elicitation. Expert elicitation is a set of formal research methods used to characterize uncertainty about existing scientific knowledge and to provide alternative parameter estimates when there are meaningful gaps in available data (7, 31, 38). Several studies have included expert elicitation to gain greater insight into attribution to food sources and other transmission pathways (9, 18, 44, 55). As part of our larger research effort, Hoffmann et al. (21–23) conducted an expert elicitation for attribution estimates on 12 of the 14 pathogens included in this study.

The elicitation was designed to characterize uncertainty about food attribution estimates for these diseases and to provide

alternative attribution estimates. Forty-five leading food safety scientific experts were identified by iterative peer nomination as having relevant, nationally recognized expertise (22). For each pathogen, experts provided their best estimate and a 90% credible interval for the percentage of foodborne illnesses associated with consumption of food in various categories. Following Clemen and Winkler (5), the percentage attributable to each pathogen-food combination was estimated as the unweighted mean of the best estimates of all the experts. The results are shown in Table 4.

The categories used in the 2003 elicitation were the same as those used to assign outbreak data to food categories, with two exceptions. First, the complex foods category necessary for evaluating outbreaks was removed after focus groups and pretesting indicated that experts could confidently attribute to single food categories, but overlaps between these categories and complex foods created ambiguity in categorization and increased uncertainty about attribution percentage estimates. Second, the elicitation included “other foods” as a residual category to ensure that attribution estimates would sum to 100%. Because focus group results showed that experts were thinking in terms of simple rather than complex foods, this category cannot be interpreted as complex foods. In analysis, the “other food” category was dropped, and remaining attribution estimates were normalized across the remaining food categories. We examined this treatment of “complex foods” through sensitivity analysis.

Choice of attribution source. Although outbreak data have been used as a primary empirical source for attribution of foodborne illness in the United States, case-control studies suggest that these data may not provide an equally accurate representation of the association between illness and food sources for all pathogens (14, 24). We conducted a series of analyses to assess when outbreak data may and may not provide good representations of food attribution. In developing our baseline estimates, we started with the presumption that outbreak-based attribution would be used, but where the totality of evidence from these analyses suggested that these data were not representative, expert-based estimates were used instead.

First, for some pathogens there are simply too few outbreaks with identified food vehicles to estimate attribution (Table 5). From 1999 through 2008, *Toxoplasma*, *Yersinia*, and *Cryptosporidium* food vehicles were identified in zero, five, and four reported outbreaks caused by each of these pathogens, respectively. However, in this same period, 1,125 norovirus-associated outbreaks, 621 *Salmonella*-associated outbreaks, and 362 *C. perfringens*-associated outbreaks with identified food vehicles were reported.

Second, we looked at the ratio of the CDC’s estimated annual number of illnesses reported by Scallan et al. (48) to the average annual number of reported outbreak cases for that pathogen from 1999 through 2008 (Table 5). The ratio represents the number of illnesses one would expect in the population for each reported outbreak case. A high ratio suggests that source attribution from outbreak data may not be representative of total foodborne illness caused by a particular pathogen. This ratio is particularly high for *Yersinia* (11,909:1), *Campylobacter* (1,712:1), and *Cryptosporidium* (1,152:1); it is lowest for *Listeria* (55:1), *Cyclospora* (87:1), and *E. coli* O157 (132:1).

Third, we analyzed the differences between outbreak-based attribution estimates and those from experts (Tables 3 and 4). Because experts draw on a range of scientific evidence, not just outbreak information, large differences may point to pathogens for which outbreak data may not be representative of food attribution. In this analysis, for each pathogen across noncomplex foods we

TABLE 3. Attribution percentages for 12 pathogens based on foodborne outbreaks with known etiology and vehicle, 1999 through 2008^a

Food	<i>Campylobacter</i> spp.	<i>Clostridium perfringens</i>	<i>Cryptosporidium parvum</i>	<i>Cyclospora cayatanensis</i>	<i>E. coli</i> O157:H7	STEC non-O157	<i>Listeria monocytogenes</i>	Norovirus	<i>Salmonella</i> (nontyphoidal)	<i>Shigella</i> spp.	<i>Vibrio</i> spp.	<i>Yersinia enterocolitica</i>
Beef	5.8	32.6	0.0	0.0	55.2	40.0	0.0	4.2	6.9	14.6	0.0	0.0
Beverages	0.0	0.0	50.0	0.0	2.1	13.3	0.0	2.0	1.1	0.0	0.0	0.0
Baked goods	0.0	0.0	0.0	0.0	0.7	0.0	0.0	7.9	2.6	0.0	0.0	0.0
Dairy	50.8	0.6	0.0	0.0	5.6	20.0	30.0	2.1	5.6	2.4	0.0	0.0
Eggs	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.6	11.8	0.0	0.0	0.0
Game	1.7	0.3	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
Deli and other meats	1.7	2.8	0.0	0.0	3.5	0.0	35.0	2.1	2.9	4.9	0.0	0.0
Complex foods	10.8	24.0	50.0	21.4	13.3	6.7	15.0	45.5	18.7	48.8	0.0	0.0
Pork	2.5	8.3	0.0	0.0	0.0	0.0	5.0	2.8	6.6	0.0	0.0	100.0
Poultry	18.3	27.3	0.0	0.0	0.7	6.7	5.0	7.7	20.9	9.8	0.0	0.0
Produce	5.8	3.0	0.0	78.6	18.2	13.3	5.0	15.6	17.6	12.2	0.0	0.0
Seafood	2.5	1.1	0.0	0.0	0.7	0.0	5.0	9.2	5.3	7.3	100.0	0.0
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Used in baseline ranking	■	■	■	■	■	■	■	■	■	■	■	■

^a No *T. gondii* outbreaks with known vehicles were identified from 1999 through 2008. These fractions were estimated by counting the number of outbreaks due to each pathogen-food combination and dividing by the total number of food attributable outbreaks for that pathogen. Food attributable outbreaks are those with known etiology and an identified food vehicle that could be placed into one of these categories. Attributions based on *Vibrio* spp. are applied to both *V. vulnificus* and *Vibrio* other.

TABLE 4. Attribution percentages for 11 pathogens based on expert elicitation^a

Food	<i>Campylobacter</i> spp.	<i>Cryptosporidium parvum</i>	<i>Cyclospora cayatanensis</i>	<i>E. coli</i> O157:H7	<i>Listeria monocytogenes</i>	Norovirus	<i>Salmonella</i> (nontyphoidal)	<i>Shigella</i> spp.	<i>Toxoplasma gondii</i>	<i>Vibrio</i> spp.	<i>Yersinia enterocolitica</i>
Beef	4.4	7.4	0.0	67.9	1.6	1.4	10.9	3.1	23.2	0.2	2.2
Beverages	0.0	9.0	1.5	3.2	0.2	4.5	1.7	4.7	0.0	0.8	1.1
Baked goods	0.0	0.3	0.3	0.0	0.2	5.8	0.3	1.9	0.0	0.0	0.0
Dairy	7.8	5.8	0.4	4.0	23.6	2.9	7.3	3.4	2.4	0.0	12.2
Eggs	2.6	0.3	0.0	0.0	0.3	1.1	21.8	0.9	0.0	0.0	0.1
Game	2.0	5.4	1.3	3.2	0.3	0.6	1.6	0.8	20.4	0.0	2.0
Deli and other meats	0.9	1.4	0.1	1.8	54.0	9.4	1.9	9.4	1.7	0.2	1.8
Complex foods	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
Pork	4.4	2.0	0.0	0.6	1.3	1.4	5.7	3.1	41.0	0.2	71.6
Poultry	72.0	1.2	0.0	0.9	2.7	1.5	35.1	4.9	3.7	0.2	1.2
Produce	5.2	59.5	96.1	18.4	8.7	37.3	11.7	60.0	7.0	1.4	3.2
Seafood	0.8	7.7	0.4	0.1	7.2	34.1	2.0	7.8	0.5	97.1	4.7
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Used in baseline ranking	■	■	■	■	■	■	■	■	■	■	■

^a The expert elicitation did not include *C. perfringens* or STEC non-O157. Attributions based on *Vibrio* spp. are applied to both *V. vulnificus* and *Vibrio* other.

TABLE 5. Factors influencing choice of attribution approach, by pathogen

Pathogen	Data decision	Total no. of attributable outbreaks (1999–2008) ^a	Total no. of outbreak cases (1999–2008) ^b	Ratio of overall incidence to outbreak cases ^c	Sum of mean difference squared ^d	Mean SD of expert estimates ^e
<i>Campylobacter</i>	Expert	120	4,936	1,712	3,307	0.91
<i>C. perfringens</i>	Outbreak	362	19,523	495		
<i>C. parvum</i>	Expert	4	500	1,152	3,622	1.64
<i>C. cayetanensis</i>	Outbreak	14	1,306	87	62	0.42
<i>E. coli</i> O157:H7	Outbreak	143	4,768	132	20	0.76
STEC non-O157	Outbreak	15	1,514	745		
<i>L. monocytogenes</i>	Outbreak	20	290	55	827	0.96
Norovirus	Outbreak	1,125	98,384	555	701	1.77
<i>S. enterica</i>	Outbreak	621	34,717	296	218	1.02
<i>Shigella</i>	Outbreak	41	5,133	256	1,198	1.68
<i>T. gondii</i>	Expert	0	0		2,706	2.02
<i>Vibrio</i> spp.	Outbreak	59	671	780	9	0.25
<i>Y. enterocolitica</i>	Expert	5	82	11,909	562	1.38

^a Number of foodborne outbreaks between 1999 and 2008 with identified etiology and food vehicle.

^b Number of foodborne outbreak cases between 1999 and 2008 with identified etiology.

^c Number of estimated annual cases from Scallan et al. (48) divided by the average annual number of foodborne outbreak cases between 1999 and 2008.

^d Sum across foods of the mean difference squared between experts' food attribution percentages and outbreak attribution percentages based on data from 1993 through 2002 (to utilize data concurrent with the expert elicitation conducted in 2003).

^e Mean across foods of the standard deviation among experts' food attribution percentages.

calculated the sum of the mean of the squared difference between experts' estimates and outbreak attribution estimates (Table 5). Outbreak attribution estimates used for this analysis were based on data from 1993 through 2002 (a 10-year window concurrent with the expert elicitation time frame). The sum of mean differences squared was highest for *Cryptosporidium* (3,622), *Campylobacter* (3,307), *Toxoplasma* (2,706), and *Shigella* (1,198) and lowest for *Vibrio* spp. (9), *E. coli* O157 (20), and *Cyclospora* (62) (Table 5). To provide a more intuitive feel for this measure of difference, outbreak estimates attributed 51% of *Campylobacter* cases to dairy and 18% to poultry, whereas experts attributed 72% to poultry and 8% to dairy on average (Tables 3 and 4). The discrepancy for dairy is likely due to the fact that many of the *Campylobacter* dairy outbreaks were associated with unpasteurized milk, a high-risk niche food consumed by a small percentage of the U.S. population. Likewise, expert judgment attributed 60% of *Shigella* infection cases to produce, whereas outbreak estimates attributed 12% of these cases to produce and 49% to complex foods.

We also looked at the mean standard deviation across experts' individual attribution estimates as an indicator of scientific agreement on food attribution relationships for a particular pathogen. This measure varies significantly across pathogens from 0.25 for *Vibrio* to 2.02 for *Toxoplasma* (Table 5). Hoffmann et al. (21) found that viewing information on multiple measures of uncertainty from expert elicitation can enhance understanding of the likely state of scientific understanding. For example, although expert and outbreak attributions for *Campylobacter* differ markedly, the low mean standard deviation among experts (0.91) suggests strong agreement about attribution. The mean standard deviation across experts is much higher for *Toxoplasma* (2.02), which points to greater uncertainty about attributing cases of toxoplasmosis.

Existing case-control studies have not included categories that are entirely congruent with our food categories, but this information can provide indications of the representativeness of outbreak attribution estimates. A FoodNet case-control study on

Campylobacter revealed that the top three foodborne hazards were chicken prepared by a restaurant, nonpoultry meat prepared by a restaurant, and turkey prepared by a restaurant (14). These results align strongly with expert judgment but not with outbreak attribution. In contrast, a recent case-control study on toxoplasmosis (24) revealed some important differences between outbreak and expert attribution. Although the present study did not include attributable fractions, published odds ratios point to much more important roles for lamb and shellfish than suggested by the percentages estimated by experts.

Together, these five pieces of evidence point to four pathogens for which outbreak attribution may not be representative (Table 5). The case for using expert elicitation is strongest for *Campylobacter*, which has a high ratio of estimated incidence to reported outbreak cases, large differences between expert and outbreak attribution, high agreement among experts, and case-control studies that support expert estimates. *Cryptosporidium* has sparse outbreak data and a high ratio of incidence to outbreak cases, although experts are not in close agreement, suggesting uncertainty in their attribution estimates. Outbreak data are nonexistent for *Toxoplasma* and plainly insufficient for *Yersinia*, although opinions about these pathogens also differ significantly among experts. Conversely, the case for using outbreak data is strongest for *Vibrio*, *Cyclospora*, and *E. coli* O157. Based on the totality of evidence, we substituted expert attribution estimates for outbreak estimates only for *Campylobacter*, *Cryptosporidium*, *Toxoplasma*, and *Yersinia* in our baseline scenario. This decision was examined through sensitivity analysis.

RESULTS AND DISCUSSION

Pathogen-food rankings. We developed rankings of pathogen-food combinations by cost of illness and QALY loss separately. Following recommendations of the National Academy of Sciences (36), we treated these metrics as

TABLE 6. Estimated annual disease burden for top 50 pathogen-food combinations, by combined QALY and cost of illness ranking^a

Rank	Pathogen-food combination	Cost of illness (\$million)	QALY loss	No. of illnesses	No. of hospitalizations	No. of deaths
1	<i>Campylobacter</i> -poultry	1,257 (606–2,988)	9,541 (5,753–18,730)	608,231 (242,588–1,159,624)	6,091 (3,095–10,960)	55 (0–239)
2	<i>T. gondii</i> -pork	1,219 (723–1,819)	4,495 (2,471–6,875)	35,537 (26,590–45,879)	1,815 (1,080–2,736)	134 (82–198)
3	<i>L. monocytogenes</i> -deli meats	902 (71–2,433)	3,281 (536–8,234)	557 (195–1,106)	509 (182–1,056)	89 (0–257)
4	<i>S. enterica</i> -poultry	693 (33–1,797)	3,513 (64–9,290)	215,109 (134,979–351,621)	4,048 (1,789–7,848)	79 (0–212)
5	<i>L. monocytogenes</i> -dairy	773 (61–2,086)	2,812 (459–7,058)	477 (167–948)	437 (156–905)	77 (0–220)
5	Norovirus-complex foods	911 (519–1,432)	2,288 (1,319–3,565)	2,485,694 (1,468,679–3,781,737)	6,673 (3,685–10,615)	68 (38–108)
7	<i>S. enterica</i> -complex foods	618 (30–1,604)	3,135 (57–8,290)	191,944 (120,443–313,754)	3,612 (1,596–7,003)	71 (0–189)
8	<i>S. enterica</i> -produce	581 (28–1,507)	2,946 (53–7,790)	180,361 (113,175–294,821)	3,394 (1,500–6,580)	66 (0–177)
8	<i>T. gondii</i> -beef	689 (409–1,028)	2,541 (1,396–3,886)	20,086 (15,029–25,931)	1,026 (610–1,546)	76 (46–112)
10	<i>S. enterica</i> -eggs	389 (19–1,009)	1,973 (36–5,217)	120,792 (75,796–197,449)	2,273 (1,004–4,407)	44 (0–119)
11	<i>L. monocytogenes</i> -complex foods	387 (31–1,043)	1,406 (230–3,529)	239 (84–474)	218 (78–453)	38 (0–110)
12	<i>S. enterica</i> -beef	229 (11–595)	1,162 (21–3,073)	71,152 (44,647–116,305)	1,339 (592–2,596)	26 (0–70)
13	<i>S. enterica</i> -pork	218 (11–567)	1,108 (20–2,930)	67,842 (42,570–110,896)	1,277 (564–2,475)	25 (0–67)
14	Norovirus-produce	313 (178–492)	786 (453–1,225)	854,457 (504,858–1,299,972)	2,294 (1,267–3,649)	23 (13–37)
15	<i>S. enterica</i> -dairy	187 (9–484)	946 (17–2,501)	57,914 (36,341–94,667)	1,090 (482–2,113)	21 (0–57)
16	<i>Y. enterocolitica</i> -pork	180 (3–1,010)	1,013 (9–5,880)	69,889 (21,748–123,620)	381 (0–839)	21 (0–124)
17	<i>T. gondii</i> -produce	209 (124–312)	772 (424–1,181)	6,104 (4,567–7,880)	312 (185–470)	23 (14–34)
18	<i>V. vulnificus</i> -seafood	291 (154–460)	557 (294–882)	96 (60–139)	93 (53–139)	36 (19–57)
19	<i>Campylobacter</i> -dairy	136 (66–324)	1,034 (623–2,029)	65,886 (26,278–125,615)	660 (335–1,187)	6 (0–26)
19	<i>S. enterica</i> -seafood	176 (8–456)	892 (16–2,358)	54,605 (34,264–89,258)	1,028 (454–1,992)	20 (0–54)
21	<i>E. coli</i> O157:H7-beef	141 (14–609)	917 (72–4,349)	34,889 (9,716–82,663)	1,181 (303–2,549)	11 (0–62)
22	Norovirus-seafood	183 (104–288)	460 (265–717)	500,052 (295,457–760,779)	1,342 (741–2,135)	14 (8–22)
23	<i>L. monocytogenes</i> -pork	129 (10–348)	469 (77–1,176)	80 (28–158)	73 (26–151)	13 (0–37)
23	<i>L. monocytogenes</i> -poultry	129 (10–348)	469 (77–1,176)	80 (28–158)	73 (26–151)	13 (0–37)
23	<i>L. monocytogenes</i> -produce	129 (10–348)	469 (77–1,176)	80 (28–158)	73 (26–151)	13 (0–37)
23	<i>L. monocytogenes</i> -seafood	129 (10–348)	469 (77–1,176)	80 (28–158)	73 (26–151)	13 (0–37)
27	<i>Campylobacter</i> -produce	91 (44–217)	693 (418–1,360)	44,178 (17,620–84,228)	442 (225–796)	4 (0–17)
27	Norovirus-bakery	158 (90–249)	398 (229–620)	432,084 (255,298–657,372)	1,160 (641–1,845)	12 (7–19)
29	Norovirus-poultry	155 (88–243)	389 (224–606)	422,374 (249,561–642,600)	1,134 (626–1,804)	12 (6–18)
30	<i>S. enterica</i> -deli meats	96 (5–249)	486 (9–1,286)	29,784 (18,689–48,686)	560 (248–1,087)	11 (0–29)
31	<i>Campylobacter</i> -pork	77 (37–183)	584 (352–1,146)	37,215 (14,843–70,952)	373 (189–671)	3 (0–15)
32	<i>Campylobacter</i> -beef	76 (37–182)	580 (350–1,138)	36,952 (14,738–70,451)	370 (188–666)	3 (0–15)
32	<i>T. gondii</i> -poultry	111 (66–166)	410 (225–627)	3,242 (2,426–4,185)	166 (99–250)	12 (7–18)
34	<i>S. enterica</i> -bakery	85 (4–221)	432 (8–1,143)	26,475 (16,613–43,276)	498 (220–966)	10 (0–26)
35	<i>C. perfringens</i> -beef	101 (6–512)	285 (27–1,285)	314,870 (62,689–809,476)	143 (14–655)	8 (0–53)
36	<i>Vibrio</i> other-seafood	103 (28–298)	210 (60–595)	52,228 (29,108–84,502)	183 (101–293)	12 (3–36)
37	<i>C. perfringens</i> -poultry	85 (5–430)	240 (23–1,078)	264,171 (52,595–679,137)	120 (12–549)	7 (0–45)
38	Norovirus-beef	84 (48–131)	210 (121–327)	228,179 (134,820–347,152)	613 (338–974)	6 (4–10)
38	<i>Shigella</i> -complex foods	59 (4–312)	266 (7–1,645)	64,026 (11,957–182,824)	710 (140–1,802)	5 (0–33)
38	<i>T. gondii</i> -dairy	71 (42–106)	261 (143–399)	2,062 (1,543–2,662)	105 (63–159)	8 (5–11)
41	<i>Campylobacter</i> -eggs	45 (22–107)	341 (206–670)	21,749 (8,675–41,467)	218 (111–392)	2 (0–9)
41	<i>E. coli</i> O157:H7-produce	46 (5–200)	302 (24–1,431)	11,482 (3,198–27,206)	389 (100–839)	4 (0–21)

TABLE 6. Continued

Rank	Pathogen-food combination	Cost of illness (\$million)	QALY loss	No. of illnesses	No. of hospitalizations	No. of deaths
43	<i>C. perfringens</i> -complex foods	74 (5-378)	210 (20-947)	232,150 (46,220-596,817)	105 (11-483)	6 (0-39)
44	<i>T. gondii</i> -deli meats	51 (30-76)	188 (104-288)	1,490 (1,115-1,923)	76 (45-115)	6 (3-8)
45	<i>E. coli</i> O157:H7-complex foods	34 (3-146)	221 (17-1,046)	8,391 (2,337-19,881)	284 (73-613)	3 (0-15)
45	Norovirus-pork	57 (32-90)	143 (82-223)	155,356 (91,792-236,359)	417 (230-663)	4 (2-7)
47	<i>S. enterica</i> -beverages	37 (2-97)	189 (3-500)	11,583 (7,268-18,933)	218 (96-423)	4 (0-11)
48	<i>C. parvum</i> -produce	28 (2-114)	203 (24-753)	34,286 (7,177-99,242)	125 (35-308)	2 (0-11)
48	Norovirus-dairy	43 (24-67)	107 (62-167)	116,517 (68,844-177,269)	313 (173-498)	3 (2-5)
48	Norovirus-deli meats	43 (24-67)	107 (62-167)	116,517 (68,844-177,269)	313 (173-498)	3 (2-5)
	Top 10 subtotal	8,032 (2,498-17,704)	36,524 (12,144-78,934)	3,858,789 (2,197,641-6,172,870)	29,878 (14,698-53,657)	759 (167-1,829)
	% of total	57%	60%	43%	56%	57%
	Top 20 subtotal	10,359 (3,092-23,447)	46,200 (14,252-104,522)	5,106,973 (2,913,058-8,141,697)	38,570 (18,708-69,571)	998 (213-2,464)
	% of total	74%	76%	57%	72%	76%
	Top 50 subtotal	13,008 (3,905-30,576)	56,907 (17,695-133,741)	8,309,592 (4,406,310-14,109,640)	50,419 (24,007-92,205)	1,225 (262-3,171)
	% of total	93%	93%	93%	94%	93%
	Total (all combinations)	14,012 (4,352-33,034)	61,166 (19,397-144,974)	8,914,713 (4,591,947-15,472,172)	53,678 (25,189-99,252)	1,322 (306-3,423)

^a Values are mean (ranges) and reflect baseline assumptions for attributing the disease burden from 14 major foodborne pathogens to 12 food categories for a total of 104 pathogen-food combinations with nonzero estimated disease burden. Combined QALY and cost of illness rank is the average of the QALY loss ranking and cost of illness ranking. Upper and lower bounds reflect estimates based on 90% credible intervals for incidence estimated by Scallan et al. (48). Number of annual illnesses, hospitalizations, and deaths include only those reported by Scallan et al. that were due to acute infection and do not include all cases of congenital illness or chronic sequelae. Illnesses caused by pathogens in game animals were not included. *Vibrio* other refers to noncholera *Vibrio* spp. other than *V. vulnificus*.

TABLE 7. Rank correlations for pathogen-food combinations, by disease burden and incidence measure^a

Comparison		Avg rank	Cost of illness rank	QALY rank	Death rank	Hospitalization rank	Illness rank
Pathogen-food pairs							
All	Avg rank	1.00					
	Cost of illness rank	1.00	1.00				
	QALY rank	1.00	0.99	1.00			
	Death rank	0.98	0.99	0.98	1.00		
	Hospitalization rank	0.96	0.96	0.96	0.93	1.00	
	Illness rank	0.81	0.81	0.80	0.75	0.89	1.00
Top 50	Avg rank	1.00					
	Cost of illness rank	0.97	1.00				
	QALY rank	0.97	0.89	1.00			
	Death rank	0.91	0.96	0.94	1.00		
	Hospitalization rank	0.87	0.86	0.87	0.80	1.00	
	Illness rank	0.01	0.03	-0.01	-0.09	0.67	1.00
Top 10	Avg rank	1.00					
	Cost of illness rank	0.89	1.00				
	QALY rank	0.89	0.59	1.00			
	Death rank	0.44	0.37	0.42	1.00		
	Hospitalization rank	0.09	0.00	0.16	-0.47	1.00	
	Illness rank	-0.04	-0.10	0.03	-0.58	0.98	1.00
			Cost of illness	QALY loss	Deaths	Hospitalizations	Illnesses
Burden measure for all pathogen-food pairs	Cost of illness		1.00				
	QALY loss		0.93	1.00			
	Deaths		0.95	0.82	1.00		
	Hospitalizations		0.36	0.80	0.69	1.00	
	Illnesses		0.48	0.36	0.36	0.75	1.00

^a Values reflect baseline assumptions for attributing the disease burden from 14 major foodborne pathogens to 12 food categories for a total of 104 pathogen-food combinations with nonzero estimated disease burden. Combined QALY and cost of illness rank is the average of the QALY loss ranking and cost of illness ranking. Number of annual illnesses, hospitalizations, and deaths include only those reported by Scallan et al. (48) that were due to acute infection and do not include all cases of congenital illness or chronic sequelae. Illnesses caused by pathogens in game animals were not included.

distinct measures of disease burden and did not monetize QALY loss. Because the Academy's recommendation was based in part on incomparability of the cardinal properties of these two metrics, we compute a unified ranking across these metrics based on ordinal rather than cardinal properties. The combined rank of each pathogen-food combination is the rank order of the average of that pair's cost of illness and QALY loss rankings.

Table 6 presents estimates of public health burden for the top 50 pathogen-food combinations based on baseline attribution assumptions and combined rank. These pathogen-food combinations account for 93% of cost of illness and QALY loss from the 14 pathogens included in this study.

Several conclusions can be drawn from these results. First, variability is high in both cost of illness and QALY loss across pathogen-food combinations; within the top 50 combinations, cost of illness ranges from \$1.3 billion (\$0.6 to \$3.0 billion) for *Campylobacter* in poultry to \$28 million (\$2 to \$114 million) for *Cryptosporidium* in produce. Second, the public health burden of foodborne illness is concentrated in the highest ranking pathogen-food combinations. The top 10 combinations caused nearly 60% of the

total cost of illness and QALY loss due to these 14 pathogens in all foods, and the next 10 combinations were responsible for another 15%. Third, a few pathogens dominated the rankings; all top 10 combinations and 39 of the top 50 pairs involved just five pathogens. Fourth, the set of top 10 combinations were the same regardless of whether they were ranked by QALY loss or cost of illness, although ranks of individual combinations differed slightly.

Although *Campylobacter* ranked fifth in cost of illness and second in QALY loss (Table 1), more than 70% of illnesses caused by this pathogen were attributed to poultry (Table 4), making *Campylobacter*-poultry the highest ranked combination. By comparison, although *Salmonella* dominated pathogen rankings (Table 1), this burden was spread across several food categories (Table 3). *Salmonella* appears eight times among the top 20 ranked pathogen-food combinations, most notably associated with poultry, produce, eggs, and complex foods. *Toxoplasma* ranked highly in our estimates because it is the second leading cause of death from foodborne illness according to the CDC (48). However, attribution of these illnesses to foods is uncertain because no outbreaks have been reported and considerable disagreement was found among experts.

TABLE 8. Estimated annual disease burden for food categories, by combined QALY and cost of illness ranking^a

Rank	Food	QALY loss	Cost of illness (\$million)	No. of illnesses	No. of hospitalizations	No. of deaths
1	Poultry	14,657 (6,369–32,025)	2,449 (810–6,067)	1,535,859 (685,972–2,898,212)	11,815 (5,679–22,040)	179 (14–578)
2	Complex foods	7,538 (1,650–19,047)	2,085 (591–4,922)	2,992,405 (1,650,512–4,922,715)	11,623 (5,583–21,056)	190 (38–494)
3	Pork	7,891 (3,019–18,582)	1,907 (817–4,150)	447,109 (213,747–796,957)	4,376 (2,095–7,712)	202 (84–460)
4	Produce	6,336 (1,479–15,770)	1,435 (393–3,378)	1,203,397 (662,055–2,008,054)	7,281 (3,374–13,557)	138 (27–353)
5	Beef	5,890 (1,997–14,931)	1,356 (526–3,226)	776,841 (291,370–1,637,898)	5,020 (2,092–9,979)	133 (50–337)
6	Dairy products	5,493 (1,319–13,827)	1,266 (205–3,351)	292,729 (142,517–520,589)	2,893 (1,250–5,589)	120 (7–350)
7	Deli and other meats	4,318 (788–10,914)	1,135 (140–3,003)	193,550 (99,616–340,533)	1,703 (721–3,313)	112 (5–317)
8	Seafood	2,906 (815–6,855)	941 (323–2,060)	644,021 (368,352–1,025,185)	2,977 (1,454–5,288)	100 (31–227)
9	Game	2,551 (1,392–4,186)	651 (377–1,033)	46,968 (24,546–81,356)	1,106 (632–1,739)	69 (41–110)
10	Eggs	2,347 (260–5,944)	447 (48–1,137)	176,766 (104,606–291,254)	2,583 (1,166–4,946)	47 (1–129)
11	Breads and bakery	843 (238–1,822)	246 (94–479)	459,188 (272,073–702,238)	1,674 (865–2,845)	22 (7–46)
12	Beverages	397 (73–1,071)	95 (27–229)	145,880 (76,581–247,180)	625 (280–1,187)	9 (2–22)
Total		61,166 (19,397–144,974)	14,012 (4,352–33,034)	8,914,713 (4,591,947–15,472,172)	53,678 (25,189–99,252)	1,322 (306–3,423)

^a Values are mean (ranges) and reflect baseline assumptions for attributing the disease burden from 14 major foodborne pathogens to 12 food categories for a total of 104 pathogen-food combinations with nonzero estimated disease burden. Combined QALY and cost of illness rank is the average of the QALY loss ranking and cost of illness ranking. Upper and lower bounds reflect estimates based on 90% credible intervals for incidence estimated by Scallan et al. (48). Number of annual illnesses, hospitalizations, and deaths include only those reported by Scallan et al. that were due to acute infection and do not include all cases of congenital illness or chronic sequelae that were included in cost and QALY estimates.

Although *Listeria* in deli meats ranks third, the number of outbreaks due to this combination has declined since the mid-2000s. Recent studies suggest that the highest risks in this category are due to retail-sliced products (11, 15). *Listeria* in dairy ranks high because of a large number of recorded outbreaks due to soft unaged cheeses such as Mexican-style *queso fresco*.

Correlation analysis provides perspective on the stability of rankings and the relative contribution of different measures of disease burden (Table 7). In the bottom set of correlations, cost of illness estimates and QALY loss estimates were highly correlated (0.93) across all pathogen-food combinations. Cost of illness and QALY loss were both highly correlated with number of annual deaths (0.95 and 0.82), although only QALY loss was highly correlated with hospitalizations (0.80). In the top set of results, correlations among pathogen-food rankings were lower for smaller subsets of all pathogen-food combinations, as expected. Average rank was highly correlated with both cost of illness rank and QALY rank (1.00 for all pairs, 0.89 for the top 10), which suggests general similarities between the two integrated measures. However, for the top 10 pairs the correlation between cost of illness rank and QALY rank dropped to 0.59. This finding suggests that from a ranking perspective the difference between QALY and cost of illness estimates matters most when assessing the relative importance of the highest ranking pathogen-food combinations.

Food rankings. Table 8 presents rankings of foods, with public health impacts summed across pathogens, using baseline attribution assumptions. Poultry was ranked in first place because of the significant disease burden caused by both *Salmonella* and *Campylobacter*. Although complex foods were associated with twice as many illnesses as was poultry, 83% of these illnesses were caused by norovirus and were relatively mild. Pork ranked third, although this ranking was largely driven by highly uncertain attribution for *Toxoplasma*. Produce ranked quite highly in part because it is a major vehicle for norovirus and *Salmonella* infection outbreaks but also because it is associated with so many pathogens; the attributable percentage for produce, averaged across all pathogens, was higher than that for any other single food category. Because outbreak-based attribution identifies foods at exposure, some portion of these produce-associated illnesses likely were caused by cross-contamination during preparation with pathogens that entered the kitchen in meat, poultry, eggs, or other animal products. Overall, food categories associated with numerous pathogens (e.g., poultry, pork, and produce) ranked much higher than those associated with few pathogens (e.g., eggs and seafood). Eggs are noteworthy because although *Salmonella* in eggs ranks within the top 10 pathogen-food combinations, eggs are one of the lowest ranking food categories overall.

The second-place ranking of complex foods is important from a food safety management perspective. The nature of outbreaks associated with complex foods suggests an important role for contamination, cross-contamination, and other mistakes during handling, preparation, and cooking. In our analysis of outbreaks associated

TABLE 9. Top 20 pathogen-food combinations under alternative attribution scenarios^a

Scenario ^b	Baseline	1	2	3	4	5	6
Attribution method	Out+Exp	Out+Exp	<i>Outbreak</i>	<i>Outbreak</i>	<i>Expert</i>	Out+Exp	Out+Exp
Outbreak approach	Events	<i>Cases</i>	Events	<i>Cases</i>	N/A	Events	Events
complex foods	Include	Include	Include	Include	Include	Include	<i>Drop</i>
Multi-source	Drop	Drop	Drop	Drop	Drop	<i>Include</i>	Drop
Pathogen-food combination							
<i>Campylobacter</i> -poultry	1	1	9	27	1	1	1
<i>T. gondii</i> -pork	2	2	—	—	4	2	2
<i>L. monocytogenes</i> -deli meats	3	4	3	3	2	4	3
<i>S. enterica</i> -poultry	4	9	4	8	3	6	4
<i>L. monocytogenes</i> -dairy	5	9	6	8	8	6	5
Norovirus-complex	5	5	5	5	—	4	—
<i>S. enterica</i> -complex	7	7	6	5	—	3	—
<i>S. enterica</i> -produce	8	3	8	3	9	9	6
<i>T. gondii</i> -beef	8	8	—	—	6	8	7
<i>S. enterica</i> -eggs	10	11	9	10	5	10	8
<i>L. monocytogenes</i> -complex	11	5	11	5	—	10	—
<i>S. enterica</i> -beef	12	18	14	17	11	12	10
<i>S. enterica</i> -pork	13	17	15	15	14	14	11
Norovirus-produce	14	12	15	11	7	17	8
<i>S. enterica</i> -dairy	15	13	17	13	12	18	13
<i>Y. enterocolitica</i> -pork	16	13	12	11	17	13	18
<i>T. gondii</i> -produce	17	15	—	—	17	15	19
<i>V. vulnificus</i> -seafood	18	19	18	16	20	19	19
<i>S. enterica</i> -seafood	19	29	19	26	29	20	14
<i>Campylobacter</i> -dairy	19	16	2	2	19	16	21
<i>E. coli</i> O157:H7-beef	21	20	20	20	16	20	17
Norovirus-seafood	22	27	21	25	10	27	12
<i>L. monocytogenes</i> -produce	23	39	22	36	14	22	22
Norovirus-bakery	27	20	28	19	27	33	15
Norovirus-poultry	29	26	29	24	45	34	16
<i>Campylobacter</i> -beef	32	30	26	18	26	29	33
<i>Campylobacter</i> -seafood	56	56	35	14	49	54	54
<i>T. gondii</i> -unknown	—	—	1	1	—	—	—
<i>Campylobacter</i> -complex	—	—	13	32	—	—	—
<i>C. perfringens</i> -unknown	—	—	—	—	13	—	—
Rank correlations with baseline^c							
All pathogen-food combinations		0.98	0.82	0.81	0.78	1.00	0.91
Top 90 pathogen-food combinations		0.94	0.77	0.70	0.64	0.99	0.75
Top 10 pathogen-food combinations		0.65	-0.03	-0.16	0.16	0.85	0.18

^a Table includes only pathogen-food combinations that rank in the top 20 in at least one of the scenarios. Shading indicates whether pairs were ranked 1 to 10, 11 to 20, or 20 and higher. Dashes indicate that a particular pathogen-food combination was not included in that scenario; for example, we did not have outbreak-based attribution percentages for *T. gondii*, so all illnesses are attributed to the “unknown” category in scenarios 2 and 3, with dashes for pork, beef, and produce.

^b Italicized assumptions indicate variation from assumptions used in the baseline scenario. “Out + Exp” refers to attribution based on both outbreak and expert attribution estimates.

^c Spearman rank correlations between baseline and alternative scenario rankings quantify the impact of changes in assumptions on rankings.

with complex food between 1998 and 2008, more than 70% of salmonellosis outbreaks and 80% of outbreaks of norovirus infection were associated with foods prepared in professional kitchens.

Sensitivity analyses. We conducted sensitivity analyses to assess the impact of key modeling assumptions. Table 9 shows pathogen-food combinations ranked within the top 20 by one of six alternate attribution scenarios as compared with baseline rankings. Shading is used to identify pairs ranked 1 through 10 for each scenario, 11 through 20, and 20 and above. Spearman rank correlations between the baseline and alternative scenario rankings quantify the impact of changes in assumptions on rankings.

The first four scenarios (1 through 4) explored the impacts of basing outbreak attribution on the number of outbreaks and of combining outbreak and expert attribution. Basing outbreak attribution on outbreak cases rather than outbreak events (scenario 1) had little impact on whether pathogen-food combinations were ranked in the top 10 or top 20 compared with the baseline, although it did change rankings within the top 10 and the next grouping of 10. Not using expert attribution estimates (scenarios 2 and 3) had a greater effect on rankings relative to the baseline when outbreak attribution was based on numbers of cases (scenario 3) than when it was based on numbers of outbreaks (scenario 2), although both rankings differed markedly from baseline estimates. The rank correlations confirm that these patterns carry through for rankings over a larger set of or all pathogen-food combinations. These differences reflect the fact that *Toxoplasma* was not represented at all in outbreak data, that expert judgment differed markedly from outbreak analysis for *Campylobacter*, and that outbreak sizes differ by food. Using expert attribution exclusively (scenario 4) resulted in some noticeable changes to rankings, primarily because the expert elicitation did not include a complex foods category. Thus, as those combinations dropped out of the analysis, others moved up. *Listeria* in deli meats rose to rank 2 from rank 4, and dairy dropped to rank 8 from rank 5, reflecting differences between experts and outbreak estimates, aside from the complex foods category.

The remaining two scenarios (5 and 6) further explored the role of the complex and multisource foods category. Including multisource outbreaks and categorizing them as complex foods (scenario 5) resulted in marginally higher attribution percentages for complex foods. Rank correlations indicated that this change had little overall impact on rankings. In contrast, dropping complex foods (scenario 6) resulted not only in removal of this category but in redistribution of outbreak attribution across remaining categories. Thus, changes from baseline were much more significant. The similarities in results for scenarios 4 and 6 reinforced that most of the differences from the baseline that resulted from relying solely on expert attribution were due to the lack of a complex foods category.

Together these sensitivity analyses suggest that our risk ranking model was most sensitive to two assumptions: the use of expert-based attribution for four pathogens and the decision to use a complex foods category in the outbreak

attribution. Basing outbreak attribution on number of events rather than number of cases had a lesser but still noticeable impact on rankings, whereas the impacts of excluding multisource outbreaks and complex foods in the expert elicitation were negligible.

Both methodological and substantive lessons can be drawn from this study. Methodologically, we found that properly structured expert elicitation can be used to characterize uncertainty about and supplement, not substitute for, attribution estimates based on empirical outbreak data. It is not necessarily more accurate to rely on a single methodology for estimating attribution percentages, but the methods must be consistent and compatible. Substantively, results from this study support risk-based prioritization by identifying which pathogens in which types of foods cause the greatest burden for public health. These estimates say nothing, however, about the relative effectiveness of public or private management efforts. This study also highlights the fact that further research is needed on the relationship between attribution foodborne illness and food sources, particularly for *Toxoplasma*, *Campylobacter*, and *Salmonella*.

ACKNOWLEDGMENTS

This research was supported by competitive grants from the Robert Wood Johnson Foundation, the Cooperative State Research, Education, and Extension Service of the U.S. Department of Agriculture (now the National Institute of Food and Agriculture), and the Milbank Memorial Fund. We thank our collaborators on the research efforts extended by this study, in particular Alan J. Krupnick, Paul S. Fischbeck, Heather Green, Michael McWilliams, and Michael R. Taylor.

REFERENCES

- Adak, G. K., S. M. Meakins, H. Yip, B. A. Lopman, and S. J. O'Brien. 2005. Disease risks from foods, England and Wales, 1996–2000. *Emerg. Infect. Dis.* 11:365–372.
- Batz, M. B., M. P. Doyle, J. G. Morris, Jr., J. Painter, R. Singh, R. V. Tauxe, M. R. Taylor, D. M. Lo Fo Wong, and the Food Attribution Working Group. 2005. Attributing illness to food. *Emerg. Infect. Dis.* 11:993–999.
- Batz, M. B., S. Hoffmann, and J. G. Morris, Jr. 2011. Ranking the risks: the 10 pathogen-food combinations with the greatest burden on public health. University of Florida, Gainesville.
- Centers for Disease Control and Prevention. 2011. Foodborne outbreak online database (FOOD). Available at: <http://wwwn.cdc.gov/foodborneoutbreaks/>. Accessed 2 September 2011.
- Clemen, R. T., and R. L. Winkler. 1999. Combining probability distributions in risk analysis. *Risk Anal.* 19:187–203.
- Codex Alimentarius Commission. 2007. Working principles for risk analysis for food safety for application by governments. GL-62/2007. Codex Alimentarius, Rome.
- Cooke, R. M. 1991. Experts in uncertainty: opinion and subjective probability in science. Oxford University Press, New York.
- Cooke, R. M., M. Nauta, A. H. Havelaar, and H. J. van der Fels. 2006. Probabilistic inversion for chicken processing lines. *Reliabil. Eng. Syst. Saf.* 91:1364–1372.
- Davidson, V. J., A. Ravel, T. N. Nguyen, A. Fazil, and J. M. Ruzante. 2011. Food-specific attribution of selected gastrointestinal illnesses: estimates from a Canadian expert elicitation survey. *Foodborne Pathog. Dis.* 8:983–995.
- Dewaal, C. S., G. Hicks, K. Barlow, L. Alderton, and L. Vegosen. 2006. Foods associated with foodborne illness outbreaks from 1990 through 2003. *Food Prot. Trends* 26:466–473.
- Endrikat, S., D. Gallagher, R. Pouillot, H. Hicks Quesenberry, D. LaBarre, C. M. Schroeder, and J. Kause. 2010. A comparative risk

- assessment for *Listeria monocytogenes* in prepackaged versus retail-sliced deli meat. *J. Food Prot.* 73:612–619.
12. Evers, E. G., H. J. Van Der Fels-Klerx, M. J. Nauta, J. F. Schijven, and A. H. Havelaar. 2007. *Campylobacter* source attribution by exposure assessment. *Int. J. Risk Assess. Manag.* 8:174–190.
 13. FDA Food Safety Modernization Act. 2011. 21 USC §2201. Available at: <http://www.gpo.gov/fdsys/pkg/PLAW-111publ353/pdf/PLAW-111publ353.pdf>. Accessed 2 September 2011.
 14. Friedman, C. R., R. M. Hoekstra, M. Samuel, R. Marcus, J. Bender, B. Shiferaw, S. Reddy, S. D. Ahuja, D. L. Helfrick, F. Hardnett, M. Carter, B. Anderson, R. V. Tauxe, and the Emerging Infections Program FoodNet Working Group. 2004. Risk factors for sporadic *Campylobacter* infection in the United States: a case-control study in FoodNet sites. *Clin. Infect. Dis.* 38(Suppl. 3):S285–S296.
 15. Gombas, D. E., Y. Chen, R. S. Clavero, and V. N. Scott. 2003. Survey of *Listeria monocytogenes* in ready-to-eat foods. *J. Food Prot.* 66:559–569.
 16. Greig, J. D., and A. Ravel. 2009. Analysis of foodborne outbreak data reported internationally for source attribution. *Int. J. Food Microbiol.* 130:77–87.
 17. Guo, C., R. M. Hoekstra, C. M. Schroeder, S. M. Pires, K. L. Ong, E. Hartnett, A. Naugle, J. Harman, P. Bennett, P. Cieslak, E. Scallan, B. Rose, K. G. Holt, B. Kissler, E. Mbandi, R. Roodsari, F. J. Angulo, and D. Cole. 2011. 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.* 8:509–516.
 18. Havelaar, A. H., A. V. Galindo, D. Kurowicka, and R. M. Cooke. 2008. Attribution of foodborne pathogens using structured expert elicitation. *Foodborne Pathog. Dis.* 5:649–659.
 19. Hennessy, T. W., L. H. Cheng, H. Kassenborg, S. D. Ahuja, J. Mohle-Boetani, R. Marcus, B. Shiferaw, F. J. Angulo, and the Emerging Infections Program FoodNet Working Group. 2004. Egg consumption is the principal risk factor for sporadic *Salmonella* serotype Heidelberg infections: a case-control study in FoodNet sites. *Clin. Infect. Dis.* 38(Suppl. 3):S237–S243.
 20. Hoffmann, S., M. B. Batz, and J. G. Morris, Jr. 2012. Annual cost of illness and quality-adjusted life year losses in the United States due to 14 foodborne pathogens. *J. Food Prot.* 75:1292–1302.
 21. Hoffmann, S., P. Fischbeck, A. Krupnick, and M. McWilliams. 2007. Elicitation from large, heterogeneous expert panels: using multiple uncertainty measures to characterize information quality for decision analysis. *Dec. Anal.* 4:91–109.
 22. Hoffmann, S., P. Fischbeck, A. Krupnick, and M. McWilliams. 2007. Using expert elicitation to link foodborne illnesses in the United States to foods. *J. Food Prot.* 70(5):1220–1229.
 23. Hoffmann, S., P. Fischbeck, A. Krupnick, and M. McWilliams. 2008. Informing risk-mitigation priorities using uncertainty measures derived from heterogeneous expert panels: a demonstration using foodborne pathogens. *Reliabil. Eng. Syst. Saf.* 93:687–698.
 24. Jones, J. L., V. Dargelas, J. Roberts, C. Press, J. S. Remington, and J. G. Montoya. 2009. Risk factors for *Toxoplasma gondii* infection in the United States. *Clin. Infect. Dis.* 49:878–884.
 25. Kassenborg, H. D., C. W. Hedberg, M. Hoekstra, M. C. Evans, A. E. Chin, R. Marcus, D. J. Vugia, K. Smith, S. D. Ahuja, L. Slutsker, P. M. Griffin, and the Emerging Infections Program FoodNet Working Group. 2004. Farm visits and undercooked hamburgers as major risk factors for sporadic *Escherichia coli* O157:H7 infection: data from a case-control study in 5 FoodNet sites. *Clin. Infect. Dis.* 38(Suppl. 3):S271–S278.
 26. Kimura, A. C., V. Reddy, R. Marcus, P. R. Cieslak, J. C. Mohle-Boetani, H. D. Kassenborg, S. D. Segler, F. P. Hardnett, T. Barrett, D. L. Swerdlow, and the Emerging Infections Program FoodNet Working Group. 2004. Chicken consumption is a newly identified risk factor for sporadic *Salmonella enterica* serotype Enteritidis infections in the United States: a case-control study in FoodNet sites. *Clin. Infect. Dis.* 38(Suppl. 3):S244–S252.
 27. Lake, R. J., P. J. Cressey, D. M. Campbell, and E. Oakley. 2010. Risk ranking for foodborne microbial hazards in New Zealand: burden of disease estimates. *Risk Anal.* 30:743–752.
 28. Little, C. L., S. M. Pires, I. A. Gillespie, K. Grant, and G. L. Nichols. 2010. Attribution of human *Listeria monocytogenes* infections in England and Wales to ready-to-eat food sources placed on the market: adaptation of the Hald *Salmonella* source attribution model. *Foodborne Pathog. Dis.* 7:749–756.
 29. Mangen, M. J., M. B. Batz, A. Kasbohrer, T. Hald, J. G. Morris, Jr., M. Taylor, and A. H. Havelaar. 2009. Integrated approaches for the public health prioritization of foodborne and zoonotic pathogens. *Risk Anal.* 30:782–797.
 30. Morgan, M. G., H. K. Florig, M. L. DeKay, and P. Fischbeck. 2000. Categorizing risks for risk ranking. *Risk Anal.* 20:49–58.
 31. Morgan, M. G., and M. Henrion. 1990. Uncertainty: a guide to dealing with uncertainty in quantitative risk and policy analysis. Cambridge University Press, Cambridge.
 32. Mullner, P., G. Jones, A. Noble, S. E. F. Spencer, S. Hathaway, and N. P. French. 2009. Source attribution of food-borne zoonoses in New Zealand: a modified Hald model. *Risk Anal.* 29:970–984.
 33. Murray, C. J. L., and A. D. Lopez (ed.). 1996. The global burden of disease: a comprehensive assessment of mortality and disability from diseases. Harvard University Press, Cambridge, MA.
 34. National Academy of Sciences. 1998. Ensuring safe food: from production to consumption. Institute of Medicine and National Research Council. National Academies Press, Washington, DC.
 35. National Academy of Sciences. 2003. Scientific criteria to ensure safe food. Institute of Medicine and National Research Council. National Academies Press, Washington, DC.
 36. National Academy of Sciences. 2006. Valuing health for cost-effectiveness analysis. Institute of Medicine. National Academies Press, Washington, DC.
 37. National Academy of Sciences. 2010. Enhancing food safety: the role of the Food and Drug Administration. Institute of Medicine and National Research Council. National Academies Press, Washington, DC.
 38. National Research Council. 2002. Estimating the public health benefits of proposed air pollution regulations. National Academies Press, Washington, DC.
 39. Painter, J. A., T. Ayers, R. Woodruff, E. Blanton, N. Perez, R. M. Hoekstra, P. M. Griffin, and C. Braden. 2009. Recipes for foodborne outbreaks: a scheme for categorizing and grouping implicated foods. *Foodborne Pathog. Dis.* 6:1259–1264.
 40. Pires, S. M., E. G. Evers, W. van Pelt, T. Ayers, E. Scallan, F. J. Angulo, A. Havelaar, T. Hald, and the Med-Vet-Net Workpackage 28 Working Group. 2009. Attributing the human disease burden of foodborne infections to specific sources. *Foodborne Pathog. Dis.* 6:417–424.
 41. Pires, S. M., and T. Hald. 2010. Assessing the differences in public health impact of *Salmonella* subtypes using a Bayesian microbial subtyping approach for source attribution. *Foodborne Pathog. Dis.* 7:143–151.
 42. Pires, S. M., A. R. Vieira, E. Perez, D. Lo Fo Wong, and T. Hald. 2012. Attributing human foodborne illness to food sources and water in Latin America and the Caribbean using data from outbreak investigations. *Int. J. Food Microbiol.* 152:129–138.
 43. Ranta, J., D. Matjushin, T. Virtanen, M. Kuusi, H. Viljugrein, M. Hofshagen, and M. Hakkinen. 2011. Bayesian temporal source attribution of foodborne zoonoses: *Campylobacter* in Finland and Norway. *Risk Anal.* 31:1156–1171.
 44. Ravel, A., V. J. Davidson, J. M. Ruzante, and A. Fazil. 2010. Foodborne proportion of gastrointestinal illness: estimates from a Canadian expert elicitation survey. *Foodborne Pathog. Dis.* 7:1463–1472.
 45. Ravel, A., J. Greig, C. Tinga, E. Todd, G. Campbell, M. Cassidy, B. Marshall, and F. Pollari. 2009. Exploring historical Canadian foodborne outbreak data sets for human illness attribution. *J. Food Prot.* 72:1963–1976.
 46. Rothman, K. J., and S. Greenland. 2005. Causation and causal inference in epidemiology. *Am. J. Public Health* 95(Suppl. 1):S144–S150.
 47. Scallan, E., P. M. Griffin, F. J. Angulo, R. V. Tauxe, and R. M. Hoekstra. 2011. Foodborne illness acquired in the United States—unspecified agents. *Emerg. Infect. Dis.* 17:16–22.
 48. Scallan, E., R. M. Hoekstra, F. J. Angulo, R. V. Tauxe, M. A. Widdowson, S. L. Roy, J. L. Jones, and P. M. Griffin. 2011. Foodborne illness acquired in the United States—major pathogens. *Emerg. Infect. Dis.* 17:7–15.

49. Shaw, J. W., J. A. Johnson, and S. J. Coons. 2005. U.S. valuation of the EQ-5D health states: development and testing of the D1 valuation model. *Med. Care* 43:203–230.
50. U.S. Food and Drug Administration. 2011. Food Safety Modernization Act. 21 USC § 2201. Available at: <http://www.gpo.gov/fdsys/pkg/PLAW-111publ353/pdf/PLAW-111publ353.pdf>. Accessed 5 September 2011.
51. U.S. Food and Drug Administration, Center for Food Safety and Applied Nutrition; and U.S. Department of Agriculture, Food Safety and Inspection Service. 2003. Quantitative assessment of relative risk to public health from foodborne *Listeria monocytogenes* among selected categories of ready-to-eat foods. Available at: <http://www.fda.gov/Food/ScienceResearch/ResearchAreas/RiskAssessmentSafetyAssessment/ucm183966.htm>. Accessed 11 August 2011
52. U.S. General Accounting Office. 1992. Food safety and quality: uniform, risk-based inspection system needed to ensure safe food supply. Report RCED-92-152. U.S. General Accounting Office, Washington, DC.
53. U.S. General Accounting Office. 2001. Food safety and security—fundamental changes needed to ensure safe food. GAO-02-47T. U.S. General Accounting Office, Washington, DC.
54. U.S. Government Accountability Office. 2011. Federal food safety oversight: food safety working group is a positive first step but government-wide planning is needed to address fragmentation. GAO-11-289 March 18. Available at: <http://www.gao.gov/products/GAO-11-289>. Accessed 10 August 2011.
55. Van der Fels-Klerx, H. J., R. M. Cooke, M. N. Nauta, L. H. Goossens, and A.H. Havelaar. 2005. A structured expert judgment study for a model of *Campylobacter* transmission during broiler-chicken processing. *Risk Anal.* 25:109–124.
56. Varma, J. K., M. C. Samuel, R. Marcus, R. M. Hoekstra, C. Medus, S. Segler, B. J. Anderson, T. F. Jones, B. Shiferaw, N. Haubert, M. Megginson, P. V. McCarthy, L. Graves, T. van Gilder, and F. J. Angulo. 2007. *Listeria monocytogenes* infection from foods prepared in a commercial establishment: a case-control study of potential sources of sporadic illness in the United States. *Clin. Infect. Dis.* 44: 521–528.
57. Voetsch, A. C., M. H. Kennedy, W. E. Keene, K. E. Smith, T. Rabatsky-Ehr, S. Zansky, S. M. Thomas, J. Mohle-Boetani, P. H. Sparling, M. B. McGavern, and P. Mead. 2007. Risk factors for sporadic Shiga toxin-producing *Escherichia coli* O157 infections in FoodNet sites, 1999–2000. *Epidemiol. Infect.* 135:993–1000.