Attribution of Illnesses Transmitted by Food and Water to Comprehensive Transmission Pathways Using Structured Expert Judgment, United States

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Illnesses transmitted by food and water cause a major disease burden in the United States despite advancements in food safety, water treatment, and sanitation. We report estimates from a structured expert judgment study using 48 experts who applied Cooke's classical model of the proportion of disease attributable to 5 major transmission pathways (foodborne, waterborne, person-to-person, animal contact, and environmental) and 6 subpathways (food handler–related, under foodborne; recreational, drinking, and nonrecreational/nondrinking, under waterborne; and presumed person-to-person-associated and presumed animal contact-associated, under environmental). Estimates for 33 pathogens were elicited, including bacteria such as *Salmonella enterica, Campylobacter* spp., *Legionella* spp., and *Pseudomonas* spp.; protozoa such as *Acanthamoeba* spp., *Cyclospora cayetanensis*, and *Naegleria fowleri*; and viruses such as norovirus, rotavirus, and hepatitis A virus. The results highlight the importance of multiple pathways in the transmission of the included pathogens and can be used to guide prioritization of public health interventions.

Illnesses transmitted commonly by food and water result in a major disease burden on both a national and a global scale (*1*). Each year in the United States, ≈9.4 million illnesses, 56,000 hospitalizations, and 1,351 deaths are caused by 31 known pathogens transmitted through food (*2*). Previous estimates of the burden of waterborne disease in the United States have largely focused on the burden of gastrointestinal illness associated with drinking water; an estimated 4–32 million cases of illness occur each year (*3*,*4*).

Source attribution is a process of estimating the proportion of illnesses resulting from various exposures for specific pathogens. Attributing illnesses to sources can guide decisions about where to target prevention and control efforts by apportioning illnesses to specific sources, thus aiding in the development of specific interventions (*5*). Attributing to the comprehensive set of transmission pathways considered in this study (foodborne, waterborne, person-to-person, animal contact, and environmental) is challenging for many reasons, including limited data and difficulty combining existing data from multiple sources. For example, outbreak surveillance data, such as those collected through the National Outbreak Reporting System (NORS), can provide information on sources of illness but are subject to reporting biases and may not be representative of endemic disease (*6*). Other studies have also raised concerns of publication bias toward novel, unique, or large foodborne outbreaks, limiting the utility of systematic reviews of published outbreaks in assessing source attribution (*7*,*8*). One method to address these barriers is structured expert judgment (SEJ), a method to use and combine estimates produced by experts and quantify uncertainty for the purpose of risk analysis when the ability to gather data is hindered by high expense, data scarcity, or lack of reliable data. This method, when executed well, is formal, reproducible, and mathematically and scientifically rigorous (*9*–*11*).

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DOI: https://doi.org/10.3201/eid2701.200316

The Centers for Disease Control and Prevention (CDC) works to control and prevent illness caused by foodborne and waterborne pathogens in the United States. To accomplish this, CDC supports states and territories in tracking disease, detects and responds to outbreaks, and uses surveillance and sentinel site data to estimate the burden of these diseases in the United States. To inform this work, we implemented an SEJ study using Cooke's classical model to estimate the proportion of domestically acquired illnesses for 33 pathogens transmitted through food and water that can be attributed to each of 5 major transmission pathways and 6 subpathways (*12*).

Methods

The process was divided into 3 stages: preparation, elicitation, and postelicitation (*11*). These stages are detailed in the following sections.

Preparation

Selection of Pathogens

We included all pathogens transmitted commonly through food or water that were examined by Scallan et al. (2) and Collier et al. (*13*) except those for which the only syndrome of interest was considered to have >95% foodborne transmission (e.g., *Listeria monocytogenes*, *Clostridium botulinum*); we added 3 free-living amoebae (*2*,*13*). For some pathogens, subdivisions into categories by serotype, patient age, or clinical manifestations of interest were included because transmission pathways were assumed to be different. For example, for *Salmonella*, the 5 most common serotypes were included along with 2 groups of rarer serotypes based on a ranking of their coefficients of variation (CVs) calculated from the patients' ages, sexes, states of residence, and the year and month specimens were obtained (group 1, lowest CVs; group 2, highest CVs) as described by Boore et al. (*14*). This compilation resulted in a total of 33 pathogens and 47 target questions, or categories, for estimation. The 47 target questions were grouped into 15 panels on the basis of similarities between pathogen microbiology and ecology (Table 1).

Transmission Pathway Definitions

We used definitions for 5 major pathways that were mutually exclusive and comprehensive (i.e., covering

Table 1. Pathogen panels, target questions, and number of experts providing estimates, structured expert judgment, United States, 2017

Panel	Pathogen and clinical manifestation target questions	No. experts who provided estimates in initial elicitation	No. experts who revised estimates	No. experts who provided re-elicitation estimates
Panel 1	*Acanthamoeba* spp., *Balamuthia mandrillaris, Naegleria fowleri*	14	4	Not required
Panel 2	Astrovirus, norovirus, rotavirus, sapovirus	17	3	Not required
Panel 3	*Brucella* spp., *Mycobacterium bovis*	16	5	Not required
Panel 4	*Campylobacter* spp., *Yersinia enterocolitica*	19	5	Not required
Panel 5	*Cryptosporidium* spp.,*Giardia* spp.	21	5	Not required
Panel 6	*Cyclospora cayetanensis*	21	4	Not required
Panel 7	Enterotoxigenic *Escherichia coli,* other diarrheagenic *E. coli, Shigella* spp.	21	3	Not required
Panel 8	Hepatitis A virus	19	2	Not required
Panel 9	*Legionella* spp., nontuberculous *Mycobacterium* spp.	9	1	Not required
Panel 10	*Pseudomonas* spp., otitis externa, pneumonia, septicemia	16	7	7
Panel 11	*Salmonella enterica*, nontyphoidal: all serotypes and ages, <5 y of age; Enteritidis, Typhimurium, Newport, I 4,[5],12:i:-, Javiana; other serotypes group 1,* other serotypes group 2†	14	3	Not required
Panel 12	Shiga toxin–producing *E. coli* O157 and non-O157	18	4	Not required
Panel 13	*Staphylococcus aureus*, group A *Streptococcus*	19	4	Not required
Panel 14	*Toxoplasma gondii*	16	3	Not required
Panel 15	*Vibrio alginolyticus*, AGI, non-AGI; *V. cholerae*, nontoxigenic, AGI, non-AGI; *V. parahaemolyticus*, AGI, non-AGI; *V. vulnificus*,‡ non-AGI; *Vibrio* spp., other, AGI, non-AGI	15	6	9

*Group 1: serotypes such as Agona, Anatum, Braenderup, Hadar, Heidelberg, Infantis, Oranienburg, Saintpaul, Senftenberg, Thompson. AGI, acute gastrointestinal illness.
†Group 2: serotypes such as Bareilly, Gaminara, Give, Mississippi, Norwich, Pomona, Rubislaw, Tennessee, Urbana, Weltevreden.
‡Clinical manifestations of interest for initial elicitation were bacteremia and wound infections.

Table 2. Major transmission pathway definitions, structured expert judgment, United States, 2017

Major transmission pathways	Description
Foodborne	Transmission occurs through eating food. Contamination can originate anywhere in the food production chain from primary production, to retail, and then to the home or restaurant. This pathway applies to all nonwater beverages and items ingested by humans as food (e.g., including raw milk and excluding items consumed for medicinal purposes).
Waterborne	Transmission occurs through the consumption of or direct contact with water or inhalation of aerosols originating from water. This includes drinking water, bottled water, recreational water (treated and untreated), and other water sources, such as water within buildings, used in medical devices, or for industry/manufacturing.
Person-to-person	Transmission occurs by direct contact with infected persons or their bodily fluids, or by contact with the local environment where an exposed person is simultaneously present with an infected person or visible excreta.
Animal contact	Transmission occurs through direct contact with an animal, its bodily fluids (excluding raw milk or other fluids consumed as food), fur, hair, feathers, scales, or skin, or by contact with the local environment where an infected animal, its visible excreta, fur, hair, feathers, scales, or skin was simultaneously present with the exposed person (e.g., barns, petting zoos, and pet stores). This pathway includes domestic animals, farm animals, wildlife, and pets.
Environmental	Transmission occurs through exposure to naturally occurring agents (e.g., free-living ameba or radon) or contact with contaminated air, mud, soil, or other outdoor or indoor surfaces or objects not attributable to foodborne, waterborne, person-to-person, or animal contact transmission, as defined for this project.

100% of transmission modes) and that reflect those used by CDC for outbreak surveillance (*15*,*16*; Tables 2, 3). We defined 3 mutually exclusive waterborne subpathways (recreational water, drinking water, and nonrecreational nondrinking water) that were comprehensive (i.e., all waterborne pathway transmission fell into 1 of the 3 subpathways). We also defined and elicited 1 foodborne (food handler-related) and 2 environmental (presumed animal associated, presumed person-to-person) subpathways that accounted for only a portion of transmission within their main pathway. We calculated the unelicited proportion remaining of their respective main pathways during analysis and assigned it to the subpathways other foodborne and other environmental. For all transmission pathways, we defined the point of attribution as the point of exposure (i.e., the event during which a person ingested, or was otherwise exposed to, the pathogen).

Expert Identification and Selection

We identified 182 experts representing a range of scientific backgrounds (e.g., epidemiologists, laboratory scientists, and environmental engineers from government, academia, nongovernmental organizations,

Table 3. Transmission subpathway definitions, structured expert judgment, United States, 2017

Subpathway	Description
Foodborne subpathway	
Food handler–related	When food processed or prepared for others is contaminated by an infected person.
Waterborne subpathways	
Recreational water, treated or untreated	Water that is used for recreational activities, such as in an aquatic facility or natural body of water. Can be treated or untreated. Treated water has undergone a systematic disinfection process (e.g., chlorination and filtration) with the goal of maintaining good microbiologic quality for recreation; untreated water has not undergone a disinfection or treatment process to maintain good microbiological quality for recreation (e.g., lakes, rivers, oceans, and reservoirs).
Drinking water	Water that is used primarily for drinking but including other domestic uses, such as washing or showering; can come from a public water system, a private well, or commercially bottled sources.
Nonrecreational, nondrinking water	Water that is used for purposes other than recreation or drinking (e.g., for agriculture, industry, medical treatment, backcountry streams or flood waters). Agricultural water includes water that is used to grow fresh produce and sustain livestock. Industrial water includes water used during manufacturing or in cooling equipment. Medical water includes any water used within medical devices or water used for washing surgical tools and equipment, and water used for hydrotherapy. This subcategory does not include transmission that can be accounted for by another major pathway, such as food or animals
Environmental subpathways	
Presumed animal contact associated	When a person becomes ill from exposure to soil, mud, or surfaces contaminated by an animal without direct contact or simultaneous presence with the animal, or when an infection is suspected to be animal associated because of previous knowledge about the pathogen.
Presumed person-to-person associated	When a person becomes ill from an exposure indirectly associated with an ill person.

and industry) on the basis of publication records, experience, expertise, or previous participation in source attribution studies. We contacted the experts directly and invited them to apply for participation (Figure 1). Fifty-eight returned a curriculum vitae and publication record and completed a questionnaire about their professional interest, knowledge, and experience for each of the 33 pathogens using a 4-level Likert scale (high, medium, low, or none) by the requested deadline. We asked experts to suggest additional experts to be considered; the 3 who were suggested were also invited.

Assignment to Panels

We evaluated expert applications based on area of expertise, education, work history, professional interest, experience, and knowledge of the individual pathogens in this study. Publication record was not used to determine eligibility because it could have led to elimination of qualified experts who do not publish frequently. We used maximum bipartite matching in R version 3.3.1 with the igraph package version 1.0.1 to assign experts to panels based on their curricula vitae, publication records, and questionnaire responses (*17*,*18*). Final assignment ensured that experts were not on pathogen panels for which they reported none or low experience. Individual experts were on panels for ≤15 pathogens (Appendix 1, https://wwwnc.cdc.gov/EID/article/27/1/20-0316-App1.pdf).

Calibration Questions

The study administrators used unpublished data to develop calibration questions (Appendix 2, https://wwwnc.cdc.gov/EID/article/27/1/20-0316-App2.pdf). We developed 14 questions to evaluate the experts' statistical accuracy and informativeness by probing the experts' ability to provide reliable estimates under uncertainty. The subject domain of the questions aimed to represent expertise in public health surveillance of foodborne and waterborne diseases, food consumption patterns in the United States, and human exposure and occurrence data about pathogens in food, water, and the environment.

Target Questions

Target questions asked the proportion of illnesses transmitted through the 5 major pathways and 6 subpathways for all study pathogens. Study administrators blocked transmission pathways and subpathways for some pathogens based on their microbiology and ecology (Table 4). We created individualized Microsoft Excel version 14.7.7 (http://www.microsoft.com) files with separate sheets for calibration questions, target questions for each assigned pathogen, and additional instructions for each expert. We included verification aids in the worksheets to assist the experts (Appendix 3, https://wwwnc.cdc.gov/EID/article/27/1/20-0316-App3.xlsm).

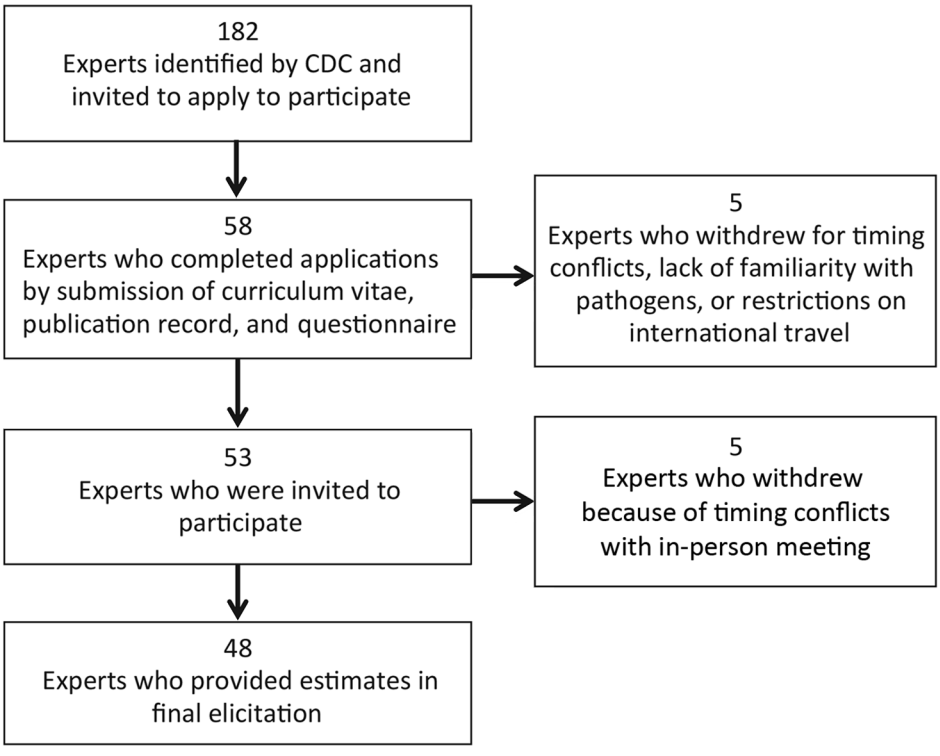

Figure 1. Expert selection process for study of attribution of illnesses transmitted by food and water to comprehensive transmission pathways using structured expert judgment, United States, 2017.

Dry Run Exercise

We conducted a dry run exercise using video web conferencing to assess calibration questions, target question answer sheets, and expert training materials for completeness, clarity, and ease of use. Six persons from academia, state health departments, and CDC participated in this trial exercise, but not in the formal elicitation itself. We modified the elicitation materials based on feedback from this exercise.

Expert Orientation

Before the formal elicitation, experts attended a training webinar to learn definitions of transmission pathways, subpathways, and point of attribution. To ensure common understanding of the definitions, experts completed a 20-question review of knowledge after the webinar (Appendix 4, https://wwwnc.cdc.gov/EID/article/27/1/20-0316-App4.pdf).

We provided a background document summarizing current surveillance data, when available, and

Table 4. Source attribution results for major transmission pathways, structured expert judgment, United States, 2017*

Pathogen name	Mean % (95% uncertainty interval)				
	Foodborne	Waterborne	Person-to-person	Animal contact	Environmental
Bacteria					
Brucella spp.	45 (13–77)	10 (0–42)	Blocked	36 (10–73)	9 (0–32)
Campylobacter spp.	57 (30–80)	13 (1–31)	7 (0–23)	16 (3–35)	7 (0–30)
Enterotoxigenic *Escherichia coli*	69 (37– 91)	9 (0–38)	7 (0–38)	Blocked	15 (2–33)
STEC O157	60 (40–77)	5 (1–13)	16 (4–33)	12 (3–25)	7 (1–17)
STEC non-O157	50 (26–75)	6 (0–17)	15 (2–34)	21 (2–46)	8 (0–24)
E. coli, other diarrheagenic	55 (27–80)	9 (0–30)	16 (2–39)	9 (0–33)	12 (0–33)
Legionella spp.	Blocked	97 (67–100)	0 (0–1)	Blocked	2 (0–28)
Mycobacterium bovis	75 (36–98)	1 (0–9)	9 (0–39)	13 (0–50)	2 (0–12)
Nontuberculous *Mycobacterium* spp.	Blocked	72 (39–94)	4 (0–21)	2 (0–35)	22 (0–49)
Pseudomonas spp., otitis externa	Blocked	81 (67–95)	3 (0–13)	1 (0–4)	15 (1–,25)
Pseudomonas spp., septicemia	Blocked	22 (3–53)	2 (0–19)	2 (0–11)	74 (41–94)
Pseudomonas spp., pneumonia	Blocked	51 (14–80)	4 (1–32)	0 (0–2)	45 (15–80)
Salmonella enterica, nontyphoidal	66 (48–81)	6 (0–22)	7 (0–16)	11 (3–24)	9 (2–21)
S. enterica, nontyphoidal, age <5 y	46 (20–66)	7 (0–26)	18 (6–35)	13 (2–30)	16 (2–36)
S. enterica serotype Enteritidis	80 (63–92)	4 (0–11)	7 (1–16)	5 (0–19)	4 (1–14)
S. enterica serotype I 4,[5],12:i:-	66 (40–82)	6 (1–15)	8 (1–17)	12 (2–27)	7 (0–20)
S. enterica serotype Javiana	56 (29–76)	7 (1–20)	9 (2–22)	14 (3–33)	14 (2–29)
S. enterica serotype Newport	74 (50–86)	2 (0–9)	7 (1–16)	8 (1–19)	8 (2–18)
S. enterica serotype Typhimurium	59 (27–78)	7 (1–18)	8 (2–19)	14 (3–29)	13 (2–30)
S. enterica, all other serotypes group 1	60 (29–79)	6 (1–18)	9 (2–21)	12 (2–29)	12 (3–,29)
S. enterica, all other serotypes group 2	40 (10–65)	7 (1–24)	10 (2–26)	17 (1–40)	26 (6–51)
Shigella spp.	8 (1–36)	4 (1–21)	81 (48–93)	Blocked	6 (0–26)
Staphylococcus aureus	Blocked	75 (23–98)	18 (1–71)	1 (0–5)	5 (0–37)
Streptococcus spp., group A	4 (0–33)	1 (0–6)	92 (55–99)	1 (0–12)	2 (0–19)
Vibrio alginolyticus	60 (24–84)	37 (13–71)	0 (0–1)	1 (0–4)	2 (0–11)
V. alginolyticus, non-AGI	2 (0–17)	97 (79–100)	0 (0–1)	0 (0–2)	0 (0–2)
V. cholerae nontoxigenic	92 (61–100)	6 (0–30)	1 (0–3)	0 (0–4)	0 (0–3)
V. cholerae nontoxigenic, non-AGI	33 (8–59)	65 (39–90)	0 (0–1)	0 (0–1)	2 (0–13)
V. parahaemolyticus	74 (59–91)	24 (7–38)	0 (0–2)	0 (0–2)	1 (0 –5)
V. parahaemolyticus, non-AGI	8 (2–39)	90 (57–97)	0 (0–1)	0 (0–1)	2 (0–8)
V. vulnificus†	20 (7–54)	77 (40–91)	0 (0–3)	1 (0–9)	2 (0–12)
V. vulnificus, non-AGI	20 (9–34)	78 (58–89)	0 (0–1)	1 (0–16)	2 (0–9)
Vibrio spp., other AGI	96 (69–100)	2 (0–23)	0 (0–1)	0 (0–2)	1 (0–8)
Vibrio spp, other non-AGI	95 (58–100)	3 (0–27)	0 (0–1)	0 (0–2)	2 (0–15)
Yersinia enterocolitica	77 (44–100)	9 (0–37)	3 (0–17)	4 (0–16)	8 (0–33)
Protozoa					
Acanthamoeba spp.	Blocked	82 (46–100)	Blocked	0 (0–0)	18 (0–54)
Balamuthia mandrillaris	Blocked	54 (5–95)	Blocked	0 (0–0)	46 (5–95)
Cryptosporidium spp.	7 (0–25)	43 (17–73)	20 (2–49)	21 (4–48)	8 (0–34)
Cyclospora cayetanensis	83 (59–99)	6 (0–25)	3 (0–14)	1 (0–9)	7 (0–28)
Giardia spp.	10 (0–35)	44 (16–78)	27 (3–59)	10 (0–38)	8 (0–37)
Naegleria fowleri	Blocked	88 (61–100)	Blocked	Blocked	12 (0–38)
Toxoplasma gondii	28 (4–60)	5 (0–27)	Blocked	58 (24–86)	9 (0–29)
Viruses					
Astrovirus	15 (1–38)	6 (0–25)	73 (44–94)	Blocked	6 (0–18)
Hepatitis A virus	42 (9–78)	8 (0–33)	41 (8–77)	Blocked	8 (0–34)
Norovirus	19 (6–37)	6 (0–25)	70 (46–88)	Blocked	5 (0–18)
Rotavirus	5 (0–20)	7 (0–28)	81 (57–98)	Blocked	5 (0–21)
Sapovirus	13 (0–34)	8 (0–30)	75 (49–94)	Blocked	4 (0–16)

*Blocked indicates pathways blocked by study administrators. AGI, acute gastrointestinal disease; STEC, Shiga toxin–producing *Escherichia coli*.
†Clinical manifestations of interest for initial elicitation were bacteremia and wound infections.

relevant research findings for each pathogen. The document contained links to selected research articles. Experts were encouraged to use any data they felt were informative to make their estimates; they were not limited to only this document.

Elicitation

For the formal elicitation, 48 experts representing a wide range of professional and scientific backgrounds participated at a 2-day, in-person workshop in May 2017. During the workshop, experts participated in a 2-hour information session on probabilistic methods and providing estimates under uncertainty.

Calibration Questions

Experts were not expected to know true values precisely and provided low (5th percentile), median (50th percentile), and high (95th percentile) estimates to represent their uncertainty on the answers provided to the calibration questions. Experts were not allowed access to any additional resources while answering the calibration questions and, after they had they had finished, they could not return to this section to change their responses.

Target Questions

After completion of the calibration questions, experts provided 5th, 50th, and 95th percentile estimates for the proportion of domestically acquired illnesses that are transmitted through each major pathway and subpathway annually for each pathogen and target question in each panel to which they were assigned. The experts were also asked to indicate if they did not agree with the pathways blocked by study administrators. One pathway, person-to-person transmission for *Legionella* spp., was unblocked based on this feedback, and experts provided this estimate with the others at the in-person elicitation. Experts could access resources and discuss them with colleagues, if desired. However, we emphasized that the final estimates should represent the expert's individual responses, not a group consensus.

Postelicitation

Re-Elicitation

After the in-person elicitation was completed, we determined that re-elicitation for some pathogens was necessary. More granular detail was needed beyond the single estimate for *Pseudomonas*, so estimates were re-elicited for otitis externa, septicemia, and pneumonia. Based on feedback we received during the elicitation, we re-elicited estimates for non–acute gastrointestinal infections (non-AGI) for nontoxigenic *Vibrio cholerae*, *V. parahaemolyticus, V. vulnificus*, and *V. alginolyticus*. Experts were provided with feedback with updated surveillance data and given the opportunity to adjust their original estimates if new data led them to reconsider their previous estimates (Figure 1). The re-elicitations were completed through follow-up emails and web conferences.

Data Analysis

We analyzed data using EXCALIBUR (*19*). We combined all individual expert assessments by linear pooling into a single uncertainty assessment for each target question (*11*). For equal-based weighting, all experts' assessments contributed to the combined uncertainty assessment evenly. We computed performance-based weighting by combining the statistical accuracy and information scores of experts in each panel. The weighted combination of experts is referred to as the decision maker. We used the item weight decision maker because this calculates and applies weights per individual target question rather than for all questions an expert answered. We performed optimization to determine the threshold by which an expert's responses would be included in the final estimate or not. This was done separately per expert for each panel, based on each expert's statistical accuracy score (*12*).

We performed a subgroup analysis to determine whether separate schools of thought existed as a result of experts' self-identified background (categorized as mainly foodborne, mainly waterborne, or both). This analysis was completed by 2 independent reviewers who analyzed EXCALIBUR panel outputs for each target question to determine whether wide divergence existed among individual responses.

We normalized random samples from the weighted distributions for major transmission pathways and waterborne subpathways such that on each sample the values across pathways summed to 1. This process was done by resampling the cumulative distribution functions generated by EXCALIBUR 5,000 times in R version 3.4.3 for each pathogen, while dividing all sampled values by the sum of their values per iteration. Point estimates and 95% uncertainty intervals (UIs) for each target question and pathway were produced. We performed robustness analysis and out-of-sample validation to assess the performance of the method and to evaluate the effect of individual experts and individual calibration questions on the final distribution (Appendix 5, https://wwwnc.cdc.gov/EID/article/27/1/20-0316-App5.pdf) (*12*).

Results

Knowledge Review

The 20 questions were designed to be challenging, to emphasize application of the study definitions, and to represent scenarios at the boundaries among different transmission pathways. For 17 (85%) questions, >75% of participants answered with the correct major pathway, and of these questions, 13 (76%) were answered with the correct subpathway as well (Appendix 4).

Figure 2. Source attribution results for major transmission pathways of bacteria in study of attribution of illnesses transmitted by food and water to comprehensive transmission pathways using structured expert judgment, United States, 2017.

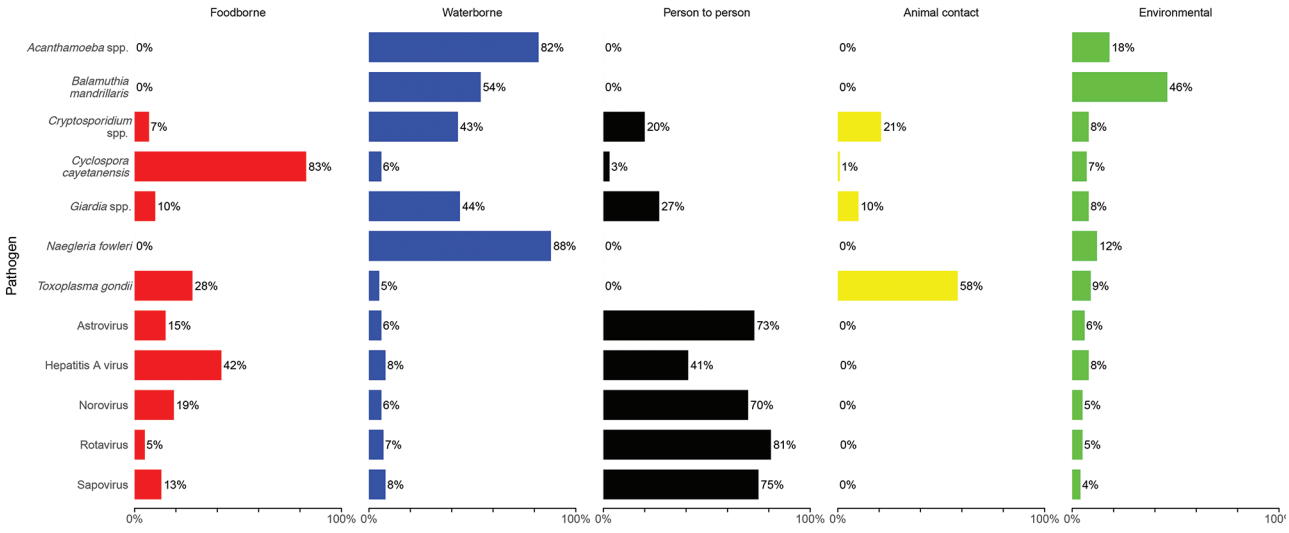

Figure 3. Source attribution results for major transmission pathways of protozoa and viruses for study of attribution of illnesses transmitted by food and water to comprehensive transmission pathways using structured expert judgment, United States, 2017.

Major and Subpathway Results

Table 4 and Figures 2 and 3 show the proportion and UI of domestically acquired illnesses attributed to the 5 major transmission pathways; Tables 5 and 6 show the subpathway results. For all panels, a satisfactory number of accurate and informative experts were included. Differing schools of thought based on experts' backgrounds were not identified (Appendix 5).

Bacteria

Most of the pathogens in this study were bacteria; they encompassed 35 of the 47 target questions. More than half of transmission (>50%) was attributed to the foodborne pathway for *Campylobacter* spp.; enterotoxigenic *Escherichia coli*; Shiga toxin-producing *Escherichia coli* (STEC) O157; other diarrheagenic *E. coli*; *Mycobacterium bovis*; nontyphoidal *Salmonella enterica* (all ages and serotypes); *S. enterica* serotypes Enteritidis, I 4,[5],12:i:-, Javiana, Newport, Typhimurium, and group 1 serotypes; *Vibrio alginolyticus*; *V. cholerae* nontoxigenic; *V. parahaemolyticus; Vibrio* spp., other AGI; *Vibrio* spp, other non-AGI; and *Yersinia enterocolitica*. In addition, *Legionella* spp.; nontuberculous *Mycobacterium* spp.; *Pseudomonas* spp., otitis externa; invasive *Staphylococcus aureus*; *V. alginolyticus*, non-AGI; *V. cholerae* nontoxigenic, non-AGI; *V. parahaemolyticus*, non-AGI; and *V. vulnificus* were all estimated to have majority transmission from the waterborne pathway. Most transmission for *Shigella* spp. and group A *Streptococcus* were estimated to be through person-to-person transmission. No bacterial pathogen had majority transmission through animal contact. *Pseudomonas* spp. septicemia was attributed primarily to the environmental pathway.

Protozoa

Cyclospora cayetanensis was the only protozoan estimated to have majority transmission through the foodborne pathway. *Acanthamoeba* spp. and *Naegleria fowleri* both had >80% transmission attributed to the waterborne pathway, and 54% (UI 5%–95%) of *Balamuthia mandrillaris* infections were estimated to occur through waterborne transmission. No protozoa had majority person-to-person or environmental transmission. Waterborne transmission was estimated at 43% (UI 17%–73%) for *Cryptosporidium* spp. and 44% (UI 16%–78%) for *Giardia* spp. Among all pathogens, *Toxoplasma gondii* had the highest attribution to animal contact transmission, 58% (UI 24%–86%).

Viruses

Most transmission for astrovirus, norovirus, rotavirus, and sapovirus was attributed to the person-to-person pathway. Hepatitis A virus was estimated to have the highest proportion of illness transmitted by the foodborne pathway at 42% (UI 9%–78%). Of this, 48% (UI 2%–93%) was considered food handler related. Of foodborne transmission, 50%–71% was estimated to be food handler related for astrovirus, norovirus, and sapovirus. For all viruses, 67%–88% of environmental transmission was attributed to the subpathway of presumed person-to-person transmission.

Discussion

This study presents a novel method for estimating the proportion of illnesses from pathogens transmitted commonly by food and water in the United States

through comprehensive and mutually exclusive pathways. It includes estimates for food handler–related, recreational water, drinking water, nonrecreational nondrinking water, and various environmental subpathways. This method enabled estimates to be informed by multiple data sources, including outbreak surveillance data, studies of sporadic illnesses, case reports, and experts' professional knowledge. The use of calibration to weight expert responses is a distinguishing characteristic of the classical model and introduces mathematical rigor not found with other elicitation methods.

Similar SEJ studies have been conducted in numerous countries, including Australia, Canada, and

Table 5. Source attribution results for foodborne and environmental transmission subpathways, structured expert judgment, United States, 2017*

	Mean % (95% uncertainty interval)				
	Foodborne		Environmental		
Pathogen name	Food handler–related	Other foodborne	Presumed person-to-person	Presumed animal contact	Other environmental
Bacteria					
Brucella spp.	Blocked	100 (100–100)	Blocked	41 (2–96)	59 (4–98)
Campylobacter spp.	12 (0–58)	88 (42–100)	12 (0–46)	62 (3–100)	26 (0–89)
Enterotoxigenic *Escherichia coli*	23 (1–71)	77 (29–99)	8 (0–43)	Blocked	92 (54–100)
STEC O157	8 (0–55)	92 (45–100)	10 (0–46)	76 (16–100)	13 (0–73)
STEC non-O157	5 (0–29)	95 (71–100)	21(2–49)	65(19–91)	14 (0–55)
E. coli, other diarrheagenic	7 (0–54)	93 (46–100)	59 (3–100)	9 (0–39)	31 (0–91)
Legionella spp.	Blocked	Blocked	0 (0–6)	Blocked	99 (91–100)
Mycobacterium bovis	1 (0–13)	99 (87–100)	3 (0–34)	45 (0–100)	53 (0–100)
Nontuberculous *Mycobacterium* spp.	Blocked	Blocked	3 (0–35)	6 (0–87)	91 (0–100)
Pseudomonas spp., otitis externa	Blocked	Blocked	8 (0–51)	2 (0–11)	90 (16–100)
Pseudomonas spp., septicemia	Blocked	Blocked	9 (0–59)	1 (0–4)	91 (39–100)
Pseudomonas spp., pneumonia	Blocked	Blocked	10 (0–61)	1 (0–6)	88 (22–100)
Salmonella enterica, nontyphoidal	10 (0–38)	90 (62–100)	20(2–52)	45 (5–89)	35 (0–83)
S. enterica, nontyphoidal, under 5 y	10 (0–39)	90 (61–100)	35 (5–78)	45 (6–84)	20 (0–75)
S. enterica serotype Enteritidis	11 (0–51)	89 (49–100)	22 (2–56)	44 (3–88)	34 (0–84)
S. enterica serotype I 4,[5],12:i:-	10 (0–38)	90 (62–100)	21 (3–52)	45 (3–89)	34 (0–84)
S. enterica serotype Javiana	11 (0–48)	89 (52–100)	36 (4–80)	44 (5–84)	20 (0–75)
S. enterica serotype Newport	10 (0–39)	90 (61–100)	21 (3–53)	48 (5–89)	30 (0–82)
S. enterica serotype Typhimurium	10 (0–39)	90 (61–100)	21 (2–50)	49 (6–88)	31 (0–81)
S. enterica, all other serotypes group 1	10 (0–38)	90 (62–100)	21 (2–52)	48 (6–89)	31 (0–81)
S. enterica, all other serotypes group 2	10 (0–39)	90 (61–100)	35 (5–79)	44 (5–83)	20 (0–74)
Shigella spp.	71 (17–96)	29 (4–83)	90 (31–100)	Blocked	10 (0–69)
Staphylococcus aureus	Blocked	Blocked	76 (30–97)	3 (0–43)	21 (0–66)
Streptococcus spp., group A	51 (0–100)	49 (0–100)	94 (29–100)	2 (0–33)	4 (0–70)
Vibrio alginolyticus, AGI	5 (0–89)	95 (11–100)	2 (0–19)	2 (0–36)	96 (9–100)
V. alginolyticus, non-AGI	0 (0–2)	100 (98–100)	1 (0–3)	96 (45–100)	3 (0–54)
V. cholerae nontoxigenic AGI	1 (0–5)	99 (95–100)	6 (0–83)	9 (0–97)	85 (0–100)
V. cholerae nontoxigenic, non-AGI	0 (0–1)	100 (99–100)	1(0–4)	96 (26–100)	3(0–73)
V. parahaemolyticus AGI	5 (0–52)	95 (48–100)	2 (0–7)	2(0–24)	96 (18–100)
V. parahaemolyticus, non-AGI	0 (0–2)	100 (98–100)	1 (0–3)	96 (30–100)	3 (0–69)
V. vulnificus†	5 (0–72)	95 (28–100)	3 (0–48)	3 (0–50)	94 (0–100)
V. vulnificus, non-AGI	0 (0–2)	100 (98–100)	1 (0–3)	96 (29–100)	3 (0–70)
Vibrio spp., other AGI	3 (0–70)	97 (30–100)	1 (0–5)	2 (0–27)	96 (21–100)
Vibrio spp., other non-AGI	3 (0–43)	97 (57–100)	1 (0–2)	2 (0–31)	97 (38–100)
Yersinia enterocolitica	9 (0–55)	91 (45–100)	23 (0–67)	56 (8–99)	20 (0–82)
Protozoa					
Acanthamoeba spp.	Blocked	Blocked	Blocked	1 (0–6)	97 (45–100)
Balamuthia mandrillaris	Blocked	Blocked	Blocked	2 (0–12)	97 (37–100)
Cryptosporidium spp.	24 (0–87)	76 (13–100)	18 (0–61)	61 (7–99)	21(0–81)
Cyclospora cayetanensis	10 (0–68)	90 (32–100)	51 (0–100)	6 (0–70)	43 (0–100)
Giardia spp.	19 (0–72)	81 (28–100)	26 (1–66)	23 (0–86)	51 (0–97)
Naegleria fowleri	Blocked	Blocked	Blocked	Blocked	97 (47–100)
Toxoplasma gondii	Blocked	100 (100–100)	Blocked	80 (22–100)	20 (0–78)
Viruses					
Astrovirus	50 (0–100)	50 (0–100)	73 (1–100)	Blocked	27 (0–99)
Hepatitis A virus	48 (2–93)	52 (7–98)	86 (27–100)	Blocked	12 (0–72)
Norovirus	71 (29–99)	29 (1–71)	73 (2–100)	Blocked	27 (0–98)
Rotavirus	27 (0–98)	73 (2–100)	88 (35–100)	Blocked	11 (0–65)
Sapovirus	51 (0–99)	49 (1–100)	67 (0–100)	Blocked	33 (0–100)

*Blocked indicates pathways blocked by study administrators. AGI, acute gastrointestinal disease; STEC, Shiga toxin–producing *Escherichia coli*.
†Clinical manifestations of interest for initial elicitation were bacteremia and wound infections.

Table 6. Source attribution results for waterborne transmission subpathways (means and 95 uncertainty interval), structured expert judgment, United States, 2017*

Pathogen name	Mean % (95% uncertainty interval)		
	Recreational water	Drinking water	Nonrecreational, nondrinking water
Bacteria			
Brucella spp.	45 (0–100)	8 (0–97)	47 (0–100)
Campylobacter spp.	32 (0–97)	44 (0–99)	24 (0–99)
Enterotoxigenic *Escherichia coli*	31 (3–85)	57 (8–94)	12 (0–58)
STEC O157	69 (33–94)	26 (3–60)	5 (0–28)
STEC non-O157	51 (18–77)	12 (0–43)	38 (12–69)
E. coli, other diarrheagenic	20 (2–53)	70 (34–92)	10 (0–38)
Legionella spp.	9 (2–35)	52 (19–78)	39 (13–69)
Mycobacterium bovis	21 (0–100)	14 (0–100)	65 (0–100)
Nontuberculous *Mycobacterium* spp.	13 (0–43)	67 (33–93)	20 (0–51)
Pseudomonas spp., otitis externa	95 (75–100)	3 (0–21)	2 (0–11)
Pseudomonas spp., septicemia	7 (2–37)	16 (1–50)	77 (37–94)
Pseudomonas spp., pneumonia	48 (17–74)	6 (1–33)	46 (18–76)
Salmonella enterica, nontyphoidal	18 (2–53)	75 (37–93)	7 (0–26)
S. enterica, nontyphoidal, <5 y	19 (3–49)	69 (38–91)	12 (1–30)
S. enterica serotype Enteritidis	20 (3–49)	71 (38–92)	9 (1–27)
S. enterica serotype I 4,[5],12:i:-	18 (2–49)	74 (38–93)	9 (0–35)
S. enterica serotype Javiana	21 (3–53)	67 (29–90)	12 (0–42)
S. enterica serotype Newport	17 (2–48)	74 (40–94)	9 (0–39)
S. enterica serotype Typhimurium	19 (3–51)	73 (39–93)	8 (1–29)
S. enterica, all other serotypes group 1	19 (3–51)	72 (36–93)	9 (0–39)
S. enterica, all other serotypes group 2	19 (2–50)	69 (36–91)	12 (1–40)
Shigella spp.	77 (41–95)	3 (0–25)	20 (3–50)
Staphylococcus aureus	91 (50–100)	5 (0–29)	4 (0–43)
Streptococcus spp., group A	73 (0–100)	10 (0–95)	18 (0–100)
Vibrio alginolyticus AGI	97 (66–100)	1 (0–6)	2 (0–21)
V. alginolyticus, non-AGI	96 (49–100)	2 (0–36)	3 (0–47)
V. cholerae nontoxigenic AGI	96 (56–100)	2 (0–11)	2 (0–22)
V. cholerae nontoxigenic, non-AGI	96 (50–100)	2 (0–14)	3 (0–43)
V. parahaemolyticus	98 (62–100)	1 (0–10)	1 (0–13)
V. parahaemolyticus, non-AGI	97 (50–100)	2 (0–35)	2 (0–37)
V. vulnificus†	98 (66–100)	1 (0–9)	2 (0–24)
V. vulnificus, non-AGI	96 (49–100)	2 (0–37)	2 (0–43)
Vibrio spp., other AGI	69 (0–100)	4 (0–69)	27 (0–100)
Vibrio spp, other non-AGI	70 (0–100)	4 (0–69)	26 (0–100)
Yersinia enterocolitica	51 (6–100)	28 (0–83)	21 (0–79)
Protozoa			
Acanthamoeba spp.	52 (8–88)	15 (0–51)	33 (3–76)
Balamuthia mandrillaris	48 (6–88)	4 (0–26)	48 (7–89)
Cryptosporidium spp.	66 (21–96)	24 (0–68)	11 (0–41)
Cyclospora cayetanensis	39 (0–99)	32 (0–97)	29 (0–100)
Giardia spp.	49 (9–93)	33 (2–82)	18 (0–67)
Naegleria fowleri	85 (51–98)	3 (0–27)	12 (1–45)
Toxoplasma gondii	37 (0–100)	27 (0–100)	36 (0–100)
Viruses			
Astrovirus	39 (0–99)	47 (0–100)	13 (0–92)
Hepatitis A virus	35 (0–100)	44 (0–100)	21 (0–97)
Norovirus	47 (8–90)	45 (6–86)	8 (0–42)
Rotavirus	41 (7–84)	50 (8–86)	9 (0–41)
Sapovirus	55 (11–97)	37 (0–84)	8 (0–41)

*AGI, acute gastrointestinal disease; STEC, Shiga toxin–producing *Escherichia coli*.
†Clinical manifestations of interest for initial elicitation were bacteremia and wound infections.

the Netherlands, as well as for global subregions, by the World Health Organization. Each of these used different transmission pathway definitions, study designs, and elicitation methods (*20*–*23*). This and other variations in methods limit comparison of estimates across studies, but provide support for some of the differences between our study results and previous US pathway attribution estimates. Previous estimates of foodborne transmission for 33 pathogens and animal contact transmission for 6 pathogens included in our study are available (*2*,*24*). We compared published foodborne and waterborne attribution studies with this study (Tables 7, 8).

Differences from previously published work on foodborne transmission attribution proportions were noted, including for *Campylobacter* spp., STEC

non-O157, other diarrheagenic *E. coli*, nontyphoidal *S. enterica*, *M. bovis, Shigella* spp., *Y. enterocolitica, C. cayetanensis, T. gondii,* astrovirus, rotavirus, sapovirus, and hepatitis A virus. These differences could be the result of changes in data availability or analytic methods. For example, previous US foodborne illness estimates used data from surveillance, risk factor studies, and literature review (*2*). Based on available data for *S. enterica* (a case-control study of sporadic illness and unpublished outbreak data [*2*,*25*]), a study used an estimate of 94% foodborne transmission, notably higher than this study's estimate of 66% (UI 48%–81%). Estimates more similar to the current study were reported in SEJ studies in the Netherlands (55%), Canada (63%), and Australia (71%) (*21*,*22*); these studies examined attribution to similar major pathways to those included in this study versus foodborne transmission only. Our estimates of foodborne transmission of astrovirus (15%), rotavirus (5%), and sapovirus (13%) are much higher than the estimate of <1% for each in an earlier study (*2*); reports of foodborne outbreaks caused by these viruses in CDC's outbreak surveillance systems informed our estimates. Reporting of enteric disease outbreaks transmitted by nonfoodborne routes has improved, and experts probably used these new data to inform their estimates (*26*).

This study provides noteworthy estimates for the food handler–related subpathway. For hepatitis A, both the World Health Organization and this study estimate 42% foodborne transmission, of which this study estimated 48% (UI 2%–93%) to be food

Table 7. Comparison of proportion of illnesses attributed to foodborne transmission from this and earlier studies*

	Study					
Details	Scallan et al. (*2*)	Hald et al. (*20*)	Havelaar et al. (*21*)	Butler et al. (*22*)	Vally et al. (*23*)	This study
Country	United States	AMR A (Canada, Cuba, USA)	Netherlands	Canada	Australia	United States
Type	Outbreak surveillance data or published studies	SEJ	SEJ	SEJ	SEJ	SEJ
Bacteria						
Brucella spp.	50	75	NE	34.6	NE	45
Campylobacter spp.	80	73	42	62.3	76	57
STEC O157	68	59	40	61.4	Combined as all STEC, 55	60
STEC non-O157	82	NE	42	59.7	Combined as all STEC, 55	50
Enterotoxigenic *Escherichia coli*	100 (only foodborne)	36	NE	44.4	Combined as other pathogenic *E. coli*, 24	69
E. coli, other diarrheagenic	30	NE	NE	41	Combined as other pathogenic *E. coli*, 24	55
Mycobacterium bovis	95	NE	NE	NE	NE	75
Salmonella spp.	94	73	55	62.9	71	66
Shigella spp.	31	12	NE	25.9	11	8
Vibrio vulnificus	47	NE	NE	70.6	NE	Non-AGI, 20
Vibrio parahaemolyticus	86	NE	NE	82.8	NE	AGI, 74
Vibrio spp. other	57	NE	NE	88.9	NE	Non-AGI, 8 AGI, 96 Non-AGI-95
Yersinia enterocolitica	90	NE	NE	82.8	NE	77
Protozoa						
Cryptosporidium spp.	8	16	12	11.3	NE	7
Cyclospora cayetanensis	99	NE	NE	83.1	NE	83
Giardia spp.	7	11	13	7.2	NE	10
Toxoplasma gondii	50	60	56	51.4	NE	28
Viruses						
Astrovirus	<1	NE	NE	9.9	NE	15
Hepatitis A virus	7	42	11	29.5	12	42
Norovirus	26	23	17	18.4	17	19
Rotavirus	<1	NE	13	7.3	NE	5
Sapovirus	<1	NE	NE	16.9	NE	13

*NE, not estimated; SEJ, structured expert judgment; STEC, Shiga toxin–producing *Escherichia coli*.

Table 8. Comparison of proportion of illnesses attributed to waterborne transmission from this and earlier published studies*

Details	Study			
	Hald et al. (*20*)	Butler et al. (*22*)	Vally et al. (*23*)	This study
Country	AMR A (Canada, Cuba, USA)	Canada	Australia	United States
Type	SEJ	SEJ	SEJ	SEJ
Bacteria				
Brucella spp.	1	4	NE	10
Campylobacter spp.	11	9.3	6	13
STEC O157	7	13.3	Combined as all STEC, 8	5
STEC non-O157	NE	11.4	Combined as all STEC, 8	6
Enterotoxigenic *Escherichia coli*	42	15.3	Combined as other *E. coli*, 14	9
E. coli, other diarrheagenic	NE	15.6	Combined as other *E. coli*, 14	9
Salmonella spp.	2	8	5	6
Shigella spp.	10	12.2	4	4
Vibrio vulnificus	NE	23.2	NE	Non-AGI, 78
V. parahaemolyticus	NE	11	NE	AGI, 24; non-AGI, 90
Vibrio spp. other	NE	7.6	NE	AGI, 2; non-AGI, 3
Protozoa				
Cryptosporidium spp.	37	36.8	NE	43
Cyclospora cayetanensis	NE	7.7	NE	6
Giardia spp.	42	NE	NE	44
Toxoplasma gondii	19	8.8	NE	5
Viruses				
Astrovirus	NE	6.8	NE	6
Hepatitis A virus	1	6.2	4	8
Norovirus	22	7.4	3	6
Rotavirus	NE	5.9	NE	7
Sapovirus	NE	1.4	NE	8

*NE, not estimated; SEJ, structured expert judgment; STEC, Shiga toxin–producing *Escherichia coli*.

handler-related (*20*). However, this study was conducted before widespread awareness of a massive increase in person-to-person transmission in the United States (*27*). Previous estimates of foodborne transmission were 11% in the Netherlands and 7% in the United States (*2*,*21*). The use of different pathway definitions, points of attribution, and inclusion of travel-related illness in these other studies might have contributed to these differences (*21*,*28*). For norovirus, 71% (UI 29%–99%) of foodborne transmission in our study was attributed to the food handler subpathway, which is supported by studies of outbreaks in the United States (*29*,*30*).

For the waterborne transmission pathway, attribution in the context of the other pathways has not been done before in the United States. Furthermore, these estimates include subpathway estimates and non-gastroenteritis clinical outcomes. For bacterial pathogens, the estimates suggest that the proportion of illnesses linked to water is higher than previously appreciated. The estimates for waterborne bacterial pathogens were associated with high rates of illness and death, including nontuberculous *Mycobacterium* spp., *Pseudomonas* spp., and *Legionella* spp. Of note, neither *Giardia* spp. nor *Cryptosporidium* spp., parasites traditionally understood to be waterborne, were assessed as predominantly waterborne; instead, person-to-person and animal contact, particularly for *Cryptosporidium*, were key pathways. For the free-living amebae *Acanthamoeba* spp., *B. mandrillaris*, and *N. fowleri*, limited data are available on exact exposures associated with these rare illnesses (*31*,*32*). The proportion of viral pathogens transmitted by water was estimated to be relatively low (6%–8%), although for norovirus this represents a substantial proportion of estimated annual waterborne disease illnesses (*32*). This study also provides estimates for 3 waterborne disease subpathways. Of note is the proportion of otitis externa infections caused by *Pseudomonas* spp. that were attributed to recreational water exposure, and the combined contribution of drinking and nonrecreational, nondrinking water exposures to nongastroenteritis outcomes of *Pseudomonas* spp. (excluding otitis externa), nontuberculous *Mycobacterium* spp., and *Legionella* spp. CDC has used results from this SEJ to help estimate that 7.2 million waterborne illnesses occur from 17 pathogens annually, including 600,000 emergency department visits, 120,000 hospitalizations, and 7,000 deaths, incurring $3.2 billion (2014 US dollars) in direct healthcare costs (*33*).

Whereas the primary focus of this SEJ study was illnesses transmitted commonly by food and water, including person-to-person, animal contact, and environmental transmission was integral to the study and led to notable findings. For example, this study estimated animal contact transmission of STEC O157 at 12% (UI 3%–25%) and of STEC non-O157 at 21% (UI 2%–46%). Previous US animal contact estimates, which were based on a FoodNet case-control study and outbreak surveillance data, estimated STEC O157 at 6% and STEC non-O157 at 8% (*24*). This discrepancy may be the result of differences in pathway definitions and the inclusion of additional data.

As with other SEJ studies, this study is subject to limitations that can affect the interpretation of results. Estimates for many pathogens had wide UIs, highlighting areas in which data gaps remain and further investment into public health surveillance and research may be warranted. More detailed attribution, such as by food category, was beyond the scope of this study. This study considered attribution at a national level and does not represent the geographic variability that exists for some pathogens. Experts provided estimates considering data available during the elicitation session, but infectious disease epidemiology can change rapidly, so these results may not reflect current transmission patterns. New information should be considered when applying these estimates (e.g., for disease burden calculations). Expert fatigue may have been a factor for participants who were asked to provide estimates for a large number of pathogens. For intervention and policy-making purposes, these results should be considered in context with results from other data-driven approaches, such as those done by the Interagency Food Safety Analytics Collaboration and for the Model Aquatic Health Code (*34*,*35*).

In conclusion, our findings provide a balanced understanding of multiple routes of transmission for 33 pathogens. This information can be used to support appropriate targeting of resources to prevent infections transmitted by all pathways and to invest in research and surveillance.

Acknowledgments

We thank all those who contributed their expertise and time to this study, especially our expert participants, dry run participants, subject matter experts at CDC, and other CDC and University of Florida staff who assisted.

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Article DOI: https://doi.org/10.3201/eid2701.200316

Attribution of Illnesses Transmitted by Food and Water to Comprehensive Transmission Pathways Using Structured Expert Judgment, United States

Appendix 1

Assigning Pathogens to Experts

Experts were polled with the question “Please indicate your professional interest, knowledge, and experience for each pathogen” for each of the 33 pathogens of interest. Answers were given on a Likert scale of high, medium, low, or none. Because we asked about professional interest, knowledge, and experience, as opposed to asking for self-ranked expertise, experts were able to indicate pathogens for which they would feel most able to provide estimates.

To support the assignment, we grouped pathogens into 15 panels with similar characteristics regarding microbiology, ecology, and/or transmission patterns, as follows:

- *Acanthamoeba* spp., *Balamuthia mandriallis*, *Naegleria fowleri*
- Astrovirus, norovirus, rotavirus, sapovirus
- *Brucella* spp., *Mycobacterium bovis*
- *Campylobacter* spp., *Yersinia enterocolitica*
- *Cryptosporidium* spp., *Giardia* spp.
- *Cyclospora cayetenensis*
- Enterotoxigenic *Escherichia coli*, other diarrheagenic *Escherichia coli, Shigella* spp.
- Hepatitis A virus
- *Legionella*, nontuberculous *Mycobacterium bovis*
- *Pseudomonas* spp.

- *Salmonella enterica*, nontyphoidal (estimates will be requested for all serotypes, as well as separately for serotypes Enteritidis, Typhimurium, Newport, i4, [5], 12:i:-, Javiana and other serotypes groups 1 and 2)
- Shiga toxin-producing *Escherichia coli* non-O157, Shiga toxin-producing *Escherichia coli* O157
- *Staphylococcus aureus* (invasive), *Streptococcus* spp., group A
- *Toxoplasma gondii*
- *Vibrio cholerae* (nontoxogenic), *Vibrio parahaemolyticus*, *Vibrio vulnificus*, *Vibrio* spp., other

Self-ratings were converted to numeric scores (0 = none, 1 = low, 2 = medium, 3 = high). The four-point Likert scale was not sufficiently informative for the algorithm used; additional information to support the assignment was based on indications of special expertise for particular pathogens. Two points were added to the expert's self-rating for any pathogen(s) about which he or she had distinctive expertise based on review of his or her curriculum vitae or publication record by the elicitation team. An average score by expert and major pathogen group (i.e., bacteria, viruses, protozoa) was calculated, and half of the average score was added to each related pathogen specific score to promote greater grouping by major pathogen group for experts. Average scores were then calculated based on the 15 sets listed previously.

Using these scores, we assigned experts to pathogens in rounds by determining the maximum bipartite graph (node type 1: expert; node type 2: pathogen set; edge weight: average set score) (*1*,*2*). This ensured that on each round the highest total score pairing of experts to pathogens was obtained. The edge order was randomly selected for each round to avoid potential issues with ties. The rounds proceeded until all matches were exhausted. The final panels were assigned based on filtering the results to include only experts with an average score of $\geq$1.5 for the pathogen set and limiting each expert to $\leq$15 pathogens.

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Article DOI: https://doi.org/10.3201/eid2701.200316

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Appendix 2

Calibration Questions

General Approach

Answers to calibration questions were required from the experts to provide weighting of their responses to the target variables. This procedure did not test experts' factual knowledge on the calibration questions, but rather their ability to provide valid estimates under uncertainty, specifically within the subject matter domain. This was done by asking for the experts' judgments of the low (5th percentile), median/best (50th percentile), and high (95th percentile) estimates that could be taken to represent their uncertainty distributions over the actual data values. The experts were not expected to know precisely these true values (but the study administrators did). However, they were expected to encompass the true values by providing suitable 90% uncertainty intervals and locate central tendency by an indicative median value. The median value need not be symmetric within the 90% uncertainty interval, but can indicate the expert's judgment of skewness (e.g., he or she might give 3 quantile values: [1; 5; 15] if he or she thought the uncertainty was right-skewed to higher values).

The initial strategy in the creation of the calibration questions was to include multiple domains in the calibration questions. The aim was to include questions that were relevant to the areas of expertise identified as desirable by CDC. The domains were as follows:

- Public health surveillance
- Occurrence data of food, water, and environmental hazards

• Exposure and frequency of exposure to hazards

• Food consumption patterns in the United States

The following expertise areas of interest were included on the expert questionnaire:

• Microbiology

• Bacteriology

• Virology

• Parasitology

• Enteric pathogens

• Epidemiology

• Public health

• Food safety

• Veterinary science

• Environmental microbiology

Calibration Questions

Preceding each calibration question, a short description was provided to orient the experts to the data sources from which the questions were derived. The wording given here is as it was provided to the experts at the time of elicitation.

FoodNet

The US Foodborne Diseases Active Surveillance Network, or FoodNet, has been tracking trends for infections commonly transmitted through food. This is done through active surveillance is in the following 10 US states: Connecticut, Georgia, Maryland, Minnesota, New Mexico, Oregon, Tennessee, and parts of California, Colorado, and New York. CDC releases preliminary data from the previous year annually, usually in the spring. The most recently available data were for 2015. Data for 2016 are expected to be published in April 2017.

Based on active surveillance data from FoodNet, what was the incidence (per 100,000 population) of laboratory-confirmed human *Cyclospora cayetanensis* infections for the year 2016?

Background information: In the year 2015, a total of 65 cases of *Cyclospora cayetanensis* were reported in the FoodNet database. This represents an incidence of 0.13 per 100,000 population.

Low (5^{th})	Median (50^{th})	High (95^{th})
_____	_____	_____

Based on active surveillance data from FoodNet, what was the incidence (per 100,000 population) of laboratory-confirmed human *Salmonella* infections for the year 2016?

Background information: In the year 2015, a total of 7,719 cases of human *Salmonella* were reported in the FoodNet database. This represents an incidence of 15.74 per 100,000 population.

Low (5^{th})	Median (50^{th})	High (95^{th})
_____	_____	_____

NNDSS

The US National Notifiable Disease Surveillance System (NNDSS) tracks all notifiable diseases that are reported to CDC by state and territorial jurisdictions. Each state has mandatory reporting criteria, but no federal-level reporting criteria exist. The state and territorial agencies voluntarily submit information to NNDSS, which the CDC oversees. The general system has been in existence since 1878. Notifiable disease surveillance is "passive" at the national level and is susceptible to underreporting. Annual reports are issued in July. The most recently available data were for 2015 and were published in *MMWR* in July 2016.

The annual number of human cases of acute hepatitis A reported to CDC through the NNDSS passive surveillance system has declined markedly over the past decade. What was the percent decrease from 2013 to 2014 in the annual number of cases of hepatitis A reported to CDC through the NNDSS system?

This would be calculated as follows:
(number of cases in 2013 – number of cases in 2014)/(number of cases in 2013) × 100%

Low (5^{th})	Median (50^{th})	High (95^{th})

NCOD

The Environmental Protection Agency (EPA) is required to assemble and maintain national drinking water contaminant occurrence for 30 regulated and unregulated contaminants in public water systems. EPA tracks these data in the National Contaminant Occurrence Database (NCOD). This database was established in 1996 in accordance with the amendments to the Safe Drinking Water Act (SDWA). EPA maintains 2 data management systems for water quality information, the Legacy Data Center and STORET. These contain raw biologic, chemical, and physical data on surface and ground water collected by federal, state, and local agencies, academics, volunteer groups, tribes, and others. These reports are released in 3-year increments and published the following summer. The most recent data are from the years 2008–2015 and were published in July 2016.

EPA uses the Unregulated Contaminant Monitoring Rule (UCMR) program to collect data for certain contaminants. This monitoring covers a representative sample of public water systems (PWS) that serve $\leq$10,000 people in the United States. *E. coli* has a minimum reporting level (MRL) of 1 MPN^3/100 mL according to NCOD. Between 2013 and 2015, a total of 1,045 samples were taken from these public water systems and tested for *E. coli*.

Based on the surveillance data in the NCOD, how many of these samples contained results with greater than or equal to the MRL for *E. coli* in 2016?

Low (5^{th})	Median (50^{th})	High (95^{th})

NHANES

The United States Department of Agriculture (USDA) publishes food consumption estimates of the average daily intake of food, by food source and demographic characteristics. These data were last updated in 2014 and include estimates from 2007–2010. These estimates are produced through the collection of data as part of the National Health and Nutrition Examination

Survey (NHANES). Data collection for these estimates began in 2003 and requires persons to record 2 nonconsecutive days using 24-hour dietary recall to obtain information about what they eat. Data on where food was purchased and eaten are included. NHANES data are released on a biannual basis for public use. NHANES oversamples from the underrepresented populations of African Americans, Hispanics, and persons ≥60 years of age.

NHANES includes fresh, canned, and frozen vegetables in its analysis of "total vegetables." This estimate does not include legumes.

Based on data collected by USDA for NHANES, what is the mean daily intake of total vegetables, in cups, for an individual, when considering the total US population age 2 and over for the year 2012?

Low (5^{th})	Median (50^{th})	High (95^{th})
_____	_____	_____

NHANES defines dairy products as fluid milk, cheese, and yogurt. Based on data collected by the USDA for NHANES, what is the mean daily intake of dairy, in cups, for a child in the US during 2012?

Low (5^{th})	Median (50^{th})	High (95^{th})
_____	_____	_____

FSIS

The Food Safety and Inspection Service (FSIS), as part of the United States Department of Agriculture (USDA), publishes data on the prevalence, volume weighted percent positive, or percent positive calculations for microbial pathogens in FSIS-regulated products. These results are released quarterly. These products include raw beef, raw pork, poultry, and ready-to-eat products. Pathogens tested for are *Salmonella*, *Campylobacter*, Shiga toxin-producing *E. coli* (STEC), *Listeria monocytogenes*, and chemical residues.

Between January 1, 2016 and December 31, 2016, a total of 11,277 samples of raw ground beef from 1,193 establishments were tested for *Salmonella* spp. Of these samples, how many tested positive for *Salmonella* spp.?

Low (5^{th})	Median (50^{th})	High (95^{th})

NARMS Background

The National Antimicrobial Resistance Monitoring System (NARMS) is a national public health surveillance system that tracks changes in the antimicrobial susceptibility of certain enteric bacteria found in ill persons, retail meats, and food animals in the United States. NARMS was established in 1996 and is a collaboration among CDC, USDA, and FDA. Reports are published annually, representing data from 2 years prior. Thus, the report of data from 2014 was published in 2016.

NARMS tests *Salmonella* samples for resistance to 9 antimicrobial classes. These include aminoglycosides, β-lactam/β-lactamase inhibitor combinations, cephems, folate pathway inhibitors, macrolides, penicillins, phenicols, quinolones, and tetracyclines.

In 2014, a total of 2,127 *Salmonella* isolates from humans were tested by NARMS for resistance to the above antimicrobial agents.

What percentage of these samples showed no resistance to any of the antimicrobial agents tested?

Low (5^{th})	Median (50^{th})	High (95^{th})

In 2014, a total of 4,122 Campylobacter isolates were tested in NARMS. Of these, 1,397 samples were from humans. What percentage of human samples tested in 2014 showed resistance to ciprofloxacin?

Low (5^{th})	Median (50^{th})	High (95^{th})

NORS

The National Outbreak Reporting System (NORS) is a web-based platform used by local, state, and territorial health departments in the United States. This system is used to report all waterborne disease outbreaks, foodborne disease outbreaks, and enteric disease outbreaks transmitted by contact with environmental sources, infected persons or animals, or unknown modes of transmission. Data are evaluated continuously as outbreaks are reported into the system. Final data are typically released 12–18 months after the end of the reporting year.

As reported in 2014, between 2009 and 2010 there were 11 outbreaks involving harmful algal blooms (HABs). What percentage of individuals affected by the HAB outbreaks were hospitalized?

_____	_____	_____
Low (5^{th})	Median (50^{th})	High (95^{th})

A total of 864 foodborne disease outbreaks were reported in NORS for the year 2014. This includes both confirmed and suspected etiologies, as is reported annually. Of the outbreaks attributed to a single food category, how many were associated with chicken products?

_____	_____	_____
Low (5^{th})	Median (50^{th})	High (95^{th})

During 2014, there were 712 hospitalizations due to illnesses associated with NORS-reported outbreaks. How many hospitalizations due to illnesses associated with NORS-reported outbreaks were there in 2016?

_____	_____	_____
Low (5^{th})	Median (50^{th})	High (95^{th})

Recreational Water Outbreaks Background

The CDC defines recreational water as treated venues (e.g., pools, hot tubs, or spas) and untreated water venues (e.g., lakes and oceans). The Waterborne Disease and Outbreak Surveillance System collects data on waterborne diseases and outbreaks associated with recreational water, drinking water, environmental, and undetermined water exposures. Outbreaks in recreational water are reported in *MMWR* annually, reflecting finalized data from 3 years prior. Thus, the 2015 report reflects 2011–2012 data.

For the years 2009–2010, there were a total of 81 outbreaks attributed to recreational water (both treated and untreated) reported to the Waterborne Disease and Outbreak Surveillance System.

For the years 2011–2012, how many outbreaks were be attributed to untreated recreational water?

_____	_____	_____
Low (5^{th})	Median (50^{th})	High (95^{th})

For the years 2009–2010, there were a total of 81 outbreaks attributed to recreational water (both treated and untreated) reported to the Waterborne Disease and Outbreak Surveillance System.

What percentage of recreational water outbreaks for the years 2011–2012 were caused by *Cryptosporidium* species?

_____	_____	_____
Low (5^{th})	Median (50^{th})	High (95^{th})

Article DOI: https://doi.org/10.3201/eid2701.200316

Attribution of Illnesses Transmitted by Food and Water to Comprehensive Transmission Pathways Using Structured Expert Judgment, United States

Appendix 4

Knowledge Review Questionnaire and Results

Review of Knowledge

Transmission pathways & definitions

Please feel free to refer to the pathway definitions as needed to complete this. There are 20 questions in total.

* Required

1. **Email address** *

2. **First Name** *

3. **Last Name** *

Transmission Pathway Questions

Please choose the transmission pathway that best fits each scenario described

1. **Norovirus illness among attendees of a banquet linked to carpet and indoor environment that had been contaminated with vomit the day before the banquet and subsequently cleaned**
   Mark only one oval.
   - ◯ Foodborne transmission
   - ◯ Foodborne transmission - Food-handler related
   - ◯ Waterborne transmission - Drinking water
   - ◯ Waterborne transmission - Recreational water
   - ◯ Waterborne transmission - Non-recreational/Non-drinking
   - ◯ Person-to-person transmission
   - ◯ Animal contact transmission
   - ◯ Environmental transmission
   - ◯ Environmental- Presumed person-to-person
   - ◯ Environmental - Presumed animal contact

2. **Salmonellosis among participants in a mud volleyball tournament linked to ingestion of mud**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

3. **Norovirus illness from a lake after someone vomited in the lake**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

4. **STEC O157 illness linked to touching the railings of an animal enclosure at an animal fair**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

5. **Campylobacteriosis among mountain bikers linked to ingestion of mud**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

6. **STEC O157 illness linked to camping on grounds that had been used as pasture area for sheep 1 month prior**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

7. **Legionellosis linked to construction activities with a water main break**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

8. **Q-fever associated with living within 3 miles of an infected goat farm**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

9. **Brucellosis acquired through wounds or inhalation among employees at a pig slaughter plant**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

10. **Mycobacterium kansasii infection among mineworkers linked to contaminated showers**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

11. **Toxoplasmosis linked to working in the home garden**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

12. **Campylobacteriosis linked to contact with contaminated packaging of chicken meat**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

13. **Legionellosis linked to a contaminated cooling tower**
Mark only one oval.

- Foodborne transmission
- Foodborne transmission - Food-handler related
- Waterborne transmission - Drinking water
- Waterborne transmission - Recreational water
- Waterborne transmission - Non-recreational/Non-drinking
- Person-to-person transmission
- Animal contact transmission
- Environmental transmission
- Environmental- Presumed person-to-person
- Environmental - Presumed animal contact

14. **Salmonella in the family of a laboratorian who routinely prepared the family's dinners**
Mark only one oval.

- ◯ Foodborne transmission
- ◯ Foodborne transmission - Food-handler related
- ◯ Waterborne transmission - Drinking water
- ◯ Waterborne transmission - Recreational water
- ◯ Waterborne transmission - Non-recreational/Non-drinking
- ◯ Person-to-person transmission
- ◯ Animal contact transmission
- ◯ Environmental transmission
- ◯ Environmental- Presumed person-to-person
- ◯ Environmental - Presumed animal contact

15. **Transmission of STEC O157 illness from a sick child to other children in a daycare**
Mark only one oval.

- ◯ Foodborne transmission
- ◯ Foodborne transmission - Food-handler related
- ◯ Waterborne transmission - Drinking water
- ◯ Waterborne transmission - Recreational water
- ◯ Waterborne transmission - Non-recreational/Non-drinking
- ◯ Person-to-person transmission
- ◯ Animal contact transmission
- ◯ Environmental transmission
- ◯ Environmental- Presumed person-to-person
- ◯ Environmental - Presumed animal contact

16. **Salmonellosis due to internalization of contaminated water by tomatoes during processing**
Mark only one oval.

- ◯ Foodborne transmission
- ◯ Foodborne transmission - Food-handler related
- ◯ Waterborne transmission - Drinking water
- ◯ Waterborne transmission - Recreational water
- ◯ Waterborne transmission - Non-recreational/Non-drinking
- ◯ Person-to-person transmission
- ◯ Animal contact transmission
- ◯ Environmental transmission
- ◯ Environmental- Presumed person-to-person
- ◯ Environmental - Presumed animal contact

17. **Salmonellosis linked to rodents contaminating food in a restaurant kitchen**
Mark only one oval.

- ◯ Foodborne transmission
- ◯ Foodborne transmission - Food-handler related
- ◯ Waterborne transmission - Drinking water
- ◯ Waterborne transmission - Recreational water
- ◯ Waterborne transmission - Non-recreational/Non-drinking
- ◯ Person-to-person transmission
- ◯ Animal contact transmission
- ◯ Environmental transmission
- ◯ Environmental- Presumed person-to-person
- ◯ Environmental - Presumed animal contact

18.. **Norovirus outbreak due to an infected food handler preparing sandwiches**
Mark only one oval.

- ◯ Foodborne transmission
- ◯ Foodborne transmission - Food-handler related
- ◯ Waterborne transmission - Drinking water
- ◯ Waterborne transmission - Recreational water
- ◯ Waterborne transmission - Non-recreational/Non-drinking
- ◯ Person-to-person transmission
- ◯ Animal contact transmission
- ◯ Environmental transmission
- ◯ Environmental- Presumed person-to-person
- ◯ Environmental - Presumed animal contact

19. **Paratyphi B var. Java linked to contact with aquariums housing fish**
Mark only one oval.

- ◯ Foodborne transmission
- ◯ Foodborne transmission - Food-handler related
- ◯ Waterborne transmission - Drinking water
- ◯ Waterborne transmission - Recreational water
- ◯ Waterborne transmission - Non-recreational/Non-drinking
- ◯ Person-to-person transmission
- ◯ Animal contact transmission
- ◯ Environmental transmission
- ◯ Environmental- Presumed person-to-person
- ◯ Environmental - Presumed animal contact

20. **STEC O157 infection after attending a dance in a barn that had been cleaned since housing animals**

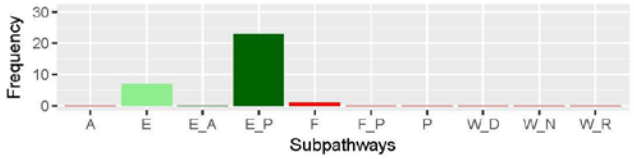
Mark only one oval.

- ◯ Foodborne transmission
- ◯ Foodborne transmission - Food-handler related
- ◯ Waterborne transmission - Drinking water
- ◯ Waterborne transmission - Recreational water
- ◯ Waterborne transmission - Non-recreational/Non-drinking
- ◯ Person-to-person transmission
- ◯ Animal contact transmission
- ◯ Environmental transmission
- ◯ Environmental- Presumed person-to-person
- ◯ Environmental - Presumed animal contact

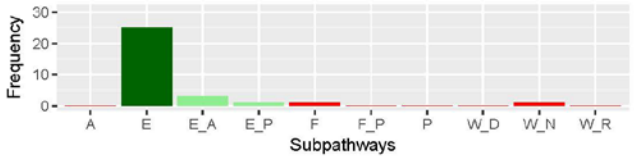
8/8

Appendix 4 Figure 1. Knowledge Review Questionnaire

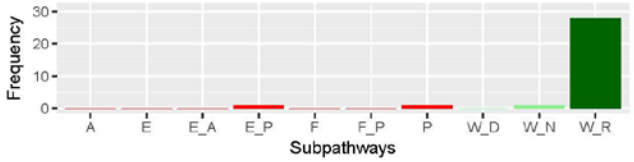
1. Norovirus illness among attendees of a banquet linked to carpet



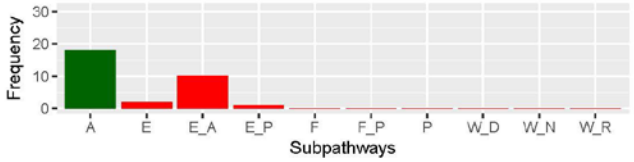
2. Salmonellosis among participants in a mud volleyball tournament linked to ingestion of mud



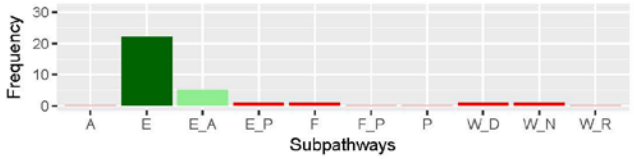
3. Norovirus illness from a lake after someone vomited in the lake

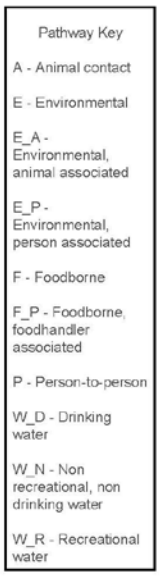


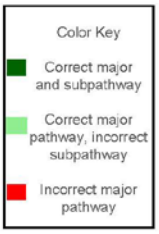
4. STEC O157 illness linked to touching the railings of an animal enclosure at an animal fair



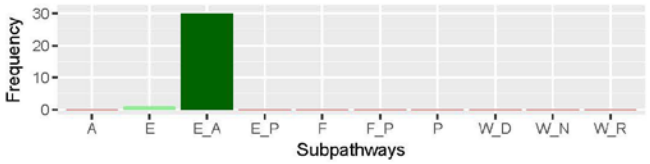
5. Campylobacteriosis among mountain bikers linked to ingestion of mud



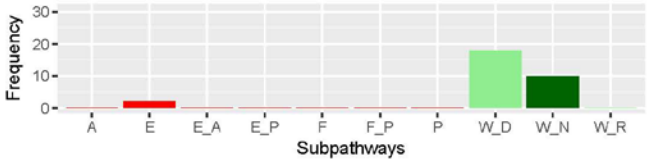




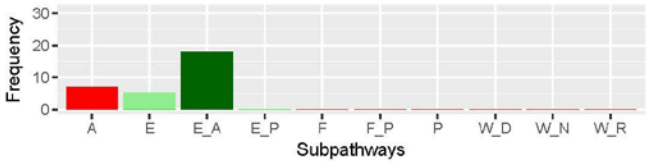
6. STEC O157 illness linked to camping on grounds that had been used as pasture area for sheep 1 month prior



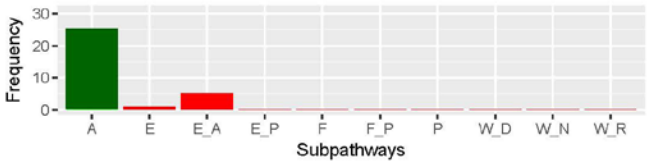
7. Legionellosis linked to construction activities with a water main break



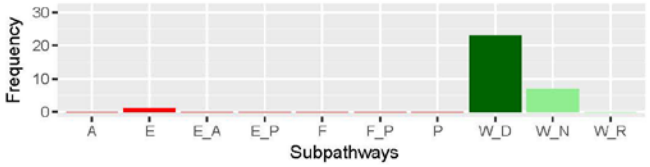
8. Q-fever associated with living within 3 miles of an infected goat farm

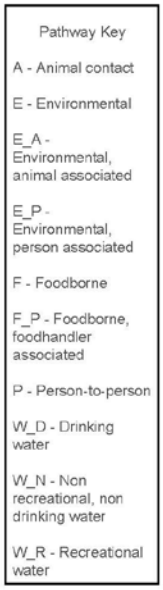


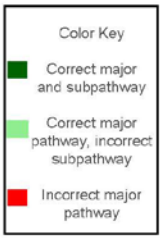
9. Brucellosis acquired through wounds or inhalation among employees at a pig slaughter plant



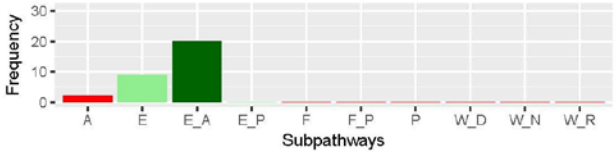
10. *Mycobacterium kansasii* infection among mineworkers linked to contaminated showers



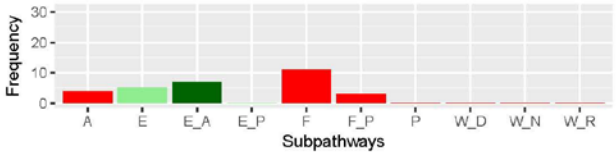




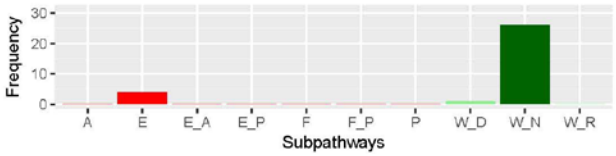
11. Toxoplasmosis linked to working in the home garden



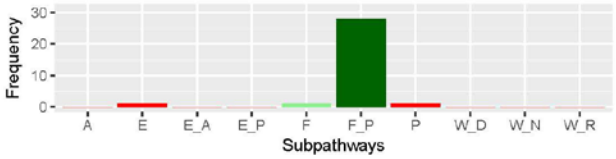
12. Campylobacteriosis linked to contact with contaminated packaging of chicken meat



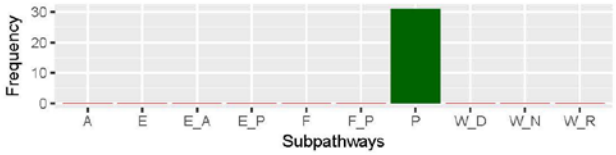
13. Legionellosis linked to a contaminated cooling tower

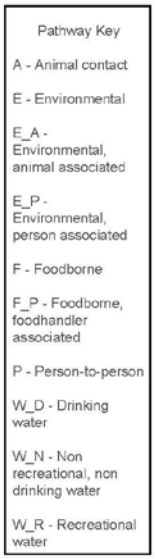


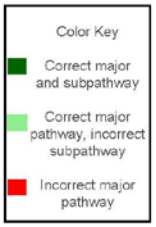
14. Salmonella in the family of a laboratorian who routinely prepared the family's dinners

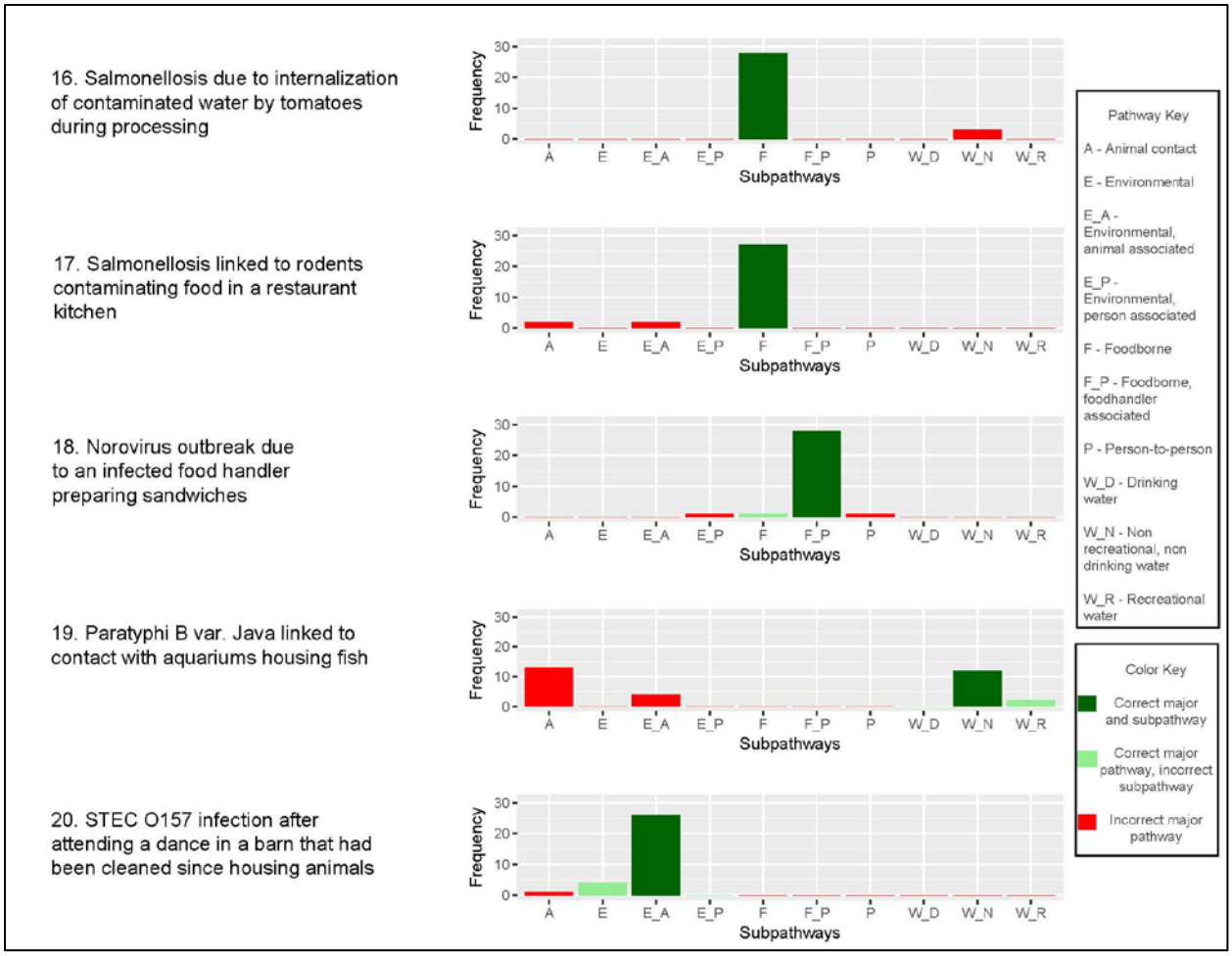


15. Transmission of STEC O157 illness from a sick child to other children in a daycare









Appendix 4 Figure 2. Expert Responses to Knowledge Review Questionnaire

Article DOI: https://doi.org/10.3201/eid2701.200316

Attribution of Illnesses Transmitted by Food and Water to Comprehensive Transmission Pathways Using Structured Expert Judgment, United States

Appendix 5

Detailed Validation Analysis

This appendix focuses on validation results for a typical panel: Panel 6, involving 21 experts. The elicitation of Panel 6 included 14 calibration questions (or variables) and 11 target questions. Experts' assessments for calibration variables were evaluated in terms of statistical accuracy and informativeness. As always, statistical accuracy is the p value at which we would falsely reject the hypothesis that an expert's probabilistic assessments were statistically accurate. Informativeness reflects the degree to which an expert's distribution was concentrated, and was measured as relative information in relation to a background measure. For all cases presented here, the background measure was uniform. Relative information of distribution A with respect to distribution B reflects the surprise we should feel if we initially believed B and drew samples exhibiting distribution A. It is related to the log likelihood ratio commonly used in goodness of fit testing. The informativeness of an expert is computed as the average over the informativeness in the calibration variables. The informativeness of an expert can also be computed for all the questions, thus including the questions of interest.

A combined score was obtained by multiplying the statistical accuracy by the informativeness, which in turn, provided performance-based weights for the experts. The weighted combination of experts is referred to as the performance weighted decision maker (PWDM). We evaluated the PWDM as compared with the equally weighted decision maker (EWDM), which assigns equal weight to all experts. Any DM can be regarded as an expert itself; thus, its assessments can also be evaluated in terms of statistical accuracy and informativeness.

Intuitive definitions of the relevant terms are offered here; for precise mathematical definitions and detailed descriptions, the reader is referred to Colson and Cooke 2017 and 2018 (*1*,*2*), especially the supplementary online material.

The Classical Model for Structured Expert Judgment admits 3 types of validation approaches: robustness analysis, in-sample validation, and out-of-sample validation.

Panel 6 In-Sample Validation

In-sample validation considers the statistical accuracy (p value) and informativeness of PWDM and EWDM, evaluated with respect to all 14 calibration variables. From Appendix 5 Table 1 we see that the statistical accuracy scores of the experts range from 0.57 (expert 3) to 0.00000064 (expert 10). Intuitively, this means that if we reject the hypothesis that expert 3 is statistically accurate, we have a 57% chance of being wrong, whereas with expert 10, the chance of being wrong is 0.00000064. Informativeness is tabulated for all variables (calibration and variables of interest combined), as well as for the calibration variables only.

As mentioned earlier, an expert's combined score is computed as the product of the p value (statistical accuracy) and informativeness for calibration variables, which, in turn, leads to experts' weights. The experts' weights can be calculated when taking into account all calibration questions, but can also be calculated for each calibration question separately. We refer to this case as item weights; experts will receive a different weight for each question, which depends on their informativeness for each question.

The expert weights should satisfy an asymptotic "proper scoring rule" property; that is, an expert maximizes his or her expected weight in the long run by, and only by, giving assessments corresponding to his or her true beliefs. Performance weights are asymptotic strictly proper scoring rules if there is some positive value α such that an expert is unweighted if his or her p value falls below α. The optimal performance weighted DM is computed by finding an optimal α cutoff for p values, which is chosen to maximize the combined score of the resulting PW. (In this exercise, PW means the item-specific PW where weights for each variable are inflected with the expert's information score for that variable.) For Panel 6, the optimal cutoff value was 0.2426, resulting in 5 experts being weighted (in bold in Appendix 5 Table 1). The expert and DM scores are given in Appendix 5 Table 1.

In-sample validation consists of ascertaining that the statistical accuracy of the PWDM and EWDM is acceptable without sacrificing informativeness. This is termed “in-sample validation” because the PWDM’s performance is assessed on the same set of calibration variables that were used to initialize the PWDM. From Appendix 5 Table 1 we see that PWDM is more statistically accurate than EWDM, but that both are acceptable. PWDM’s informativeness is comparable to the lower values of the experts, whereas EWDM’s informativeness is well below that of the experts. This replicates a recurring finding that EWDM tends to purchase acceptable statistical performance at the expense of informativeness.

Robustness

Robustness analysis removes 1 expert or 1 calibration variable at a time and recomputes the PWDM. The statistical accuracy and informativeness of the “perturbed decision makers” are compared with the original statistical accuracy and informativeness and the “discrepancy” between the perturbed DM and the original DM is computed. Mathematically, this corresponds to the relative information of each expert’s distribution with respect to the PW combination. We compare this discrepancy with the discrepancy between each expert and the EWDM. The later discrepancy gives an indication of the disagreement among the experts themselves. When the latter discrepancies are much greater than the former, we may conclude that the PWDM is indeed robust: the change induced by loss of expert or loss of item is then small relative to the differences between the experts themselves. These discrepancies between each expert and EWDM are given in Appendix 5 Table 2, whereas the discrepancies relative to the original PWDM are given in Appendix 5 Table 3.

The average of these discrepancies gives an index for the disparity within the expert panel. The higher the expert’s discrepancy relative to EWDM, the higher the disagreement with the DM. Note that the discrepancy for all 5 weighted experts is below the average discrepancy over all experts. This indicates that the weighted experts among themselves show better agreement than the experts overall.

Appendix 5 Table 3 shows the results for robustness analysis on calibration variables. That is, each of the 14 calibration questions has been excluded, one at a time, from the analysis. The optimal performance-based DM, using item weights, for the remaining 13 calibration

variables is obtained and its resulting informativeness and p value are provided. Furthermore, the discrepancy is also reflected by the total relative information with respect to the original DM, based on the 14 calibration questions. The informativeness of the new DM varies between 0.93 and 1.62, and therefore does not change significantly when removing calibration variables. However, the p value increases significantly, to 0.92, when removing CAL022, CAL055, CAL088, CAL099, or CAL1111, in turn. Nonetheless, the average of the perturbed discrepancies is 0.269, which is much smaller than the discrepancy among the experts themselves in Appendix 5 Table 2 (0.807). The PWDM is therefore shown to be robust against the loss of a single calibration variable.

Appendix 5 Table 4 shows the results of robustness on experts. Similarly to the robustness on calibration variables, experts were excluded one at a time and the optimal PWDM, using item weights, was obtained for the remaining 20 experts. The informativeness and statistical accuracy, as well as discrepancy compared to the original PWDM, are provided. The statistical accuracy of the new DM is, except when excluding expert 48, the same as the initial DM's p value. Similarly, the informativeness accounts for small variations. Finally, the average discrepancy is 0.07, which indicates a very small discrepancy with respect to the original DM.

We may conclude that the PWDM results for Panel 6 are robust with respect to loss of a single calibration variable and are extremely robust relative to the loss of a single expert.

Out-of-Sample Validation

Out-of-sample validation requires that the PWDM and EWDM be scored on a different set of variables as those used to initialize the weighting model. Because we cannot observe the variables of interest, we must recourse to cross validation: every non-empty subset of calibration variables is used to initialize the model (usually referred to as the training set) and performance is scored using predictions of variables in the complementary set (usually referred to as the test set). With 14 calibration variables, this involves $2^{14} - 2 = 16{,}832$ training set/test set computations. This accounts for training sets of size varying from 1 to 13, which include all possible combinations of calibration variables. A small training set has low statistical power for resolving the experts' performance and thus produces combinations that are not representative of the final expert panel. On the other hand, a small test set has low statistical power for resolving

the performance of the PWDM and EWDM. As the test set size decreases, statistical accuracy is evaluated by tests of decreasing statistical power and all statistical accuracy scores tend to rise. It is argued that using 80% of the calibration variables in the training set is a good compromise (*1*). (These results are computed with the MATLAB code graciously provided by Lt. Col. Justin Eggstaff.) For the results presented here, the EWDM and global PWDM scores were averaged over all same-sized training sets.

Whereas Appendix 5 Table 1 used item-specific performance weighting, for out-of-sample validation, computational constraints impose global performance weighting: instead of weighting experts for each variable using the experts' information scores for the given variable, an expert's average information over all calibration variables is used to derive weights that apply to all variables. With item-specific weights, an expert can up- or downweight himself or herself variable-wise by choosing a more or less informative distribution for the given variable. Item-specific weighting usually outperforms global weighting, and this was true for Panel 6.

The out-of-sample scores for statistical accuracy averaged over same-sized training sets are shown in Appendix 5 Figure 1 panel A. There is an out-of-sample penalty for the statistical accuracy score, but this penalty is small in absolute terms. As the training set grows, the penalty shrinks, and the PWDM resembles the PWDM of original study based on all calibration variables. Out-of-sample informativeness of PWDM is consistently higher than that of EWDM (Appendix 5 Figure 1 panel B). Putting these two together in Appendix 5 Figure 2, the combined score of PWDM is clearly superior to that of EWDM out-of-sample. The advised training set sample size of 80% of all calibration variables is highlighted.

All Experts: In-Sample

Because all 48 experts assessed the same 14 calibration variables, it is also possible to consider a fictitious panel consisting of all 48 experts. Robustness analysis does not make sense, as the 48 experts did not assess the same variables of interest. However, in- and out-of-sample validation can be performed.

In Appendix 5 Table 5 the scores for all 48 experts are shown ranked according to their combined scores. The 15 best performing experts are highlighted (shaded yellow). The last 4 rows compare 4 different DMs. PWDM is the optimal performance item weighted DM. PWDM

minus 15 represents a mass extinction robustness analysis: the 15 top performing experts, which are shaded in yellow, are removed and PWDM is computed for the remaining experts. PWDMNoOpt uses all 48 experts but sets the cutoff at zero; all experts are weighted with weights proportional to their combined score. EWDM is the equal weighted combination of all 48 experts. Experts' information scores in Appendix 5 Table 5 are higher than those in Appendix 5 Table 1 because informativeness is scored relative to the uniform distribution spanning all assessments of all experts. Increasing the number of experts expands the range of this uniform distribution, making all experts appear more informative.

PWDM minus 15 scores better than PWDMNoOpt and better than EWDM. This shows the robustness of the classical model under massive expert loss: removing the top performing third of the experts still produces higher performance scores than equally weighting all experts. The role of optimization is also highlighted. If optimization is not performed, the result PWDMNoOpt is only marginally better than EWDM.

All Experts: Out-of-Sample

The explanations given for Panel 6 apply here as well. Appendix 5 Figures 3 and 4 correspond to Appendix 5 Figures 1 and 2.

Conclusion

This appendix illustrates the 3 types of validation that are available within the Classical Model for Structured Expert Judgment: robustness analysis, in-sample validation, and out of-sample validation. With regard to the data from the CDC study, we may conclude that all three types of validation are strongly attested.

References

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2. Colson A, Cooke RM. Expert elicitation: using the classical model to validate experts' judgments. Rev Environ Econ Policy. 2018;12:113–32. https://doi.org/10.1093/reep/rex022

Appendix 5 Table 1. Panel 6 performance scores of the 21 experts, the PWDM, and EWDM*

Expert	p value	Informativeness, all variables	Informativeness, calibration variables	Combined score
Expert 01	0.000720	2.394	1.894	0.001
Expert 04	0.0135	2.361	1.906	0.026
Expert 15	0.00984	2.12	2.169	0.021
Expert 18	0.000000738	3.662	3.221	0
Expert 29	0.0334	2.498	1.396	0.047
Expert 33	**0.243**	**2.331**	**1.468**	**0.356**
Expert 43	0.00126	2.751	1.923	0.002
Expert 48	**0.569**	**2.458**	**1.541**	**0.877**
Expert 03	**0.569**	**1.686**	**1.526**	**0.868**
Expert 07	**0.243**	**2.043**	**1.671**	**0.405**
Expert 10	0.000000638	1.21	1.07	0
Expert 17	0.144	2.327	1.613	0.231
Expert 24	0.00984	1.708	1.734	0.017
Expert 25	0.00984	2.377	1.416	0.014
Expert 27	0.000101	1.664	1.514	0
Expert 32	0.0543	1.869	1.353	0.073
Expert 47	**0.569**	**1.02**	**0.8906**	**0.507**
Expert 16	0.0724	1.821	1.502	0.109
Expert 42	0.223	2.284	2.114	0.47
Expert 06	0.185	2.186	2.177	0.403
Expert 22	0.00217	3.319	2.718	0.006
PWDM	0.659	1.473	1.093	0.72
EWDM	0.1325	0.8184	0.6998	0.093

*EWDM, equally weighted decision maker; PWDM, performance weighted decision maker.The experts included in the optimal DM are in bold.

Appendix 5 Table 2. Expert discrepancies for each expert in Panel 6 with respect to the EW combination of the experts' distributions

Expert	Discrepancy relative to EWDM,* all variables
Expert 01	1.472
Expert 04	1.189
Expert 15	1.013
Expert 18	2.19
Expert 29	0.947
Expert 33	0.835
Expert 43	0.986
Expert 48	0.803
Expert 03	0.699
Expert 07	0.854
Expert 10	0.815
Expert 17	0.837
Expert 24	1.117
Expert 25	1.017
Expert 27	1.07
Expert 32	0.949
Expert 47	0.664
Expert 16	0.747
Expert 42	1.084
Expert 06	1.36
Expert 22	1.474
Average	1.003

*EWDM, equally weighted decision maker.

Appendix 5 Table 3. Robustness on calibration variables

Excluded variable	Informativeness calibration variables	p value	Discrepancy with respect to original decision maker (DM) calibration variables
CAL011	1.37	0.6894	0.2476
CAL022	1.134	0.9281	0.2195
CAL033	1.126	0.614	0.1117
CAL044	1.094	0.4209	0.171
CAL055	0.928	0.9281	0.2293
CAL066	0.919	0.614	0.06939
CAL077	1.309	0.614	0.2772
CAL088	1.62	0.9281	0.4339
CAL099	1.142	0.9281	0.2263
CAL1010	1.149	0.614	0.093
CAL1111	0.951	0.9281	0.4727
CAL1212	1.522	0.5285	0.4966
CAL1313	1.217	0.6894	0.1641
CAL1414	1.621	0.5285	0.5567
Original	1.093	0.659	
Average discrepancy			0.269

Appendix 5 Table 4. Robustness on experts

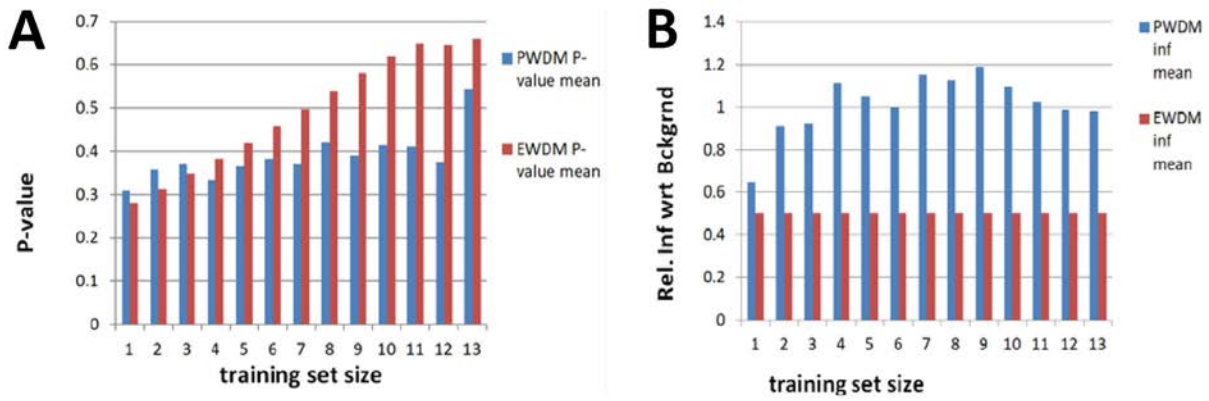
Excluded expert	Informativeness calibration variables	p value	Discrepancy with respect to original PWDM,* all variables
Expert 01	1.093	0.659	0.000000127
Expert 04	1.093	0.659	0.0000000653
Expert 15	1.093	0.659	0.0000000273
Expert 18	1.093	0.659	0.00233
Expert 29	1.093	0.659	0.0000000203
Expert 33	1.114	0.659	0.102
Expert 43	1.093	0.659	0.0000000189
Expert 48	1.076	0.968	0.485
Expert 03	1.074	0.659	0.179
Expert 07	1.083	0.659	0.182
Expert 10	0.665	0.659	0.018
Expert 17	1.093	0.659	0.0000000348
Expert 24	1.08	0.659	0.000361
Expert 25	1.092	0.659	0.000289
Expert 27	1.093	0.659	0.0000000243
Expert 32	1.093	0.659	0.00746
Expert 47	1.319	0.659	0.479
Expert 16	1.089	0.659	0.012
Expert 42	1.103	0.659	0.09
Expert 06	1.093	0.659	0.000000121
Expert 22	1.093	0.659	0.00000124
None	1.093	0.659	
Average discrepancy			0.0744

*PWDM, performance weighted decision maker.

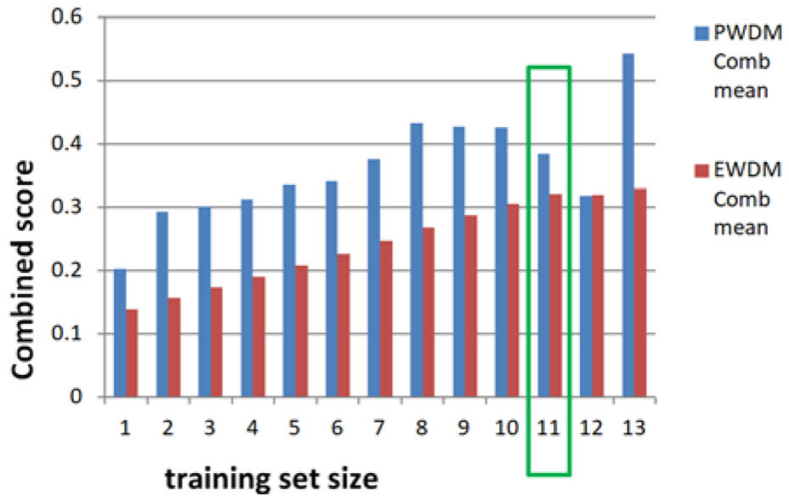
Appendix 5 Table 5. All experts statistical accuracy (p value), informativeness, and combined scores*

Expert	p value	Informativeness calibration variables	Combined score
Expert013	0.968	2.54	2.46
Expert019	0.569	2.57	1.47
Expert041	0.569	2.28	1.30
Expert048	0.569	2.27	1.29
Expert003	0.569	2.26	1.28
Expert050	0.569	1.72	0.981
Expert047	0.569	1.59	0.906
Expert028	0.321	2.19	0.701
Expert042	0.223	2.85	0.633
Expert007	0.243	2.39	0.580
Expert006	0.185	2.91	0.540
Expert033	0.243	2.20	0.533
Expert049	0.223	2.19	0.487
Expert035	0.144	2.65	0.380
Expert017	0.144	2.34	0.336
Expert030	0.0909	2.91	0.264
Expert005	0.0909	2.69	0.244
Expert026	0.0909	2.22	0.201
Expert039	0.0724	2.55	0.185
Expert016	0.0724	2.21	0.160
Expert012	0.0483	2.44	0.118
Expert040	0.0483	2.41	0.116
Expert032	0.0543	2.08	0.113
Expert014	0.0339	2.47	0.0836
Expert021	0.0334	2.46	0.0820
Expert029	0.0334	2.12	0.0709
Expert004	0.0135	2.64	0.0355
Expert020	0.0124	2.73	0.0340
Expert044	0.00984	2.92	0.0287
Expert015	0.00984	2.90	0.0285
Expert002	0.00984	2.59	0.0255
Expert045	0.0119	2.04	0.0243
Expert024	0.00984	2.47	0.0243
Expert025	0.00984	2.14	0.0211
Expert011	0.00678	2.93	0.0199
Expert022	0.00217	3.45	0.00748
Expert034	0.00220	2.60	0.00573
Expert043	0.00126	2.66	0.00335
Expert001	0.000720	2.63	0.00189
Expert037	0.000276	2.53	0.000696
Expert009	0.000157	2.54	0.000398
Expert027	0.000101	2.24	0.000228
Expert036	0.0000190	3.66	0.0000698
Expert046	0.0000123	2.30	0.0000283
Expert008	0.00000211	3.38	0.00000713
Expert018	0.000000738	3.96	0.00000292
Expert023	0.000000580	2.07	0.00000120
Expert010	0.000000638	1.80	0.00000115
PWDM	0.968	2.54	2.46
PWDM minus 15	0.659	1.97	1.30
PWDMNoOpt	0.250	1.42	0.356
EWDM	0.250	1.08	0.270

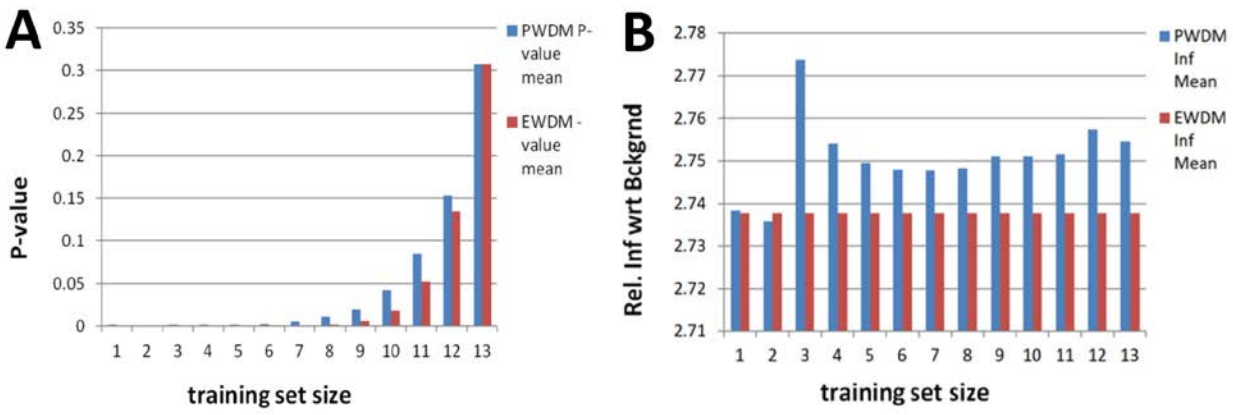
*EWDM, equally weighted decision maker; PWDM, performance weighted decision maker. PWDM is optimal performance weighted DM, using item weights. PWDM minus 15 is the result of removing the 15 experts with best statistical accuracy, shaded yellow. PWDMNoOpt is a performance-based DM, with no optimization. For EWDM, each expert receives equal weight.



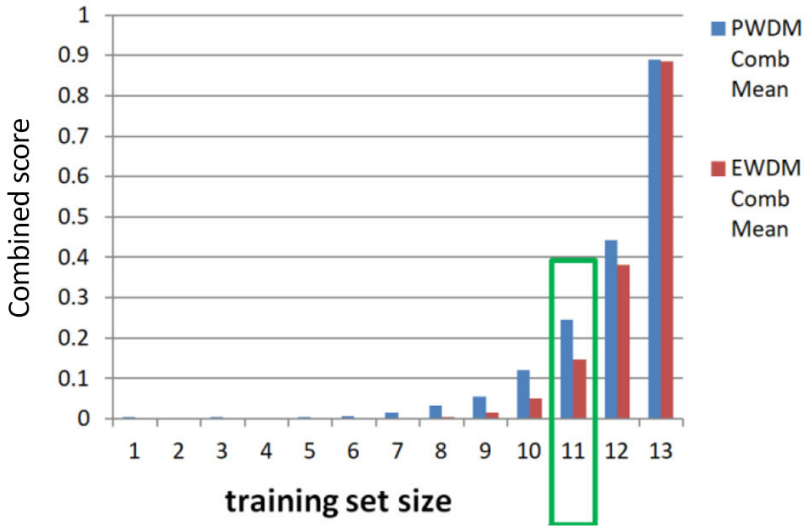
Appendix 5 Figure 1. A) Statistical accuracy and B) informativeness scores out of sample. EWDM, equally weighted decision maker; PWDM, performance weighted decision maker.



Appendix 5 Figure 2. Combined scores out of sample. Score for training set at 80% of calibration variables is highlighted. EWDM, equally weighted decision maker; PWDM, performance weighted decision maker.



Appendix 5 Figure 3. All experts, A) statistical accuracy and B) information scores out of sample. EWDM, equally weighted decision maker; PWDM, performance weighted decision maker.



Appendix 5 Figure 4. All experts combined scores out of sample. Score for training set at 80% of calibration variables is highlighted. EWDM, equally weighted decision maker; PWDM, performance weighted decision maker.