Attribution of Foodborne Pathogens Using Structured Expert Elicitation

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Abstract

Objectives: To estimate the fraction of human cases of enterically transmitted illness by five major pathways (food, environment, direct animal contact, human–human transmission, and travel) and by 11 groups within the food pathway.

Methods: Food safety experts were asked to provide their estimates of the most likely range for each of the parameters. Joint probability distributions were created by probabilistic inversion (PI).

Results: Sixteen experts participated in the study. PI resulted in good fits for most pathogens. Qualitatively, expert estimates were similar to earlier published studies but the estimated fraction of foodborne transmission was lower for most pathogens. Biologically less plausible pathways were given some weight by the experts. Uncertainties were smallest for pathogens with dominant transmission routes.

Conclusions: Structured expert studies are a feasible method for source attribution, but methods need further development.

Applications: These estimates can be combined with data on incidence, disease burden and costs to provide specific estimates of the public health impact of foodborne illness, and to identify the food groups that have the highest impact.

Introduction

PRIORITY SETTING OF PATHOGENS that can (also) be transmitted by food is a complex process that includes evaluation of several indicators such as disease burden and cost of illness, which are typically available at an aggregate level. That is, the total burden and costs for a pathogen are calculated, irrespective of transmission route, see for example Havelaar *et al.* (2000, 2004, 2007) and Vijgen *et al.* (2007). For food safety policy, it is important to know which fraction of the total burden and costs are

attributable to foods, and which foods are contributing to that fraction. Attribution of illness to different sources is a difficult process that can be based on different approaches that do not necessarily give the same answers, see for example Batz *et al.* (2005). These include outbreaks, analytical epidemiology (i.e., case–control studies), microbial subtyping, risk assessment, and intervention studies. No single approach may be expected to produce definitive data. Currently, the best possible approach is to combine data from these different approaches.

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This necessitates subjective interpretation by a group of experts. The major challenge is to make this process transparent and acceptable to a broad group of stakeholders. We present a structured expert study to estimate the fraction of human cases of enterically transmitted illness by five major pathways (food, environment, direct animal contact, human–human transmission, and travel) and by 11 groups within the food pathway. As we did not consider precise estimates to be possible, uncertainty was quantified. A description of general principles of food attribution is followed by a description of the expert elicitation method. Data analysis by probabilistic inversion is described in general terms, as well as in detail as applied in this study. The results of the study are presented and discussed in the context of other published studies on attribution of foodborne pathogens.

Methods

Principles of food attribution

A two-step process was followed, firstly assessing the proportion of all cases that is foodborne and secondly assigning the proportion of foodborne cases to specific food groups. The total foodborne transmission was compared to three other major pathways as indicated in Fig. 1. The analysis took into account that exposure may take place in the country of residence but also during foreign travel. Such cases are typically considered as a separate category, because national hygiene legislation does not impact exposures abroad. Hence, the primary differentiation of exposure pathways included a separate category of travel-associated cases. A detailed description of these five pathways is given in Table 1.
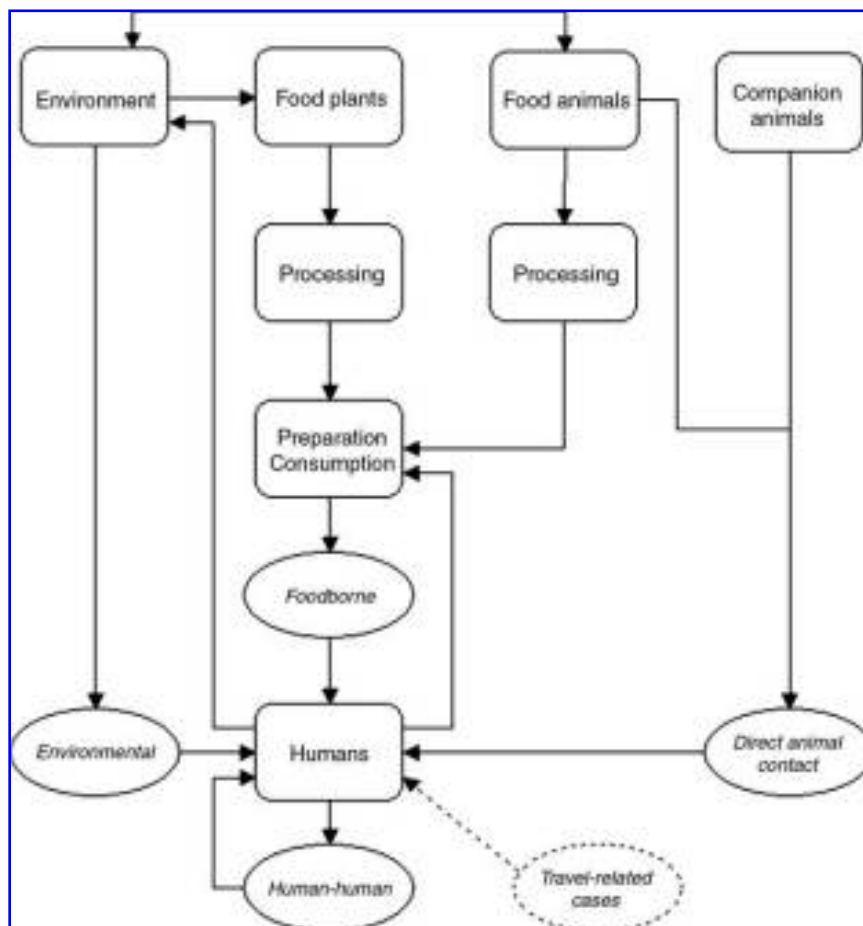

FIG. 1. Major transmission pathways for enteric pathogens.

TABLE 1. MAJOR TRANSMISSION PATHWAYS AND FOOD GROUPS FOR ATTRIBUTION

Major transmission pathways

Foodborne	Transmission through food that is contaminated when it enters the kitchen or during preparation (e.g., by food handlers)
Environmental	Transmission through contaminated water (drinking water, recreational water), soil, air or other environmental media (fomites[a])
Human–human	Transmission from person to person by the fecal–oral route
Direct animal	Transmission by direct contact with live animals including pets, farm animals, petting zoos, etc.
Travel-associated	Cases when exposure takes place by any of the above pathways during foreign travel

Food groups[b]

Beef and lamb	Beef, veal, lamb, and mutton. Includes processed and nonprocessed beef products (sausages, filet américain [steak tartare], hamburgers, etc.)
Pork	Includes processed and nonprocessed pork products (sausages, luncheon meats, etc.)
Chicken and other poultry	Includes duck, goose, ostrich, and turkey. Includes processed and nonprocessed poultry products (chicken wings, marinated chicken, confits, etc.)
Eggs	Including egg products
Dairy products	Milk, cheese, butter, cream, etc.
Fish and shellfish	Includes all finfish, shellfish (mussels, oysters, etc.) and crustaceans (lobster, shrimp, etc.)
Fruit and vegetables	Includes (mixtures of) vegetables that are consumed raw or cooked
Beverages	Includes all nonalcoholic and alcoholic beverages, except milk
Bread, grains, pastas, and bakery products	Includes pastries
Other foods including composite foods	Includes all categories not listed above (e.g., nuts, oils, confectionery, spices) and all foods that are sold to the consumer as a composite of two or more of the above categories (e.g., pizzas, lasagna, nasi-goreng [fried rice], sandwiches)
Infected humans or animals	Includes food handlers, vermin, pets, etc.

[a]Inanimate objects or substances capable of absorbing, retaining, and transporting contagious or infectious organisms (e.g., doorknobs and toys).

[b]Contamination is assigned to the food category as it enters the kitchen. Cross-contamination to other products or the environment does not change this assignment (e.g., if chicken contaminates a salad, contamination is still assigned to chicken). Food contaminated by infected humans or animals during preparation is a separate category.

A more detailed examination of Fig. 1 shows that there are usually different transmission routes from a single reservoir. For example, if the reservoir of a pathogen is in food animals, transmission may be foodborne, environmental, or by direct contact. In this study, the point of exposure approach was used instead of the point of reservoir approach (Pires *et al.*, submitted for publication).

Within the foodborne category, many subdivisions are possible. The Food Safety Research Consortium (http://www.thefsrc.org/) is developing the Foodborne Illness Risk Ranking Model (Batz *et al.*, 2004). There are 14 major food categories and numerous subcategories for attribution in this model. Adak *et al.* (2005) have presented estimates of foodborne illness in England and Wales. These authors used a scheme with 10 major food groups and numerous food types. There are similarities as well as differences between these two schemes. At the level of major food categories or groups, the U.S. scheme is somewhat more disaggregated than the U.K. scheme. For example, the red meat category in the United Kingdom is split up into game, beef, and pork in the United States. There are also differences where a group of commodities is a major group in one scheme and a subgroup in the other. For example, rice and other dairy products are subgroups in the U.S. scheme and major groups in the U.K. scheme. Van Duynhoven *et al.* (2005) give annual reports on outbreaks of enteric illness in the Netherlands. The classification scheme used generally corresponds with but is more aggregated than the U.S. and U.K. schemes. For example, the Dutch scheme involves a category poultry and eggs that is disaggregated in the other schemes. Preferably, a classification scheme should not contain overlapping categories and if such categories are included, clear guidelines on classification must be given. Given the paucity of

and sources of bias in the available data, it does not seem appropriate to use very detailed food groups. Based on these considerations, a simple classification scheme comprising 11 food groups was used in this study (see Table 1).

The elicitation

The experts invited to participate in this elicitation study included members from both industry and research (academia and institutes) with different scientific backgrounds including microbiology, epidemiology, and food science. Some experts had a broad perspective on food safety issues whereas other experts had studied particular foods or pathogens for several years, thus having a deeper but narrower knowledge.

The study included 17 pathogens that are currently being evaluated in a Dutch study on priority setting of foodborne pathogens (Kemmeren *et al.*, 2006; Vijgen *et al.*, 2007). Experts were presented with a detailed, written summary of the principles of attribution as applied to this study and the relevant (national and international) data, but were asked to evaluate possible biases in the data and the applicability to the Dutch situation themselves. Uncertainty was included by asking the experts to give an interval that contained, according to their assessment, the probability of transmission through a particular pathway or ingestion of a food group with 90% certainty. Appendix 1 gives an example of the questions included in the elicitation. Asking experts for intervals not only allows them to express their uncertainty but also reduces respondents' fatigue and allows them to answer questionnaires for more pathogens. The elicitation was done entirely by e-mail. After sending the invitation, experts were asked to indicate which combinations of pathogens and pathways and food groups they felt competent to complete. They were then sent a spreadsheet containing a separate form for each combination, which they completed electronically and returned by e-mail. Originally, 37 experts were invited and 28 agreed to participate. After the questionnaires were sent, two experts declined to participate, while 10 never sent their assessments. As a result, 16 experts participated in the elicitation. The number of experts participating per pathogen varied between 2 and 12.

Data analysis

For each pathogen and each pathway that pathogen might take, each expert gave an interval for which he or she is 90% certain contains the true probability that the given pathogen takes a certain pathway. Of course the probabilities of all pathways must sum to one, but the experts were not asked for their joint probability over all pathways. The joint probability complying with the experts' assessments for individual pathways was constructed in the manner described below.

Illustrative data from three experts are shown in Fig. 2, for pathway X and for pathogen Y. The intervals are converted to density functions, also shown in Fig. 2. These densities are the minimally informative densities complying with each expert's 90% interval. Combining these densities with equal weight results in the bold black line in Fig. 3. Suppose we now have these equal weight decision maker (EWDM) combinations for each of the five pathways that pathogen Y can take. Each individual density represents the combined uncertainty over the probability that this pathway is chosen.

The next step is to convert these distributions over each pathway's probability into a distribution over the set of probability vectors of
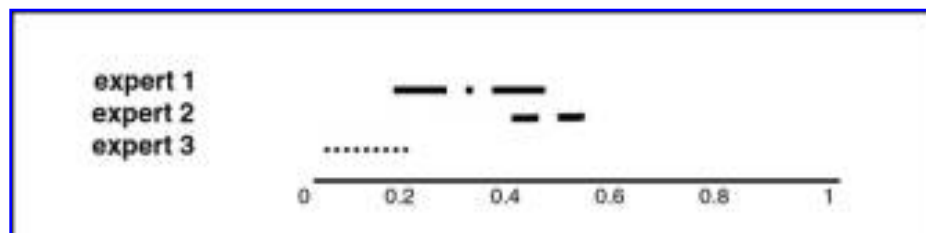

FIG. 2.   Three experts' 90% intervals for the probability that pathogen X takes pathway Y.
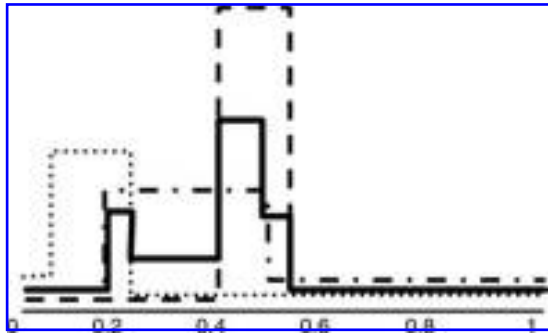
FIG. 3. Equal weight combination (solid) of three experts' density functions (dashed) that pathogen X takes pathway Y.

TABLE 2. PROBABILISTIC INVERSION RESULTS FOR MAJOR PATHWAYS OF *CAMPYLOBACTER* SPP.

Pathways	Estimated fraction	DM		Resampling	
		5%	95%	5%	95%
Food	0.4210	0.2270	0.852	0.158	0.837
Environment	0.2060	0.0003	0.7310	0.0003	0.7310
Human	0.0628	0.0001	0.1230	0.004	0.1230
Animal	0.1910	0.0022	0.5980	0.0022	0.05980
Travel	0.1200	0.0020	0.2840	0.0022	0.2880
	No. of experts		12	Method	IPF

DM, Decision Maker; IPF, iterative proportional fitting. See text for explanation.

length 5. There may be substantial uncertainty surrounding each pathway, but we know that the sum of the probabilities over all pathways must equal 1, since only one pathway is chosen in each instance of the disease.

The method for accomplishing this is called probabilistic inversion. Further details are given in Appendix 2.

Results

The number of experts who completed a questionnaire varied between 12 and 2 per pathogen, and was somewhat higher for food groups than for major pathways. Even though the present elicitation lacks seed variables that would enable the analyst to filter some experts (Cooke, 1995), there was enough evidence to consider filtering one of the experts as these results were negatively affecting the Decision Maker (DM) distribution but also the interpretation of the questions in the elicitation was not considered correct. After filtering this expert, the results in general were satisfactory. To illustrate the method, Table 2 shows the probabilistic inversion results for *Campylobacter* spp. The 5% and 95% columns under DM are the percentiles of each pathway that we would like to recover with probabilistic inversion. The 5% and 95% columns under "Resampling" show the results of the probabilistic inversion. The "Estimated fraction" is the mean of the resampled probabilities, for each pathway. Note that these fractions sum to one, as required. The results in Table 2 are quite good.

The results of fitting the 5% and 95% quantiles for the 17 pathogens are summarized in Tables 3 and 4. The fit was good enough for the majority

of the pathogens, being slightly better for the pathways compared to the food groups. This is due to the number of elements. It is simpler for both the assessment and the analysis step to manage a smaller number of items. For the experts it is easier to give estimates for a smaller number of items, because it is easier to compare fewer options and it is easier to be aware of probabilities that are of bigger magnitude. Naturally, as the number of items increases the comparisons and the assessments are harder because the analysis demands from the expert a more accurate knowledge and a larger capability of taking all the options into account.

Evaluation of the 5th and 95th percentiles in Tables 3 and 4 shows that for most estimates, there is considerable uncertainty. Experts' individual estimates did not agree in many cases which results in wide uncertainty intervals in the absence of seed variables. The broad intervals for parameter estimates may be considered to reflect current uncertainty about the proportion of pathogens that is transmitted by food or specific food groups. Note that for pathogens that are typically considered to be almost exclusively foodborne (e.g., *Clostridium perfringens* and *Staphylococcus aureus*), the 90% intervals for major pathways are much smaller than for typical multi-source pathogens such as Campylobacter and STEC O157. For food groups, the uncertainty is smaller for pathogens with a single reservoir, e.g., viruses (humans, pigs) in comparison to *S. aureus*.

Discussion

Because of a lack of definitive data, there is no way to formally validate the results. One option

Table 3. Transmission of 17 Enteropathogens by Major Pathways

Pathogen	Experts	Fraction (%) transmitted by pathway[a]				
		Food	Environment	Human	Animal	Travel
Campylobacter spp.	12	42 (16–84)	21 (0–73)	6 (0–12)	19 (0–60)	12 (0–29)
Shiga toxin–producing *E. coli*						
O157	3	40 (15–83)	17 (0–47)	10 (0–23)	21 (0–76)	12 (0–27)
Non-O157	3	42 (21–78)	14 (0–29)	10 (0–20)	28 (11–48)	6 (0–10)
Listeria monocytogenes	7	69 (47–98)	7 (0–18)	5 (0–13)	5 (0–13)	13 (0–40)
Mycobacterium avium	4	42 (0–79)	19 (0–58)	18 (0–57)	9 (0–27)	12 (0–39)
Salmonella spp.	8	55 (32–88)	13 (0–29)	9 (0–19)	9 (0–19)	14 (3–26)
Bacillus cereus toxin	4	90 (68–100)	1 (0–4)	1 (0–4)	1 (0–4)	7 (0–91)
Clostridium perfringens toxin	4	91 (72–100)	2 (0–5)	2 (0–5)	2 (0–5)	3 (0–9)
Staphylococcus aureus toxin	4	87 (73–100)	4 (0–9)	3 (0–8)	2 (0–5)	4 (0–10)
Enterovirus	2	6 (0–16)	25 (0–60)	60 (30–92)	2 (0–2)	7 (0–15)
Hepatitis A virus	2	11 (0–20)	11 (0–19)	18 (0–**42**)	0 (0–0)	60 (7–80)
Hepatitis E virus	2	14 (0–38)	25 (0–75)	8 (0–20)	11 (0–29)	43 (0–68)
Norovirus	5	17 (16–47)	14 (0–43)	55 (42–88)	5 (0–10)	9 (0–20)
Rotavirus	3	13 (13–28)	17 (0–46)	58 (43–90)	3 (0–5)	9 (0–19)
Cryptosporidium parvum	2	12 (0–20)	28 (10–39)	27 (10–38)	13 (5–19)	20 (4–29)
Giardia lamblia	3	13 (0–24)	24 (10–37)	35 (10–56)	11 (0–20)	18 (5–29)
Toxoplasma gondii	3	56 (26–88)	36 (6–66)	1 (0–1)	3 (0–3)	5 (**0**–9)

[a]Mean (5th and 95th percentile) after resampling. Bold type indicates poor fit with Decision Maker.

is to compare the results with those from other (usually less comprehensive) studies. Complete studies that break down transmission pathways in the above-mentioned categories are not available in the literature. Some authors have provided estimates of the fraction of foodborne illness. Table 5 gives an overview of published (international) data for the 17 pathogens that are included in this study. At first glance the results of the present study appear logical. The pathogens can be grouped in several categories with respect to their major pathways. Toxins (*Bacillus cereus* [Bc], *Clostridium perfringens* [Cp], *Staphylococcus aureus* [Sa]) are predominantly considered foodborne whereas other bacterial pathogens (*Campylobacter* spp. [Ca]; STEC O157 and non-O157 [STEC]; *Listeria monocytogenes* [Lm]; *Mycobacterium avium* [Ma]; *Salmonella* spp. [Sa]) and the protozoan parasite *Toxoplasma gondii* (Tg) are considered to be transmitted by multiple pathways with food as the most important one. The other protozoan parasites (*Cryptosporidium parvum* [Cp] and *Giardia lamblia* [Gl]) are considered to be predominantly transmitted between humans and through the environment with a small fraction by food. A similar fraction of viruses is considered to be foodborne with mainly transmission between humans (enterovirus [Ev], norovirus [Nv], rotavirus [Rv]) or during travel (hepatitis-A

virus [Hav] and hepatitis-E virus [Hev]). From a qualitative point of view, these estimates are consistent with the general epidemiological data on these pathogens. While results may be expected to vary internationally due to differences in food production and consumption, it is worth noting that for most pathogens the fraction transmitted by food is considerably lower than other international estimates (cf. Table 5). The data are closer to an earlier Dutch report, but also in comparison with these data the proportion of cases of salmonellosis in the present study is low (55% vs. >90%). Several pathogens are attributed in low percentages (<5%) to pathways that are biologically implausible. This is the case for Bc, Cp, Sa, and Lm by the environment, humans and animals as growth of these bacteria is usually required to produce illness. Direct transmission of Tg by humans or animals is biologically impossible as humans do not excrete infectious oocysts and those excreted by felines need to mature in the environment for several days before becoming infectious. There is no evidence that Ev, Nv, and Rv are zoonotic, hence transmission by animals is unlikely.

Within the food pathway, results are also generally consistent with the overall epidemiology of the pathogens. Beef and lamb are considered the main food involved in transmission of STEC and Cp, poultry of Ca, and pork of

TABLE 4. TRANSMISSION OF 17 ENTEROPATHOGENS BY FOOD GROUPS WITHIN THE FOOD PATHWAY

| | | Fraction (%) transmitted by food group[a] | | | | | | | | | | |
Pathogen	Experts	B&L	Pork	Poultry	Eggs	Dairy	(S)F	F&V	Bev	Grains	Comp	H&A
Campylobacter spp.	11	4 (0–17)	5 (0–19)	54 (17–86)	3 (0–10)	9 (0–44)	7 (0–27)	5 (0–25)	2 (0–4)	2 (0–6)	3 (0–10)	5 (0–18)
Shiga toxin–producing E. coli												
O157	7	44 (16–88)	6 (0–25)	3 (0–9)	2 (0–5)	7 (0–28)	3 (0–8)	7 (0–28)	4 (0–12)	3 (0–8)	4 (0–12)	17 (0–7)
Non-O157	3	62 (0–79)	9 (0–19)	3 (0–9)	1 (0–4)	5 (0–25)	3 (0–5)	4 (0–19)	4 (0–13)	2 (0–9)	2 (0–9)	6 (0–22)
Listeria monocytogenes	9	11 (5–29)	9 (0–26)	7 (0–17)	4 (0–12)	25 (14–50)	18 (0–46)	8 (0–25)	3 (0–7)	6 (0–16)	6 (0–19)	5 (0–9)
Mycobacterium avium	4	6 (0–45)	41 (0–86)	6 (0–7)	2 (0–0)	5 (3–3)	7 (0–15)	6 (0–9)	5 (0–8)	1 (0–1)	4 (0–15)	20 (0–35)
Salmonella spp.	13	13 (5–28)	14 (6–36)	15 (5–47)	22 (11–54)	7 (0–25)	4 (0–10)	6 (0–20)	3 (0–9)	4 (0–12)	6 (0–18)	6 (0–18)
Bacillus cereus toxin	5	7 (4–4)	3 (0–18)	2 (0–0)	4 (0–2)	6 (0–30)	2 (0–0)	2 (0–10)	2 (0–7)	17 (7–95)	54 (0–75)	2 (0–4)
Clostridium perfringens toxin	4	48 (20–94)	8 (0–65)	7 (0–54)	3 (0–9)	4 (0–21)	6 (0–37)	7 (0–35)	2 (0–8)	3 (0–9)	8 (0–53)	4 (0–18)
Staphylococcus aureus toxin	4	8 (0–28)	8 (0–29)	8 (0–29)	3 (0–10)	15 (0–29)	6 (0–20)	2 (0–5)	2 (0–4)	7 (0–29)	30 (5–49)	12 (0–77)
Enterovirus	2	**Problem**	*in–feasible*									
Hepatitis A virus	2	0 (0–0)	0 (0–0)	0 (0–0)	0 (0–0)	0 (0–0)	13 (0–40)	13 (0–39)	4 (0–10)	4 (0–10)	3 (0–5)	63 (0–99)
Hepatitis E virus	2	0 (0–0)	74 (0–100)	0 (0–0)	0 (0–0)	0 (0–0)	5 (0–11)	7 (0–19)	4 (0–6)	0 (0–0)	0 (0–0)	10 (0–31)
Norovirus	5	3 (0–9)	3 (0–10)	3 (0–9)	2 (0–5)	2 (0–5)	16 (0–57)	7 (0–41)	3 (0–9)	5 (0–19)	5 (0–19)	51 (0–87)
Rotavirus	3	0 (0–0)	3 (0–5)	0 (0–0)	0 (0–0)	2 (0–2)	19 (0–59)	24 (2–59)	4 (0–9)	7 (0–19)	5 (0–10)	36 (5–77)
Cryptosporidium parvum	2	26 (24–56)	4 (2–9)	3 (1–5)	3 (0–5)	9 (6–20)	22 (21–38)	21 (20–38)	3 (0–4)	0 (0–0)	3 (0–5)	6 (4–11)
Giardia lamblia	3	20 (0–49)	5 (0–9)	3 (0–5)	0 (0–0)	8 (0–18)	13 (0–28)	33 (0–69)	3 (0–5)	0 (0–0)	3 (0–5)	12 (0–30)
Toxoplasma gondii	3	23 (0–47)	50 (21–99)	5 (0–14)	0 (0–0)	5 (0–14)	4 (0–10)	6 (0–18)	0 (0–0)	0 (0–0)	2 (0–50)	6 (0–19)

[a]Mean (5th and 95th percentile) after resampling. Bold type indicates poor fit with Decision Maker.
B&L, beef and lamb; (S)F, fish and shellfish; F&V, fruit and vegetables; bev, beverages; grains: bread, grains, pastas and bakery products; comp, other foods including composite foods; H&A, infected humans or animals.

Table 5. Proportion of Illness Cases That Are Attributed to Food

	Reference[a]					
	Mead	*Adak*	*Duyn*	*Anon*	*Hall*	*This study*
Country	USA	UK	NL	France	Australia	NL
Period	1990s	1992–2000	1990s	1990s	2000	2006
Data sources[b]	E/O/R	O	E/CC	E	E	E
Travel-related cases	Included	Excluded	Included	Included	Excluded	Included
Campylobacter spp.	80%	80%	30–80%	80%	75%	42%
Shiga toxin–producing *E. coli*						
O157	85%	63%	50–90%	50%	65%	40%
Non-O157	85%	NA[c]	NA	NA	65%	42%
Listeria monocytogenes	99%	99%		99%	NA	69%
Mycobacterium avium	NA	NA	NA	NA	NA	42%
Salmonella spp.	95%	92%	>90%	95%	87%	55%
Bacillus cereus toxin	100%	100%	100%	100%	100%	90%
Clostridium perfringens toxin	100%	94%	100%	100%	100%	91%
Staphylococcus aureus toxin	100%	96%	100%	100%	100%	87%
Enterovirus	NA	NA	NA	NA	NA	6%
Hepatitis A virus	50%	NA	NA	5%	NA	11%
Hepatitis E virus	NA	NA	NA	NA	NA	14%
Norovirus	40%	11%	10–20%	14%	25%	17%
Rotavirus	1%	3%	0–10%	NA	2%	13%
Cryptosporidium parvum	10%	6%	??	NA	10%	12%
Giardia lamblia	10%	10%	<30%	NA	5%	13%
Toxoplasma gondii	50%	NA	NA	50%	NA	56%

[a]Mead, Mead *et al.* (1999); Adak, Adak *et al.* (2002); Duyn, Van Duynhoven *et al.* (2002); Anon, Anonymous (2004); Hall, Hall *et al.* (2005).
[b]E, expert estimates; O, outbreaks; R, reported cases; CC, case–control studies.
[c]NA, not applicable.

Ma, Hev, and Tg (the latter with a substantial contribution by beef and lamb). Sa is the only pathogen that is attributed to eggs in a substantial amount, with all meat groups also considered important. The pathogens for which humans are the only reservoirs (Hav, Nv, Rv) are mainly attributed to infections by humans and animals with (shell)fish and fruits and vegetables as secondary food groups. These latter groups are also considered of importance for the Cp and Gl, which are also attributed to beef and lamb.

Quantitatively, it is noteworthy that for the specific human pathogens Hav and Rv, the foods of animal origin receive a score of 0%; while Hev is only attributed to pork, consistent with its detection in slaughter pigs. For Nv, the experts are less consistent in their dismissal of zoonotic transmission. Bc and Sa are mainly attributed to composite foods with secondary routes being bread, grains, etc. for Bc and dairy for Sa. Again, this is consistent with the general epidemiology.

To evaluate in how far the relatively high scores attributed to less plausible routes were related to the chosen methods, additional data analysis was carried out. First, the probabilistic inversion was repeated with addition of a fit to the 50th percentile (arbitrarily set as the midpoint between the 5th and 95th percentiles). Secondly, some biologically implausible results were defined as seed variables (Cooke, 1995) and the experts were weighed according to their score on these seed variables. For both methods, the results were hardly different from the baseline model and it is concluded that the scores were not a result of the data analysis but did represent the experts' beliefs.

As for pathways, it is remarkable, that biologically less plausible routes do score a small percentage of transmission, e.g., Ca in bread, grains, etc. (Ca survives very poorly on dry products) and several pathogens in eggs (only two Salmonella serovars are able to invade the oviduct of laying hens).

Hoffmann *et al.* (2007) recently published an expert survey on attribution in the United States. The study was limited to the food pathway. Experts were asked for their best estimates and 90% confidence bounds. Weighted means

were reported and combined with incidence estimates of foodborne illness as published by Mead *et al*. (1999). Uncertainty estimates and their implications are discussed in a separate paper (Hoffmann *et al*., in press). Results are difficult to compare with the present study because of different food groupings and different definitions. For example, in the U.S. study, a salad that was cross-contaminated during preparation was assigned to the produce group in the U.S. study, but was assigned to the contaminated food entering the kitchen (say chicken) in our study. Such details in definitions should be carefully considered by decision makers. Results should not be expected to be similar as the epidemiology of foodborne illness differs between the United States and the Netherlands. For example, experts assign a far greater role to produce in the United States, which is in line with the far greater number of reported outbreaks. On the other hand, eggs are considered to be the dominant source of salmonellosis in the Netherlands, in contrast to poultry in the United States. Similar results are obtained, for example, for the importance of poultry in the transmission of campylobacteriosis and of beef for STEC O157.

The response rate in our study was 43% (16/ 37). The background of the invited experts was in microbiology (25), epidemiology (5), and food science (7); the respondents were 11 microbiologists, 4 epidemiologists, and 1 food scientist. Thus, while among the invitations, microbiologists were overrepresented, this was less so among the respondents, but food scientists were underrepresented. The low response may have been due to a high burden to complete all data sheets. We have no information on a possible influence on our results by the nonresponse.

An expert study may not be expected to provide an unbiased estimate of the relative importance of different transmission routes. Rather, it should be regarded as a structured way to obtain a consensus opinion, based on evaluation of all available data. For policy-making purposes, this consensus opinion may be highly valuable. Future developments should aim at developing more data-driven approaches, combining information from different sources in a single analytical framework.

To provide more comparable data, international harmonization of definitions, groupings, protocols, and data analysis methods should be aimed for.

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APPENDIX 1

Example Excel® Sheet for Expert Elicitation

APPENDIX 2

We first describe a simple implementation of the probabilistic inversion method and then indicate how this simple method was adapted to deal with particular problems.

We first draw a large sample of probability 5 vectors, say 100,000. This is simply a list of numbers $(p_1, \ldots, p_5)$, such that $p_i \geq 0$ and $\Sigma_i p_i = 1$. There are many ways to do this, a convenient method is to sample independent gamma variables $g_1, \ldots, g_5$ with the same shape and scale parameters, and then define, on each sample

$$p_i = g_i / \Sigma_j g_j$$

If we now consider the marginal distribution of, for example, p_2 in this list of 100,000 vectors, this will not agree with the distribution in Fig. 2. The idea is now to re-weight this sample so that the marginal distributions of $p_1, \ldots p_5$ in the re-weighted sample fit as closely as possible the distributions of the EWDM. The method for finding these weights is called *iterative proportional fitting* (IPF), and a description of this method, and some of its variations, may be found in Cooke *et al*. (2006). There is no reason why there should be a distribution over probability 5 vectors whose margins agree exactly with those from the EWDM. Indeed, the experts were asked only for marginal distributions of probabilities; asking the experts to insure that these margins were consistent with a joint distribution over probability 5 vectors would impose a daunting task. Moreover, the simplifications involved in constructing the densities in Fig. 2 might undo any such effort. Hence, it may happen that there is no distribution over probability 5 vector that exactly recovers the EWDM's distributions. The probabilistic inversion in such cases is infeasible. Where infeasibility was an issue, the PARFUM variant of IPF was applied, as this algorithm generally has better behavior in case of infeasibility.

To do the probabilistic inversion with fully specified densities would require sample sizes beyond the capability of current platforms. To keep the sample sizes manageable, we approximated each density as a piece-wise uniform density whose 5th and 95th percentiles agreed with the equal weight decision maker's density. We compared the results to the results obtained by adding the (interpolated) 50% value, and found little difference. Even with this simplification it is not always possible to find such a set of weights: that is, it may not be possible to recover all the marginal distributions in this way. When this happens we may either draw a larger sample, or sample the starting p_i's more intelligently. In particular, if we know that the mean of the distribution in Fig. 3 is 0.35, then we could choose the shape factors of our gamma distributions differentially (the scale factors must be the same). If the shape factor of g_i is a_i, then we can arrange that $a_3 / \Sigma_j a_j = 0.35$. This will insure that the mean of p_i in the starting distribution, before re-weighting, is 0.35, and this will make an "infeasible" problem "less infeasible" without increasing the sample size. In cases of difficult fitting, such techniques were employed, but most of the fitting problems were feasible, or nearly feasible, without such special nursing.

There were some cases when there was absolute consensus among the group of experts. In these cases, where all experts agreed that the probability of contamination is equal to zero the respective random variable was deleted beforehand.