Citation (APA)
Wijnen, L. I., Nane, G. F., Benincà, E., Pijnacker, R., Franz, E., Cooke, R. M., & Mughini-Gras, L. (2026). Source attribution of foodborne pathogens in the Netherlands using structured expert elicitation. *International Journal of Food Microbiology*, *454*, Article 111735. https://doi.org/10.1016/j.ijfoodmicro.2026.111735

International Journal of Food Microbiology 454 (2026) 111735

Contents lists available at ScienceDirect

International Journal of Food Microbiology

journal homepage: www.elsevier.com/locate/ijfoodmicro

Source attribution of foodborne pathogens in the Netherlands using structured expert elicitation

Lena I. Wijnen [a,b], Gabriela F. Nane [c], Elisa Benincà [a], Roan Pijnacker [a], Eelco Franz [a], Roger M. Cooke [c,d], Lapo Mughini-Gras [a,b,*,**]

[a] Centre of Infectious Disease Control (Cib), National Institute for Public Health and the Environment (RIVM), Bilthoven, the Netherlands
[b] Institute for Risk Assessment Sciences (IRAS), Faculty of Veterinary Medicine, Utrecht University, Utrecht, the Netherlands
[c] Department of Applied Mathematics, Delft University of Technology, Delft, the Netherlands
[d] Resources for the Future, Washington, DC, USA

ARTICLE INFO

Keywords:
Foodborne pathogens
Source attribution
Kitchen door level approach
Transmission pathways
Food items
Structured expert judgment
Calibration questions

ABSTRACT

Foodborne pathogens represent a significant public health burden. Quantifying the relative importance of various potential sources of foodborne infection is challenging due to data scarcity and uncertainty in empirical studies. Structured expert judgment (SEJ) provides a valuable methodological alternative to gain insights into source attribution of foodborne pathogens. We conducted a SEJ study to attribute human cases of 26 foodborne pathogens in the Netherlands to seven major transmission pathways, 20 food groups, and two animal groups, in a typical post-COVID19 year, using Cooke's classical model. The elicitation process involved snowball recruitment, expertise self-assessment, and a workshop where experts answered calibration questions to capture their uncertainty as input for the model. Subsequently, experts completed the target questions to obtain attributable proportions at the 'kitchen door' level. Results indicated that transmission was predominantly (>50%) foodborne for *Staphylococcus aureus*, *Listeria monocytogenes*, *Yersinia* spp., *Bacillus cereus*, *Clostridium perfringens*, certain non-typhoidal *Salmonella* serotypes, *Campylobacter* spp., hepatitis E virus and *Toxoplasma gondii*, whereas person-to-person transmission was the primary pathway for astrovirus, rotavirus, norovirus, and sapovirus. *Brucella* spp. and typhoidal *Salmonella* were attributed primarily (>85%) to international travel. All other pathogens showed attributions of <50% to any individual pathway. Substantial differences were observed when dividing foodborne transmission into food groups. Key contributors included food handlers and vermin, various meats (e.g., pork, beef, chicken), and shellfish. These SEJ-derived estimates complement existing data by providing pathogen-specific insights in the Dutch context.

1. Introduction

Approximately 1 in 10 people worldwide were estimated to fall ill due to foodborne pathogens in 2010 (Havelaar et al., 2015). Although the associated public health burden is higher in low- and middle-income countries, foodborne diseases remain a significant concern in high-income countries as well (Havelaar et al., 2015; WHO, 2015). For example, in the Netherlands (population 17.6 million), approximately 1.8 million incident cases of foodborne diseases caused by 14 selected pathogens were estimated in 2023. These cases represent a substantial public health burden, corresponding to roughly 11,000 Disability-Adjusted Life Years (DALYs) and an economic cost of €538 million in 2023 (Benincà et al., 2024). For context, the burden of these 14 pathogens is comparable to that of influenza in the Netherlands, estimated at 10,900 DALY during the 2023/2024 respiratory infection season. This highlights the substantial contribution of foodborne infections to the national infectious disease burden (Bos et al., 2024).

Although various methods to estimate the burden of foodborne diseases are available, it remains challenging to uncover their true burden. Indeed, most people who fall ill do not seek medical care, meaning that

---

* Corresponding author at: National Institute for Public Health and the Environment (RIVM), Antonie van Leeuwenhoeklaan 9, 3721 MA, Bilthoven, the Netherlands.

** Corresponding author at: Institute for Risk Assessment Sciences (IRAS), Faculty of Veterinary Medicine, Utrecht University, Yalelaan 2, 3584 CL, Utrecht, the Netherlands.

E-mail addresses: lapo.mughini.gras@rivm.nl, l.mughinigras@uu.nl (L. Mughini-Gras).

https://doi.org/10.1016/j.ijfoodmicro.2026.111735
Received 20 January 2026; Received in revised form 11 March 2026; Accepted 13 March 2026

many cases are not captured by surveillance systems (Mead et al., 1999; Haagsma et al., 2013; Pires et al., 2021). Another challenge in fully understanding the burden of foodborne diseases is accurately attributing their sources. This challenge arises from the multifactorial nature of transmission pathways, the variability in source attribution methodologies, differences in incubation periods, and the constantly evolving epidemiology of foodborne pathogens. Failure to account for all relevant sources of infection can skew public health responses and policy decisions (Mughini-Gras et al., 2018a, 2019). An additional challenge lies in attributing the foodborne disease burden to specific food groups. This is due to the diversity of food products, potential for cross-contamination along the food production chain, and limited data on pathogen prevalence and diversity in different food categories (Hoffmann et al., 2017).

Source attribution is crucial for identifying where human infections are most likely to originate, guiding resource allocation for surveillance and control efforts, and assessing the effectiveness of these interventions (Havelaar et al., 2008; WHO, 2015). In absence of empirical data, or when data is overwhelming and evidence is conflicting, source attribution estimates derived from structured expert judgment (SEJ) offer a valid approach (Cooke, 1991). The Classical Model for SEJ is a widely used method that objectively validates experts' assessments of uncertainty and aggregates mathematically their distributions by employing performance-based weights. A SEJ study was conducted in the Netherlands (Havelaar et al., 2008). This study estimated the source attribution for 17 pathogens across 5 transmission pathways and 11 food groups within the foodborne transmission pathway. The study concluded that combining these estimates with other types of data, such as incidence of disease burden data, can provide insights in the public health impact of different foodborne pathogens.

Multiple SEJ studies have been performed worldwide for source attribution of foodborne diseases (Beshearse et al., 2021; Hoffmann et al., 2017; Sapp et al., 2022). A systematic review on this topic concluded that this approach is especially valuable for identifying knowledge gaps (Butler et al., 2015). In the Netherlands, the study of Havelaar et al. (2008) provides a solid foundation for SEJ-based source attribution of foodborne pathogens. However, it represents an epidemiological context from several years ago that may no longer reflect the current situation. In particular, the COVID-19 pandemic had a substantial impact on the epidemiology of foodborne pathogens (Lazarakou et al., 2024; Mughini-Gras et al., 2021b; Pijnacker et al., 2024) and led to long-lasting changes in Dutch society, such as reduced long-distance travel and the widespread adoption of regularly working from home (Faber et al., 2023). Therefore, we conducted a new SEJ study to update the current attribution estimates for foodborne pathogens in the Netherlands. We expanded our study to include additional pathogens and a broader range of potential food sources, and we employed calibration questions alongside the target questions. Calibration questions are a core component of the Classical Model, enabling the empirical validation of experts' uncertainty assessments. They have also been used in several recent studies (Beshearse et al., 2021; Hoffmann et al., 2017; Sapp et al., 2022), which facilitates comparison across studies.

The aim of this study was to estimate the proportions of human infections caused by 26 foodborne pathogens attributed to seven major transmission pathways, as well as to 20 food groups within the foodborne pathway and to two animal groups within the animal contact pathway.

2. Methods

For this SEJ study, a two-step process was followed. First, the proportion of all human cases caused by each pathogen (Table 1) was attributed to seven different transmission pathways (Table 2). Second, the proportion of foodborne cases was attributed to 20 food groups and the proportion of cases attributed to animal contact was further attributed to two animal groups (Table 3).

Table 1
Pathogens included in the present structured expert elicitation.

Bacteria	Viruses	Parasites
Brucella spp.	Astrovirus	*Giardia* spp.
Campylobacter spp.	Hepatitis A virus	*Toxoplasma gondii*
Listeria monocytogenes	Hepatitis E virus	*Cryptosporidium* spp.
Legionella spp.	Rotavirus	
Leptospira spp.	Norovirus	
Typhoidal *Salmonella*	Sapovirus	
Salmonella Enteritidis		
Salmonella Typhimurium		
Other non-typhoidal *Salmonella* serotypes		
STEC O157		
STEC non-O157		
Other pathogenic *E. coli*		
Yersinia spp.		
Vibrio spp.		
Bacillus cereus		
Clostridium perfringens		
Staphylococcus aureus		

The elicitation process consisted of three different steps: 1) preparation for the elicitation (pre-elicitation), 2) elicitation, and 3) post-elicitation (Fig. 1).

2.1. Pre-elicitation

2.1.1. Pathogens

For the selection of pathogens (hazards) we included all the pathogens from the previous Dutch SEJ (Havelaar et al., 2008), with the exception of *Mycobacterium avium* and enterovirus, as these could not be reliably attributed in that study. For *Escherichia coli*, next to Shiga toxin-producing *Escherichia coli* (STEC) serogroups O157 and non-O157, an extra hazard was added as 'other pathogenic *E. coli*'. Additionally, *Salmonella* spp. was split into typhoidal and non-typhoidal serotypes. The non-typhoidal *Salmonella* serotypes were further split into Enteritidis, Typhimurium, and other serotypes, as Enteritidis and Typhimurium together account for the largest proportion (~70%) of notified human salmonellosis cases in the Netherlands and other European countries (Teunis et al., 2025). Moreover, seven additional pathogens were included because estimating their attribution was of particular interest to the research team. This led to a total of 26 pathogens included in the present study (Table 1). Not all pathogens could be attributed to all exposure pathways, as some combinations are biologically implausible *a priori* (Havelaar et al., 2008). For example, *Legionella* cannot plausibly be attributed to the foodborne pathway, nor rotavirus to the animal contact pathway. Therefore, certain pathogen–pathway combinations were excluded by design (see Table 1 C.1, Appendix C).

2.1.2. Transmission pathways

We considered seven major transmission pathways: 1) food, 2) drinking water, 3) environmental water, 4) other environmental pathways, 5) animal-to-human (animal contact), 6) person-to-person, and 7) international travel. Additionally, foodborne transmission and animal contact were further subdivided into several food and animal groups, respectively (Tables 2 and 3). The definitions of the transmission pathways and groups therein followed the approach of Beshearse et al. (2021) and Havelaar et al. (2008), with some minor adaptations considering the different study setting. For pathways 1 to 6, the Netherlands was the country where transmission occurred (i.e., domestically-acquired cases), whereas pathway 7 referred generically to international travel to indicate that transmission occurred outside the Netherlands (i.e., travel-related or imported cases), without further specification as to where and how transmission occurred.

The foodborne transmission pathway was further divided into 20 food groups: 1) processed chicken meat, 2) non-processed chicken meat, 3) other poultry meat, 4) processed beef, 5) non-processed beef, 6)

Table 2
Major transmission pathways used for source attribution in the present structured expert elicitation.

Major transmission pathways	Description
Food	Foodborne transmission occurs through preparing and eating food. Contamination can originate anywhere in the food production chain, from primary production to retail. Transmission can occur at home or elsewhere (e.g., in a restaurant). Transmission occurs through food that is contaminated before it enters the kitchen, i.e., attribution at the "kitchen door" level, thereby excluding cross-contamination from other products or the environment in the kitchen. This pathway also includes contamination during preparation by food-handlers or vermin/pests, which introduced the pathogen into the kitchen. The foodborne pathway applies also to all non-water beverages and items ingested as food (e.g., milk, juices, candies, etc. but excluding items consumed for medicinal purposes). This pathway refers to transmission occurring in the Netherlands (i.e., domestically acquired infections).
Drinking water	Transmission occurs through the consumption of drinking water. This includes drinking tap or bottled water. Transmission occurs through water that is contaminated when it enters the kitchen (or comes out of the tap), i.e., attribution at the 'kitchen door' level. Water that is used primarily for drinking but also for other domestic uses, such as washing or showering, can originate from a public water system, a private well, or commercially bottled sources. This pathway refers to transmission occurring in the Netherlands (i.e., domestically acquired infections).
Environmental water	Water that is used for recreational activities, such as a swimming pool or a natural body of water (e.g., a lake or canal). It can be treated or untreated. Treated water has undergone a purification process (e.g., through chlorination or filtration) with the goal of controlling microbiologic quality (e.g., swimming pool), whereas untreated water has not undergone such process (e.g., natural ponds). Transmission occurs through direct exposure to this water source (e.g., through swimming, splashing). This also includes contact with water where infected animals live. This pathway refers to transmission occurring in the Netherlands (i.e., domestically acquired infections).
Other environmental pathways	Transmission occurs through exposure to the natural and man-made environment via exposure to contaminated air, mud, soil, or other outdoor or indoor surfaces or objects (fomites), but excluding water itself, so not attributable to the other transmission routes as defined in this study. It also includes exposure to the environment where infected animals live. This pathway refers to transmission occurring in the Netherlands (i.e., domestically acquired infections).
Animal-to-human (animal contact)	Transmission occurs through direct contact with a live animal, its bodily fluids (excluding those consumed as food like milk), excreta, fur, hair, feathers, scales or skin. This pathway includes companion animals, farm animals, and wildlife. This pathway refers to transmission occurring in the Netherlands (i.e., domestically acquired infections).
Person-to-Person	Transmission occurs by direct contact with infected persons or their bodily fluids and excreta (e.g., fecal-oral route), or by contact with the living environment where the exposed person is simultaneously present with the infected person or visible fluids/excreta. This pathway refers to transmission occurring in the Netherlands (i.e., domestically acquired infections).
International travel	Transmission has occurred abroad (i.e., anywhere outside the Netherlands), regardless of the specific transmission pathway involved, so it includes all transmission pathways mentioned above in cases where transmission occurred in another country than the Netherlands (i.e., travel-related or imported infections). Travel-related transmission is therefore excluded from the other transmission pathways. International travel is not specified into more detail or one or more of the above.

processed pork, 7) non-processed pork, 8) veal calf meat, 9) sheep meat, 10) goat meat, 11) other meats, 12) eggs, 13) dairy products, 14) shellfish, 15) fish and crustaceans, 16) fruit, 17) vegetables, 18) grains, cereals, pasta, bread and other bakery products, 19) food handler and vermin, and 20) other foods. The animal contact pathway was further divided into 1) pets and 2) livestock and wildlife (Table 3). Following Havelaar et al. (2008), the point of attribution was the so-called 'kitchen door', which considers the source of human infection to be the vehicle that was already contaminated with the pathogen when it entered the kitchen, i.e., the food that brought the pathogen to the place of preparation before consumption. Therefore, cross-contamination from other food products or the environment occurring within the kitchen was not considered (e.g., if raw chicken meat contaminated a vegetable salad during preparation in the kitchen and this led to human infection, the resulting case had to be attributed to the chicken meat and not to the salad). Food contaminated by infected people (e.g., food handler) or animals (e.g., vermin) during preparation was considered a separate category, as in this case the vehicle bringing the pathogen to the kitchen was not a food item, but a person or a pest (Havelaar et al., 2008).

All transmission pathways and subgroups therein were mutually exclusive, with their attributions adding to 100%.

2.1.3. *Experts*

The research team identified an initial group of 74 national experts in different topics of food safety, mainly microbiology, epidemiology and food science, working in different Dutch organizations, defined as academic or public bodies (i.e., public health services, veterinary inspectorates, national competent authorities, ministries, universities, colleges, and research institutes). Experts working in commercial organizations (e.g., industry, food business operators, consultancy bureaus, etc.) were excluded to avoid potential conflicts of interests. The same applied to some experts at the Netherlands Food and Consumer Product Safety Authority (NVWA) that were directly involved in the funding of this study, to maintain independence of the study outputs from the funders. Some experts had a broad perspective on food safety, whereas others had studied specific foods or pathogens for an extended period, developing a deeper and more specialized knowledge.

Experts were formally invited to participate via email. To broaden the expert pool, snowball sampling was applied, allowing the experts to refer additional experts from their professional networks. The invitation email contained an information letter and a link to an initial online survey. This survey aimed to assess the availability of the relevant expertise for the elicitation and included self-assessment questions in which experts rated their knowledge level for each of the 26 pathogens. The knowledge level was expressed on a 5-level Likert scale (no knowledge, basic knowledge, average knowledge, good knowledge, and excellent knowledge). Experts who indicated a good to excellent knowledge for a given pathogen were included in the elicitation of that pathogen. After enrolment, the experts received an information package with background material about the study (i.e., a detailed summary of the principles of source attribution, as applied to this study, and the relevant data) and an agenda for the meeting. A total of 45 experts were initially enrolled in the study; however, two withdrew due to unforeseen circumstances, resulting in 43 participating experts (see Section 2.2).

2.1.4. *Elicitation method*

The method used here was the Classical Model for SEJ, or Cooke's method (Cooke et al., 1988; Cooke and Goossens, 2008). This is a mathematical model that aggregates experts' uncertainty assessments for quantities of interest, referred to as target variables or questions of interest, in a calibrated manner. The model is calibrated using calibration questions (see Section 2.1.5), while experts provide their assessments using target questions (see Section 2.1.6).

Experts are asked to quantify their uncertainty regarding quantities of interest with respect to a best estimate's (50th percentile), lower uncertain bound (5th percentile) and upper uncertain bound (95th

Table 3
Sub-groups used in the present structured expert elicitation for source attribution within the foodborne transmission pathway and within the animal contact transmission pathway.

Subgroups for foodborne transmission	Description
Processed chicken meat	Any chicken meat that has been modified/transformed in order to either improve its taste and/or to extend its shelf life (through salting, curing, fermentation, heating or smoking), e.g., chicken sausages, chicken nuggets, smoked chicken, cold meats, etc. Processed meat does not include processes that change fresh meat through simple mechanical processes only, such as cutting, grinding or mixing. Cooked chicken meat is also considered processed.
Non-processed chicken meat	Fresh chicken meat, i.e., any chicken meat that has ***not*** been modified/transformed in order to either improve its taste and/or to extend its shelf life as described above (only simple mechanical processes, such as cutting, grinding or mixing are allowed), e.g., whole-chicken carcass, chicken breast, drumsticks, minced chicken meat, etc.
Other poultry meat	Includes duck, goose, ostrich and turkey, both processed and unprocessed meat.
Processed beef	Any beef that has been modified/transformed in order to either improve its taste and/or extend its shelf life (through salting, curing, fermentation, heating or smoking), e.g., beef sausages, corned beef, cold meats, etc. Cooked beef is also considered processed.
Non-processed beef	Fresh beef, i.e., any beef that has ***not*** been modified/transformed in order to either improve its taste and/or to extend its shelf life as described above (only simple mechanical processes, such as cutting, grinding or mixing are allowed), e.g., sirloin steak, filet mignon, filet Americain, steak tartare, hamburgers, etc.
Processed pork	Any pork that has been modified/transformed in order to either improve its taste and/or to extend its shelf life (through salting, curing, fermentation, heating or smoking), e.g., pork sausages, bacon, ham, salami, cold meat, etc. Cooked pork is also considered processed.
Non-processed pork	Fresh pork, i.e., any beef that has ***not*** been modified/transformed in order to either improve its taste and/or to extend its shelf life as described above (only simple mechanical processes, such as cutting, grinding or mixing are allowed), e.g. pork tenderloin, pork chops, pork ribs, minced pork, etc.
Veal calf meat	Includes both processed and non-processed veal calf meat.
Sheep meat	Includes both processed and non-processed sheep meat.
Goat meat	Includes both processed and non-processed goat meat.
Other meats	Includes deer, wild boar, rabbit, hare, exotic animal meat like kangaroo, alligator, etc.
Eggs	Eggs of all kinds of poultry.
Dairy products	Milk, cheese, butter, cream, etc. both raw and pasteurized products are included.
Shellfish	E.g., mussels, oysters, clams, scallops, etc.
Fish and crustaceans	Fish of all kinds, and crustaceans like lobster, shrimp, crabs, etc.
Fruit	Includes (mixtures of) fresh fruit that are consumed raw or cooked. Includes also fruit juices and fruit smoothies (non-dairy).
Vegetables	Includes (mixtures of) fresh vegetables that are consumed raw or cooked. Includes vegetable juices, vegetable smoothie (non-dairy).
Grains, cereals, pasta, bread and other bakery products	E.g., rice, bread, pasta, noodles, muffins, etc.
Food handler and vermin	A food handler is any person who has direct contact with food in different phases (e.g., food preparation, packaging, storage, sale, transport, etc.). When a food handler is the source of contamination of the food that is being prepared, it means that the person itself brought the pathogen into the kitchen. This also applies to vermin (e.g., mice, rats, insects) bringing pathogens into the kitchen and contaminating the food that is there.
Other foods	E.g., chocolates, candies, complex and ultra-processed foods, dietary supplements, alcohol and soda beverages, etc.

Subgroups for animal contact	Description
Pets/companion animals	Includes small animals (dogs, cats, rabbits, hamsters, etc.), horses, and amphibians and reptiles kept as pets/companion animals in the Netherlands.
Livestock and wildlife	Includes domesticated animals raised in in the Netherlands to provide labor and produce diversified products for consumption, such as meat, eggs, milk, honey, fish, fur, leather, wool, etc. It also includes wild animals.

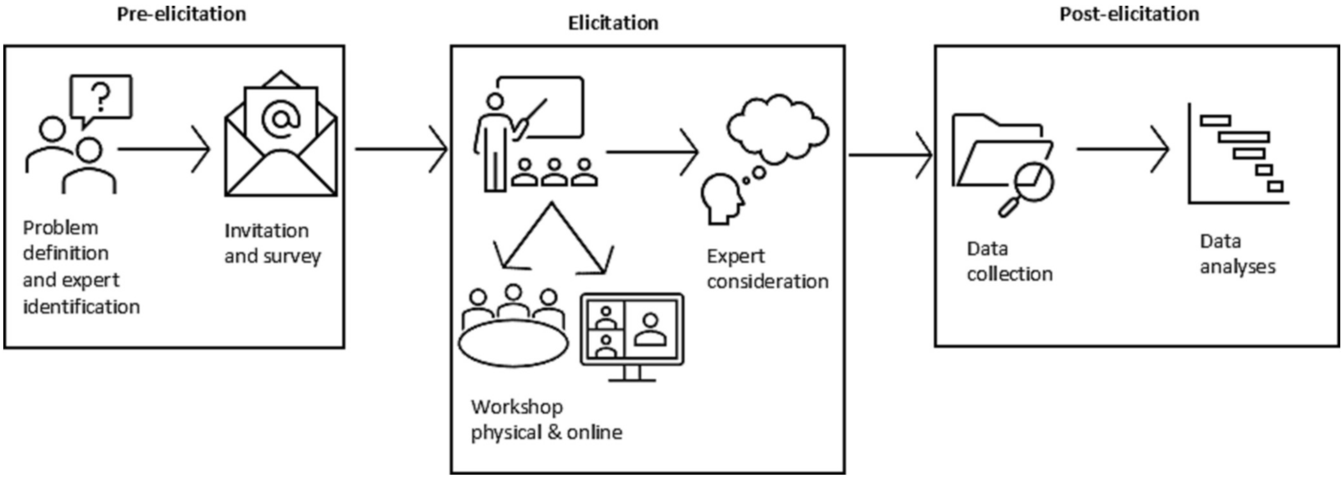

Fig. 1. Schematic description of the expert elicitation process.

percentile). Distribution functions are constructed for all questions, where the support is obtained from all experts' assessments. The interval defined by the minimum of the elicited 5th percentiles and the maximum of the 95th percentiles is then extended by an overshoot, typically chosen to be 10% of the interval's width. The resulting support of the distribution is preserved when aggregating experts' distributions.

Expert's uncertainty assessments for calibration questions are used to determine weights, referred to as performance-based weights. The weights are obtained from a calibration and an information score. The calibration score accounts for the statistical accuracy of the uncertainty assessments, that is, if the intervals defined by experts' percentiles capture the realizations (i.e., the answers to the calibration questions) at the expected frequencies. Statistical accuracy measures the expert's ability to choose these percentiles such that, statistically speaking, 90% of the realizations fall within the 90% band and 50% of the realizations fall below the median. The information score measures the expert's ability to give narrow uncertainty bands and is obtained by averaging the information score of each calibration question (Cooke et al., 2021; Cooke, 1991).

The calibration and information scores yield a combined score, which is the product of the two scores. The normalized combined scores yield performance-based weights. Experts' uncertain distributions are aggregated using the performance-based weights into a Performance-Weight Decision Maker (PWDM). When the information score of each distinct question is considered, the resulting decision maker is called Item-Weight Decision Maker (IWDM). The resulting distribution is subject to the same validation approach as individual assessments and calibration and information scores are calculated for the resulted PWDMs and IWDMs. The scores reflect how statistically accurate and informative the assessments resulting from aggregated distributions are. With this respect, it is investigated whether excluding experts' assessments results in DMs with improved performance in quantifying uncertainty (combined score). Experts' assessments are excluded successively and the performance of the resulted DMs compared. The DMs with the highest combined scored yields an optimized decision maker. Within the Classical Model, an optimized PWDM (PWDM_opt) and an optimized IWDM (IWDM_opt) are considered along with their non-optimized versions. Finally, experts' distributions are also aggregated using equal weights, which gives an Equal Weight Decision Maker (EWDM). The performance of all decision makers is compared and the decision maker with the highest performance is chosen. Further methodological and theoretical details of the Classical Model are reported elsewhere (Cooke et al., 2021; Cooke, 1991; Hanea, 2021).

2.1.5. *Calibration questions*

The calibration questions are relevant to the topic under study and enable the calibration of the mathematical model used to aggregate experts' uncertain assessments. Calibration is obtained by evaluating experts' assessments using calibration and information scores. Therefore, the calibration questions must have answers known to the study team (*post-hoc*), but unknown to the experts during the elicitation (Cooke and Goossens, 2008).

Fifteen calibration questions were developed based on unpublished data at the moment of the elicitation from five widely consulted annual reports on foodborne pathogens, infectious diseases and antimicrobial resistance (in humans, animals and food) in the Netherlands (Appendix A). The calibration questions were thus true predictions and the most desirable type of calibration questions (Hanea, 2021). The questions required numeric answers and handled different pathogens and a wide range of topics, covering the main knowledge domains of the SEJ study. All experts provided assessments for the same fifteen calibration questions.

2.1.6. *Target questions*

The target questions aimed to estimate the proportions of cases attributed to the transmission pathways and food groups therein, by asking the experts to provide, according to their subjective belief, a lower, medium and upper uncertainty bound corresponding statistically to the 5th, 50th (median) and 95th percentiles. Eliciting percentile estimates from experts not only enables them to explicitly express their uncertainty, but also helps reduce respondent fatigue, thereby facilitating the assessment of a larger number of pathogens per expert (Havelaar et al., 2008). Experts provided attribution estimates for the seven major transmission pathways, 20 food groups within the foodborne pathway, and two animal groups within the animal contact pathway, for each pathogen separately (Appendix B).

These estimates were expressed in percentage for a “typical post-COVID19 year” in the Netherlands. Indeed, during the COVID19 pandemic, several diseases, including foodborne infections, dropped significantly as a consequence of the measures implemented (e.g., distancing, closure of dine-in restaurants, ban on gatherings, travel restrictions, etc.), as well as improved hygiene and altered diagnostic procedures and healthcare-seeking behaviours (Van Deursen et al., 2022; Lazarakou et al., 2024; Nielsen et al., 2022; Pijnacker et al., 2024). Although the COVID19 pandemic has passed and most diseases have resumed their typical epidemiological patterns, it has induced long-lasting changes in society (e.g., less frequent long-distance traveling, increased hand hygiene, widespread work/study-from-home, online gathering, etc.) (Faber et al., 2023), which could influence, to varying extent, the epidemiology of the pathogens included. Therefore, experts were asked to consider these changes in their assessments.

As mentioned in 2.1.1, some pathogen pathway or combinations were blocked *a priori* because they are considered biologically implausible (Table C.1, Appendix C). For modelling purposes, very small values were pre-filled for those blocked pathways (10^{-8}, 10^{-6} and 10^{-4}). Experts were given the opportunity to update these assessments if they disagreed with the blocked pathways. A rationale text box was available for the experts to explain their motivation for particular assessments.

2.2. *Elicitation*

All 45 enrolled experts were invited to a hybrid-format workshop held at the Dutch National Institute for Public Health and the Environment (RIVM) on 19 September 2023; a total of 28 experts attended, of which 14 physically and 14 online. During the workshop, experts were presented with detailed information about the study and the SEJ method, and they had the opportunity to ask clarifying questions. The workshop was recorded. While experts were requested to complete the calibration questions during the workshop, they could complete the target questions within two weeks after the workshop. Moreover, for the calibration questions, the experts could not consult any resource, whereas for the target questions they were encouraged to do so. A background document with various relevant resources was also prepared by the study team. The background document included the previous elicitation study (Havelaar et al., 2008), reports on recent foodborne outbreaks, surveillance data on foodborne pathogens, figures on zoonoses in humans and animals, antimicrobial resistance, disease burden of food-related pathogens, and other relevant literature for the Netherlands. Resources for specific pathogens were also listed.

For the 17 experts who could not attend the workshop, 10 separate online meetings (with 1 to 3 experts at a time) were organized. During these meetings, the experts were guided through the presentations of the workshop, which were shared beforehand along with the workshop recording, so that they could ask for clarifications during the meeting. Experts were then asked to complete the calibration questions. Also these experts provided their assessments within two weeks from the online meeting. The online meetings took place from 22 September 2023 to 10 October 2023. Two experts did not complete the elicitation after the workshop (one physically and one online). From all other 43 experts, we received the informed consent and both calibration and target questions.

There were too few expert assessments for three pathogens (*Staphylococcus aureus, Clostridium perfringens*, and astrovirus). For these pathogens, therefore, an active recruitment took place, for which the initial survey was investigated and the average reported knowledge of experts was compared to their publications and research projects, in order to evaluate if experts' knowledge was desired for the elicitation of the considered pathogens. In most cases, this was applicable, and these experts were then asked to provide assessments for these additional pathogens too. The number of experts who provided assessments for each pathogen is presented in Table C.2 (Appendix C).

2.3. Post-elicitation

2.3.1. Data analysis

With a Macro, the Excel files used to collect the assessments were converted into dtt files, the format required by the Delft University of Technology's software EXCALIBUR. EXCALIBUR is a graphical user interface software that is often used to analyse expert judgment data within the Classical Model. The dtt files of individual experts were merged per pathogen, and EXCALIBUR was employed separately for each pathogen. The various DMs were evaluated with respect to their combined scores and the best performing one was selected for the aggregation of experts' distributions.

The resulting aggregated distributions, for major transmission pathways and food/animal groups, were further subjected to a normalization procedure, which was adapted from Hald et al. (2016). The procedure ensures that the resulting mean estimates for major pathways sum to 100%, as required by the mutual exclusive assumption. Similarly, the sum of the resulting mean estimates of food groups sum to 100%, and the same holds for the mean estimates of animal groups.

3. Results

3.1. Experts per pathogen

Of the 43 experts answering both calibration and target questions, two experts assessed one pathogen, while all other experts assessed more than one pathogen. The assessed pathogens per expert ranged from 1 to 18, with an average of 6 pathogens. Of the 26 pathogens included, *Campylobacter* spp. was the most assessed one ($n = 22$ experts). *Vibrio* spp. and *Yersinia* spp. were assessed by the lowest number of experts (4 experts each). For all 26 pathogens, there was sufficient data to provide interpretable results (Table C.2). The calibration questions yielded informative and sufficiently statistical accurate assessments. That is, the aggregation of expert' uncertainty distributions using performance-based weights led to aggregated models that were both highly informative and statistically accurate. Additionally, the information scores were checked for differences in way of eliciting (physical or online during the workshop or individually/with others on another date). There were no effects found.

3.2. Transmission pathways

3.2.1. Bacteria

Most pathogens included in this study were bacteria (17/26). Of these bacterial pathogens, seven were predominantly attributed (>50%) to the foodborne transmission pathway. These pathogens were *Staphylococcus aureus* (77.37%), *Listeria monocytogenes* (76.51%), *Yersinia* spp. (74.74%), *Bacillus cereus* (73.27%), *Clostridium perfringens* (70.36%), other non-typhoidal *Salmonella* serotypes (65.4%), and *Campylobacter* spp. (53.43%). Furthermore, there were five bacterial pathogens that had an estimated attribution to the foodborne pathway of <50%, although the foodborne pathway still had the highest estimated attribution among all major transmission pathways. These pathogens were STEC O157 (48.91%), STEC non-O157 (48.82%), *Salmonella* Enteritidis (44.07%), *Salmonella* Typhimurium (43.77%), and *Vibrio* spp. (30.98%). For *Vibrio* spp., there were two other major pathways with >20% estimated attribution, namely environmental water (25.59%) and international travel (23.61%). *Brucella* spp. and typhoidal *Salmonella* had an estimated attribution above 50% for the international travel pathway (97.77% and 86.12%, respectively). There were three other bacterial pathogens for which international travel was the main pathway. These were *Legionella* spp. (33.25%), which had environmental water (26.81%) and drinking water (22.64%) as the other two major pathways, other pathogenic *E. coli* (30.49%), for which the foodborne pathway was 28.27%, and *Leptospira* spp. (48.06%), which had 42.51% of cases attributed to environmental water (Fig. 2 and Table C.2).

3.2.2. Viruses

Of the six viruses included in the study, Hepatitis E virus (HEV) had the highest attribution to foodborne transmission (66.37%). For astrovirus, rotavirus, norovirus, and sapovirus, the primary transmission pathway was person-to-person (>72%). Hepatitis A virus (HAV) did not have a single pathway attributed over 50%, but two pathways were equally important: person-to-person (34.2%) and international travel (33.92%) (Fig. 2 and Table C.2).

3.2.3. Parasites

Toxoplasma gondii was mostly attributed to foodborne transmission (66.06%). Neither *Giardia* spp. nor *Cryptosporidium* spp. had a single pathway with an estimated attribution greater than 50%. *Giardia* spp. had the highest estimated attribution to person-to-person transmission (29.8%), followed by international travel (25.64%). For *Cryptosporidium* spp., the highest proportion of cases was attributed to international travel (23.61%), but other pathways also had notable attributions: animal contact (16.94%), foodborne (16.83%), person-to-person (15.49%), and environmental water (14.76%) (Fig. 2 and Table C.2).

3.2.4. Travel-related cases

International travel was included as one of the major transmission pathways for all pathogens. This category encompasses all infections acquired abroad, without distinguishing the specific origin or route of transmission. While international travel is included in the overall estimates, the attributions could differ if the exact pathways were known. For example, many travel-related *Salmonella* infections are also foodborne. If these cases were included under foodborne transmission, the estimated contribution of this route to *Salmonella* infections would exceed 70%. An overview of attribution estimates for domestically-acquired cases (i.e., excluding international travel) across the main transmission routes is provided in Table C.3.

On average, the highest uncertainty was observed for foodborne transmission and international travel as pathways. This pattern was consistent across bacteria, viruses and parasites alike. Nevertheless, variation was observed within individual pathogens, with *Toxoplasma gondii*, HEV, and *Bacillus cereus* showing the highest levels of uncertainty in attribution to foodborne transmission.

3.3. Food groups

3.3.1. Bacteria

Among the 17 bacteria included in the study, *Legionella* spp. was the only one for which the foodborne transmission pathway was blocked *a priori*. Among the remaining 16 bacteria, *Brucella* spp. was the only pathogen with estimated attributions to only four different food groups: dairy products (64.59%), goat meat (17.81%), sheep meat (14.86%), and other foods (2.7%).

In addition to dairy products for *Brucella* spp., there were two other food groups with an estimated attribution of >50%: eggs for *Salmonella* Enteritidis (70.85%) and food handler and vermin for typhoidal *Salmonella* (58.66%). The food handler and vermin category also had the highest attribution for *Leptospira* spp. (29.7%) and *Staphylococcus aureus* (20.75%). For *Leptospira* spp., fruit (20.41%) and vegetables (19.64%) had an attribution exceeding 10%. Additionally, food handler and vermin were the highest attributed source for other pathogenic *E. coli* (15.92%), but there were also three other important sources for this pathogen: non-processed beef (12.16%), non-processed pork (12%), and veal calf meat (11.7%).

A pathogen with the highest attributions across various meat categories was *Salmonella* Typhimurium, for which non-processed pork had

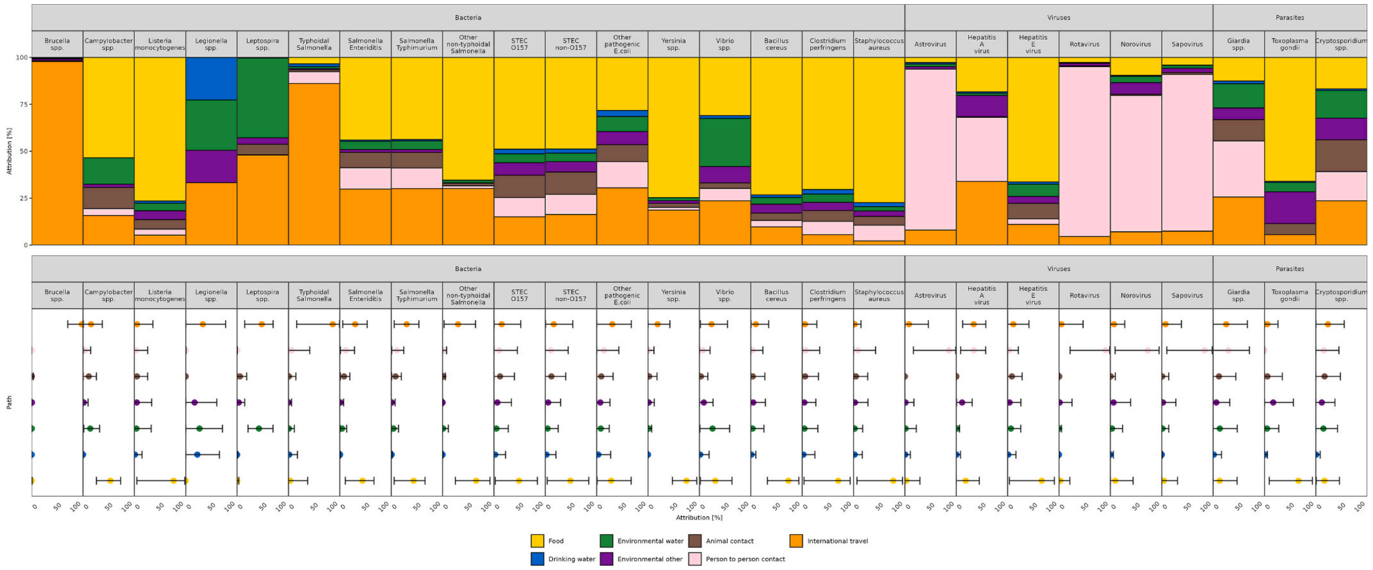

Fig. 2. The percentage-based source attribution, with a stacked bar plot illustrating the percentages per major transmission pathways and a dot plot summarizing including their 95% confidence intervals.

an estimated attribution of 44.9%, followed by processed pork (23.05%). Non-processed pork was also the second-highest attribution for *Yersinia* spp. (16.65%), with the highest attribution being 38.11% for processed pork.

Non-processed beef was the highest attributed source for both STEC non-O157 (24.79%) and STEC O157 (24.29%). Non-processed chicken meat was the highest attributed source for *Campylobacter* spp. (30.63%), but there were two other important food sources (>10%): non-processed beef (16.2%) and other poultry meat (15.28%). For other non-typhoidal *Salmonella* serovars, non-processed chicken meat also had the highest estimated attribution (14.02%). In contrast, processed chicken meat was the highest attributed source for *Clostridium perfringens* (11.25%), with processed beef following closely (10.56%), and all other estimates being <10%.

Fish and crustaceans were considered the most important source of exposure for *Vibrio* spp. (33.65%), followed by shellfish (28.73%). The fish and crustacean's category was also the most attributed source for *Listeria monocytogenes* (13.01%). *Bacillus cereus* had the highest attributions for grains, cereals, pasta, bread, and other bakery products (27.65%). More detailed results are in Fig. 3, and Tables C.4.1 and C.4.2.

3.3.2. Viruses

Among the viral pathogens, rotavirus, astrovirus, sapovirus and norovirus had the highest attributions to food handler and vermin within the foodborne transmission pathway, with 74.74%, 69.45%, 68.13% and 53.5%, respectively. Another category with attribution estimates >10% was shellfish, with attributions of 18.92%, 11.57%, 11.26% and 10.29% for HAV, sapovirus, astrovirus, and norovirus, respectively. For HAV, shellfish ranked third, after fruit (38.68%) and food handler and vermin (21.04%). HEV was predominantly attributed to processed pork (47.43%) and non-processed pork (24.92%). More detailed results are in Fig. 3, and Table C.4.3.

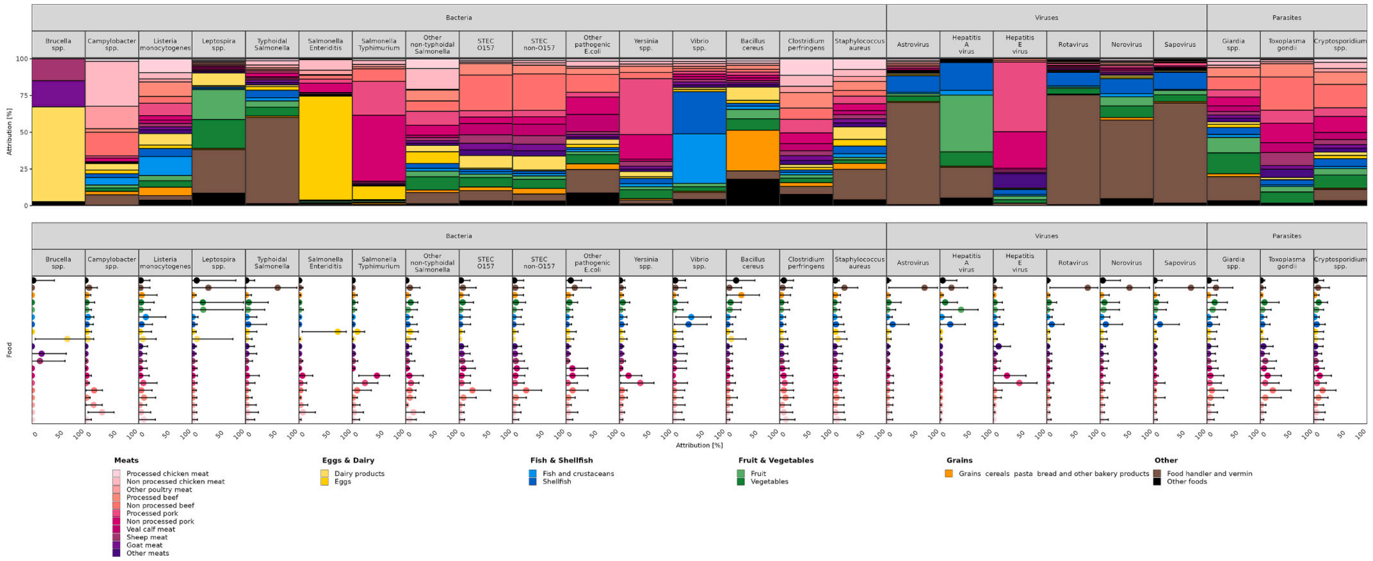

Fig. 3. The percentage-based source attribution for each pathogen, with a stacked bar plot illustrating the percentages per food item and a dot plot summarizing including their 95% confidence intervals.

3.3.3. Parasites

Both *Toxoplasma gondii* and *Cryptosporidium* spp. had the same two food groups within the foodborne transmission pathway with estimated attributions >10%: non-processed beef (22.59% and 16.01%) and non-processed pork (13.26% and 10.85%). For *Giardia* spp., three categories had attributions >10%: food handler and vermin (16.5%), vegetables (14.16%), and fruit (10.48%). See more details in Fig. 3 and Table C.4.4.

3.4. Animal contact

3.4.1. Bacteria

In total, 16 pathogens were included in the animal contact pathway, with *Legionella* spp. being blocked *a priori*. Nine bacteria were mainly attributed to the livestock and wildlife category: *Listeria monocytogenes* (80.4%), *STEC O157* (77.3%), *Yersinia* spp. (74.05%), *Bacillus cereus* (71.2%), *STEC non-O157* (70.6%), *Leptospira* spp. (65.12%), other pathogenic *E. coli* (64%), *Staphylococcus aureus* (54.8%), and other non-typhoidal *Salmonella* (50%). The other 7 bacteria were mainly attributed to pets/companion animals: *Campylobacter* spp. (94.5%), *Salmonella* Typhimurium (94%), *Salmonella* Enteritidis (94.2%), *Brucella* spp. (70.2%), *Clostridium perfringens* (63.1%), *Vibrio* spp. (51.9%), and typhoidal *Salmonella* (50.9%) (Table C.5).

3.4.2. Viruses

For all viruses except HEV, the animal contact transmission pathway was blocked *a priori*. Although the pathways were blocked, the experts could still estimate the attribution if they thought this exposure route was a possibility. These attributions were small, ranging from 0.01% to 0.88%, and were not further specified within the animal contact pathway. For HEV, the main attribution was estimated to be within the livestock and wildlife category, with an attribution of 90.3% (Table C.5).

3.4.3. Parasites

Cryptosporidium spp. and *Giardia* spp. were mainly attributed to the livestock and wildlife category, with attributions of 85.16% and 56.81%, respectively. In contrast, *Toxoplasma gondii* had its main attribution to pets/companion animals (63.96%) (Table C.5).

Uncertainty varied substantially across food groups (Fig. 3). For parasites, the highest average uncertainty was observed for non-processed beef, followed by food handler and vermin. For viruses, estimates for shellfish and vegetables showed, on average, the highest uncertainty. Bacterial pathogens exhibited broadly similar levels of uncertainty across food groups. Nevertheless, variability was observed within each food group, with the highest levels of uncertainty associated with food handler and vermin, as well as dairy.

4. Discussion

We conducted a SEJ study in the Netherlands to estimate the proportions of human cases attributed to seven major transmission pathways for 26 pathogens. Additionally, we assessed the contribution of 20 specific food groups within the foodborne pathway and two subgroups within the animal contact pathway. This study builds upon and further elaborates the work of Havelaar et al. (2008). A comparison of the main transmission pathways for the pathogens included in both studies shows that in both studies infection with *Campylobacter* spp., *Listeria monocytogenes*, certain non-typhoidal *Salmonella* serotypes, *Bacillus cereus*, *Staphylococcus aureus*, *Clostridium perfringens*, HEV and *Toxoplasma gondii* is predominantly attributed to foodborne transmission, while norovirus and rotavirus were mainly (>50%) attributed to person-to-person transmission.

Campylobacter spp. was identified by previous studies as being mainly a foodborne pathogen (Mughini Gras et al., 2012; Mulder et al., 2024). However, source attribution studies of human campylobacteriosis based on meta-analytical modelling approaches have shown less distinct differences between transmission pathways like food consumption, environmental exposure, and animal contact, with food- and waterborne routes together accounting for only about half of all cases (Mughini-Gras et al., 2022). Similar to these studies, the present study also identified traveling as an important transmission route for campylobacteriosis. While travel is not a source of infection *per se*, it encompasses a range of potential risk exposures, such as food, the environment, etc., which may all contribute to infection. Since these exposures occur outside national borders, the associated transmission pathways are more difficult to manage. While we could not identify specific risk factors involved in transmission during travel, risk factors for travel-related campylobacteriosis among Dutch travellers traveling outside Western Europe, consuming chicken meat and eating vegetable salads, among others, are known (Mughini-Gras et al., 2014b). Environmental exposures, such as swimming in surface water, as well as contact with animals, have been associated with increased campylobacteriosis risk (Mughini Gras et al., 2012, 2021a). A Dutch source attribution study based on whole-genome sequencing (WGS) data attributed 11% of human campylobacteriosis cases to surface water (Mughini-Gras et al., 2021a). This is of the same order of magnitude as the attributions in our study, where environmental water was estimated to account for approximately 14% of cases. In contrast, Mulder et al. (2024) concluded that residing in livestock-dense areas in the Netherlands is not a consistently significant, spatially confined risk factor for acquiring campylobacteriosis, thereby reinforcing the view that human infections are predominantly foodborne (Mulder et al., 2024). While surface water plays a key role in the spread of *Campylobacter* (Mughini-Gras et al., 2016; Mulder et al., 2020), it is not a true reservoir itself, but rather serves as a proxy for various animal reservoirs (Dingle et al., 2001; Kärenlampi et al., 2007; Mughini Gras et al., 2012; Mullner et al., 2009a; Mullner et al., 2009b; Strachan et al., 2009).

WGS-based attribution analysis estimated that 48.2% of campylobacteriosis cases originate from meat-producing poultry (Mughini-Gras et al., 2021a). Similarly, our food group estimates show that all chicken/poultry meat-related exposures combined accounted for 47.6% of cases. In the ranking of food groups in the present study, non-processed beef ranked next, contributing 16.2%, which is similar to the 12.1% contribution of adult cattle reported in the WGS-based study (Mughini-Gras et al., 2021a). That same study reported an attribution of 18% of campylobacteriosis cases to non-food producing animals, such as pet dogs and cats. Our results indicate 11% of cases being attributable to animals, with pets as the main animal group. While the role of pets/companion animals in *Campylobacter* epidemiology remains largely unknown, previous studies have identified owning dogs, particularly puppies, as a risk factor for human campylobacteriosis (Mughini Gras et al., 2012, 2013, 2021a).

Listeria monocytogenes is known to survive and grow in different environments, such as the food production environment, even at refrigeration temperatures (Gandhi and Chikindas, 2007). Attribution estimates based on meta-analytical approaches show that cases of *L. monocytogenes* in the Netherlands are mainly attributable to food (78.8%), followed by travel (7.3%) and the environment (5.2%) (Mughini-Gras et al., 2022). These estimates are similar to the ones of the present study where *L. monocytogenes* was mainly attributed to foodborne transmission (76.5%) and travel (5.3%). Within the foodborne transmission pathway, 13% of listeriosis cases were attributed here to fish and crustaceans. This is a similar estimate as in a recent WGS-based source attribution study of human listeriosis in the Netherlands, where 16.9% of cases were attributed to seafood (Mughini-Gras et al., 2025). However, the importance of cattle (62.3%), including fresh beef (43.7%), and chicken (19.4%), including fresh chicken meat (39.3%), in the aforementioned WGS-based study, was not reflected in the present study (non-processed beef 4.7% and non-processed chicken 4.3%, respectively). These discrepancies may arise from differences in methodology, data sources, or food categorization, with the WGS-based study directly linking human isolates to specific products and thus potentially attributing more cases to cattle and poultry. Nonetheless, no single factor fully explains the differences, which remain unresolved.

Despite STEC O157 and STEC non-O157 cases being both almost 50% attributable to foodborne transmission, there were multiple transmission pathways with attributions of around 10%. These were international travel, animal contact, and person-to-person transmission. This aligns well with the conclusions of Friesema et al. (2024) where a limited genetic clustering of human and domestic livestock isolates of STEC O157, among other serogroups, was found. That study also hypothesized international travel and person-to-person transmission as potential contributing factors of STEC transmission in the Netherlands. A meta-analysis of risk factors of STEC also found similar results, with travel, person-to-person transmission, contact with farm animals, environmental transmission and certain food exposures being risk factors for sporadic STEC infection (Augustin et al., 2021). In the present study, within the animal contact pathway, livestock and wildlife showed the highest estimated attributions across all *E. coli* groups. Among the food-related risk factors identified by Augustin et al. (2021), beef consumption was associated with an increased risk of sporadic STEC infection. Furthermore, a STEC source attribution study in the Netherlands based on serotyping data found serotype O157 to be primarily linked to cattle, followed by small ruminants. Similarly, STEC non-O157 was also mainly attributed to cattle, with small ruminants playing a more prominent role as compared to O157 (Mughini-Gras et al., 2018b). These studies are consistent with the results of the present study. Here, non-processed beef was estimated to account for 24.3% and 24.8% of STEC O157 and STEC non-O157, respectively. Moreover, the ranking of attributed sources of STEC infections, i.e., cattle, sheep and goats, pigs, and poultry (Mughini-Gras et al., 2018b) is similar to the ranking of the food items within the current study.

For *Salmonella* Enteritidis, *Salmonella* Typhimurium, and other non-typhoidal *Salmonella*, the most important transmission pathway was foodborne. Our study results were similar to those from outbreak data analyses of human salmonellosis in Europe (Chanamé Pinedo et al., 2022), with eggs being the food group with the highest attribution for *Salmonella* Enteriditis, and non-processed pork for *Salmonella* Typhimurium. Previous source attribution studies based on genotyping data support these findings, and also identified cattle as an important source of *Salmonella* Typhimurium, right after pigs (Mughini-Gras et al., 2014a).

For typhoidal *Salmonella*, the predominant transmission pathway was international travel. A systematic review on global trends in typhoidal salmonellosis support this finding, indicating that most typhoid and paratyphoid cases in high-income countries are indeed travel-related, mainly to sub-Saharan Africa, South and East Asia (Als et al., 2018).

In our study, the main transmission routes of *Leptospira* were similarly attributed to international travel (48.1%) and environmental water (42.5%). This aligns with the findings from a recent study on leptospirosis in the Netherlands, with 43.8% of cases being travel-related and most cases acquiring the infections through surface water contact (Obels et al., 2025),

For both HAV and HEV, notable differences were observed between this study and that of Havelaar et al. (2008). In the case of HAV, attribution to international travel decreased significantly (60% to 34%), while person-to-person and foodborne transmission increased (from 18% to 34.2% and 11% to 18.4%, respectively). These changes are consistent with indications that the transmission pathways of HAV have shifted over the past two decades. A systematic review reported an increase in domestic cases of HAV and a decline in travel-related cases across Europe (Andani et al., 2023), which aligns with both the 2008 and current SEJ findings. The apparent rise in person-to-person transmission may be linked to a shift in the affected population, from children to adults, with recent outbreaks affecting particularly men who have sex with men (MSM). Foodborne outbreaks of HAV also continue to occur regularly in Europe (Andani et al., 2023). These are often associated with contamination during production, particularly in fruit, vegetables, and shellfish (Friesema et al., 2022). These food groups are also reflected as most important in this study.

In this study, foodborne transmission was the predominant pathway for HEV, accounting for 66.4% of cases, followed by travel-related transmission at 11%. In contrast, Havelaar et al. (2008) identified travel (43%) and environmental exposure (25%) as the main sources. In the 15 years between the study by Havelaar et al. (2008) and the present study, research on the epidemiology of HEV has increased significantly. It is now well established that HEV has a broad host reservoir, being found in domestic farm animals, pets such as dogs and cats, as well as a variety of wild animals (Kenney, 2019). Various transmission pathways, such as foodborne and waterborne routes, and sources like the consumption of raw or undercooked meat are increasingly considered potential contributors to HEV infection (Haase et al., 2025). A Dutch study from 2015 found that many HEV patients had not travelled outside of Europe in the preceding three months and were not immunosuppressed (Koot et al., 2015). Furthermore, a study among blood donors in the Netherlands found that several pork products, particularly dry sausages, and contaminated water were associated with past HEV infections (Mooij et al., 2018). Similar results were observed in a case-control study on risk factors for acute HEV in the Netherlands, where dry raw pork sausages were identified as the major source of infection (Tulen et al., 2019). This suggests that, in the Netherlands and other Western countries, the number of HEV acquired cases without travel may previously have been underestimated (Havelaar et al., 2008; Koot et al., 2015).

For *Toxoplasma gondii*, the findings were consistent with those of the previous SEJ study, identifying foodborne transmission as the dominant pathway, followed by environmental exposure (Havelaar et al., 2008). A difference lies in the inclusion of the person-to-person transmission pathway. Here, this pathway was excluded, whereas the previous SEJ study included the pathway but specifically for fecal-oral transmission, which had an estimated attribution of 1%. None of the experts in the present study provided estimates for person-to-person transmission. Nevertheless, some experts noted that excluding person-to-person transmission might not be entirely accurate, as organ transplants could represent a potential route of infection. Although congenital toxoplasmosis is considered a form of person-to-person transmission, our focus was on identifying the sources of infection in the mother, who subsequently transmitted the infection to the child, rather than on the transmission route to the child itself (Van Den Berg et al., 2023).

For *Cryptosporidium*, there were differences in the species included in both studies. The study of Havelaar et al. (2008) included *Cryptosporidium parvum*, while the current study includes *Cryptosporidium* spp. The current results showed multiple transmission routes with higher attribution estimates (>10%) in all but one category, similar to the previous SEJ study. For *Cryptosporidium* spp., international travel was identified as the main pathway (23.6%), with animal contact (17%) and foodborne transmission (16.8%) following closely. The slight differences in the estimated attributions between the current study and Havelaar et al. (2008) could be caused by the inclusion of other species. A study examining both human and cattle isolates in the Netherlands found *C. hominis* and *C. parvum* in human isolates (Nic Lochlainn et al., 2019). Here, the dominant genotype of *C. parvum* in the Netherlands was found in both humans and farm animals, while the most dominant *C. hominis* genotype was solely found in human. Hence, inclusion of more *Cryptosporidium* species likely led to a higher attribution to person-to-person transmission (Wielinga et al., 2008).

Similar SEJ studies on source attribution of food- and waterborne pathogens have been conducted in several countries, as well as by the WHO across different world regions. However, each of these studies used varying definitions for transmission pathways and included different sets of pathogens. In addition, the methodologies differed slightly between studies, and most relied on data collected in 2020 or earlier (Beshearse et al., 2021; Hald et al., 2016; Butler et al., 2015). This limits the possibilities of comparison between studies. In the United

States of America (USA), a SEJ study was conducted in 2021. This study included eight of the same bacteria (*Brucella*, *Campylobacter*, STEC O157, STEC non-O157, *Legionella*, *Salmonella* Enteritidis, *Salmonella* Typhimurium, and *Staphylococcus aureus*), all three parasites, and five viruses (astrovirus, norovirus, rotavirus, sapovirus, and HAV). When comparing the results of the USA study to those of the current study, it became apparent that international travel, only considered in the current study, influenced the attributions. A notable example is *Brucella*: while the USA study identified foodborne transmission (45%) and animal contact (36%) as the main pathways, the current study attributed 97.8% of *Brucella* cases to international travel. Livestock in the Netherlands is proven *Brucella*-free, and the reported human brucellosis cases are rare and linked to international travel. This aligns with broader trends observed in Europe, where the incidence of human brucellosis is generally low, with higher rates reported around the south and east Mediterranean region (Liu et al., 2024). A recently identified potential source of brucellosis in the Netherlands is imported dogs. In November 2016, a dog in the Netherlands tested positive for *Brucella canis*, which had never been isolated previously in the Netherlands. Of the 16 dogs suspected to be infected, 10 were positive. All dogs infected with *Brucella canis* were rescue dogs from Eastern Europe (Van Dijk et al., 2021). In 2022, the first human case of *Brucella canis* infection in the Netherlands was reported. This human case had followed after exposure to an infected rescue dog (Kolwijck et al., 2022). Accordingly, experts in the present study attributed most human brucellosis cases (70.2%) to pets/companion animals within the animal contact transmission pathway. In the USA, the number of reported human brucellosis cases range from 79 to 165 annually, with about 6000 cases reported between 2000 and 2019. Most cases were attributed to foodborne transmission or animal contact. Notably, foodborne cases are often linked to the consumption of unpasteurized dairy products, including those consumed while traveling outside the USA (Pinn-Woodcock et al., 2023). This is in line with the findings of the present study where 64.6% of foodborne brucellosis cases were also attributed to (unpasteurized) dairy products.

For *Legionella*, the USA study identified water as the primary transmission pathway, accounting for 97% of cases (Beshearse et al., 2021), whereas we found international travel to be the main pathway, followed by environmental water. For the other bacteria, the estimated transmission pathways were largely similar between the studies, though the inclusion of international travel in the current study influenced the attributions in some cases. All three parasites included here could be compared to the USA findings (Beshearse et al., 2021). For *Giardia* and *Cryptosporidium*, the USA study highlighted waterborne transmission as the dominant pathway. However, international travel played a much more prominent role in the current study. *Toxoplasma gondii* was attributed here primarily to foodborne transmission (66%), differing from the 28% attribution reported in the USA study, where animal contact (58%) was the most common pathway (Beshearse et al., 2021). For astrovirus, norovirus, rotavirus, and sapovirus, both studies indicated person-to-person transmission as the primary route.

In addition to point estimates, the associated uncertainties are highly relevant. Uncertainty varied substantially across pathogens and, within pathogens, across transmission pathways and food groups, reflecting their epidemiological complexity and the related challenges of source attribution. Similar patterns were observed at the individual assessment level, with experts expressing greater uncertainty for certain pathways or food groups. Some experts consistently reported higher uncertainty across pathogens.

The high overall uncertainty reflects diversity in expert opinions, a common outcome of SEJ studies. While increasing the number of expert assessments can reduce uncertainty, this has not consistently been observed, as also seen in this study. Moreover, diversity in opinions may occur even when overall uncertainty is low, and general agreement combined with high individual uncertainty can still result in high overall uncertainty. Indeed, there are multiple sources of uncertainty.

In this study, high uncertainty arose from several sources, including general disagreement among experts (e.g., food and animal contact for *Campylobacter*), general agreement combined with high individual uncertainty (e.g., environmental water), agreement on the best estimate (median) with one or a few experts expressing higher uncertainty (e.g., animal contact for *Listeria*), or general agreement with a few discrepant assessments by a small number of experts (e.g., dairy for *Brucella*).

Some limitations may have influenced the outcomes of this study. Although a relatively large number of experts participated, the number of experts per pathogen varied considerably, ranging from 4 to 22. Experts who were asked to assess a high number of pathogens may have experienced expert fatigue, potentially affecting the accuracy or consistency of their responses. Additionally, the impact of the COVID-19 pandemic may not have fully stabilized at the time of data collection. The last national restrictions in the Netherlands were lifted in March 2022, and the WHO formally declared the end of the global health emergency in May 2023. An additional limitation concerns the wide uncertainty intervals (UIs) observed for some estimates. A wide UI that includes the central estimate indicates a high degree of uncertainty and suggests a substantial variability in expert opinion. This variability can be due to the limited empirical data and complexity of the existing foodborne pathogen data. The experts need to rely on assumptions that are influenced by their background and experience. Their interpretation of existing evidence can introduce subjective bias which reduces the reliability of the aggregated estimates. It can also skew the results away from the objective reality. While wide UIs have to be interpreted with cautions, the same accounts for narrow UIs. These may suggest a higher confidence among experts, but they might reflect overconfidence and can mask the true extent of uncertainty. Therefore, it is essential to critically evaluate the width of the intervals and the robustness of the evidence. Such evaluation is equally important for estimates where the UI does not include the estimate, as this may indicate a lack of consensus between the experts.

In conclusion, this study presents the results of a SEJ on the source attribution of 26 foodborne pathogens across several transmission pathways, as well as various food groups and animal contact groups. It offers a more comprehensive analysis of potential sources for a wide set of pathogens than previous studies conducted. These findings can complement data-driven approaches to strengthen the evidence base needed for food safety interventions in public health. Moreover, they provide valuable insights for developing policies aimed at preventing infections via the most relevant transmission pathways by guiding future research as well as disease surveillance and control strategies.

CRediT authorship contribution statement

Lena I. Wijnen: Writing – review & editing, Writing – original draft, Resources, Investigation, Data curation, Conceptualization. **Gabriela F. Nane:** Writing – review & editing, Validation, Supervision, Software, Methodology, Investigation, Formal analysis, Conceptualization. **Elisa Benincà:** Writing – review & editing, Visualization, Resources, Investigation. **Roan Pijnacker:** Writing – review & editing, Validation, Investigation. **Eelco Franz:** Writing – review & editing, Validation, Investigation. **Roger M. Cooke:** Writing – review & editing, Supervision, Software, Methodology, Formal analysis, Data curation. **Lapo Mughini-Gras:** Writing – review & editing, Validation, Supervision, Resources, Project administration, Methodology, Investigation, Funding acquisition, Conceptualization.

Funding information

This research was supported by the Netherlands Food and Consumer Product Safety Authority (Nederlandse Voedsel- en Warenautoriteit, NVWA).

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

We thank everyone who contributed to this study especially all experts who generously shared their time and expertise.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ijfoodmicro.2026.111735.

Data availability

Data will be made available on request.

References

Als, D., Radhakrishnan, A., Arora, P., Gaffey, M.F., Campisi, S., Velummailum, R., Zareef, F., Bhutta, Z.A., 2018. Global trends in typhoidal salmonellosis: a systematic review. Am. J. Trop. Med. Hyg. 99 (3_Suppl), 10–19. https://doi.org/10.4269/ajtmh.18-0034.

Andani, A., Bunge, E., Kassianos, G., Eeuwijk, J., Mellou, K., Van Damme, P., Mukherjee, P., Steffen, R., 2023. Hepatitis A occurrence and outbreaks in Europe over the past two decades: a systematic review. J. Viral Hepat. 30 (6), 497–511. https://doi.org/10.1111/jvh.13821.

Augustin, J.-C., Kooh, P., Mughini-Gras, L., Guillier, L., Thébault, A., Audiat-Perrin, F., Cadavez, V., Gonzales-Barron, U., Sanaa, M., 2021. Risk factors for sporadic infections caused by Shiga toxin-producing Escherichia coli: a systematic review and meta-analysis. Microb. Risk Anal. 17, 100117. https://doi.org/10.1016/j.mran.2020.100117.

Benincà, E., Pijnacker, R., Friesema, I., Kretzschmar, M., Franz, E., Mughini Gras, L., 2024. Disease burden of food-related pathogens in the Netherlands, 2023. Rijksinstituut voor Volksgezondheid en Milieu RIVM. https://doi.org/10.21945/RIVM-2024-0146.

Beshearse, E., Bruce, B.B., Nane, G.F., Cooke, R.M., Aspinall, W., Hald, T., Crim, S.M., Griffin, P.M., Fullerton, K.E., Collier, S.A., Benedict, K.M., Beach, M.J., Hall, A.J., Havelaar, A.H., 2021. Attribution of illnesses transmitted by food and water to comprehensive transmission pathways using structured expert judgment, United States. Emerg. Infect. Dis. 27 (1), 182–195. https://doi.org/10.3201/eid2701.200316.

Bos, J., de Boer, P., Franz, E., 2024. Staat van infectieziekten in Nederland, 2023. Rijksinstituut voor Volksgezondheid en Milieu RIVM. https://doi.org/10.21945/RIVM-2024-0135.

Butler, A.J., Thomas, M.K., Pintar, K.D.M., 2015. Systematic review of expert elicitation methods as a tool for source attribution of enteric illness. Foodborne Pathog. Dis. 12 (5), 367–382. https://doi.org/10.1089/fpd.2014.1844.

Chanamé Pinedo, L., Mughini-Gras, L., Franz, E., Hald, T., Pires, S.M., 2022. Sources and trends of human salmonellosis in Europe, 2015–2019: an analysis of outbreak data. Int. J. Food Microbiol. 379, 109850. https://doi.org/10.1016/j.ijfoodmicro.2022.109850.

Cooke, R.M., 1991. Experts in Uncertainty: Opinion and Subjective Probability in Science. Oxford University Press, Incorporated (with Shrader-Frechette, K.).

Cooke, R.M., Goossens, L.L.H.J., 2008. TU Delft expert judgment data base. Reliab. Eng. Syst. Saf. 93 (5), 657–674. https://doi.org/10.1016/j.ress.2007.03.005.

Cooke, R., Mendel, M., Thijs, W., 1988. Calibration and information in expert resolution; a classical approach. Automatica 24 (1), 87–93. https://doi.org/10.1016/0005-1098(88)90011-8.

Cooke, R.M., Marti, D., Mazzuchi, T., 2021. Expert forecasting with and without uncertainty quantification and weighting: what do the data say? Int. J. Forecast. 37 (1), 378–387. https://doi.org/10.1016/j.ijforecast.2020.06.007.

Dingle, K.E., Colles, F.M., Wareing, D.R.A., Ure, R., Fox, A.J., Bolton, F.E., Bootsma, H.J., Willems, R.J.L., Urwin, R., Maiden, M.C.J., 2001. Multilocus sequence typing system for *Campylobacter jejuni*. J. Clin. Microbiol. 39 (1), 14–23. https://doi.org/10.1128/JCM.39.1.14-23.2001.

Faber, R., Hamersma, M., De Haas, M., Krabbenborg, L., 'T Hoen, A., 2023. Estimating post-pandemic effects of working from home and teleconferencing on travel behaviour. Eur. J. Transp. Infrastruct. Res. 23 (1). https://doi.org/10.18757/ejtir.2023.23.1.6733.

Friesema, I.H., Slegers-Fitz-James, I.A., Wit, B., Franz, E., 2022. Surveillance and characteristics of food-borne outbreaks in the Netherlands, 2006 to 2019. Eurosurveillance 27 (3). https://doi.org/10.2807/1560-7917.ES.2022.27.3.2100071.

Friesema, I.H., Van Der Voort, M., Wit, B., Van Hoek, A.H., Van Den Beld, M.J., Van Der Weijden, C., Franz, E., 2024. Cross-sectoral genomic surveillance reveals a lack of insight in sources of human infections with Shiga toxin-producing Escherichia coli, the Netherlands, 2017 to 2023. Eurosurveillance 29 (49). https://doi.org/10.2807/1560-7917.ES.2024.29.49.2400264.

Gandhi, M., Chikindas, M.L., 2007. Listeria: A foodborne pathogen that knows how to survive. Int. J. Food Microbiol. 113 (1), 1–15. https://doi.org/10.1016/j.ijfoodmicro.2006.07.008.

Haagsma, J.A., Polinder, S., Stein, C.E., Havelaar, A.H., 2013. Systematic review of foodborne burden of disease studies: quality assessment of data and methodology. Int. J. Food Microbiol. 166 (1), 34–47. https://doi.org/10.1016/j.ijfoodmicro.2013.05.029.

Haase, J.A., Schlienkamp, S., Ring, J.J., Steinmann, E., 2025. Transmission patterns of hepatitis E virus. Curr. Opin. Virol. 70, 101451. https://doi.org/10.1016/j.coviro.2025.101451.

Hald, T., Aspinall, W., Devleesschauwer, B., Cooke, R., Corrigan, T., Havelaar, A.H., Gibb, H.J., Torgerson, P.R., Kirk, M.D., Angulo, F.J., Lake, R.J., Speybroeck, N., Hoffmann, S., 2016. World Health Organization estimates of the relative contributions of food to the burden of disease due to selected foodborne hazards: a structured expert elicitation. PLoS One 11 (1), e0145839. https://doi.org/10.1371/journal.pone.0145839.

Hanea, A.M., 2021. with Nane, G. F., Bedford, T., & French, S. Expert Judgement in Risk and Decision Analysis. Springer International Publishing AG.

Havelaar, A.H., Galindo, Á.V., Kurowicka, D., Cooke, R.M., 2008. Attribution of foodborne pathogens using structured expert elicitation. Foodborne Pathog. Dis. 5 (5), 649–659. https://doi.org/10.1089/fpd.2008.0115.

Havelaar, A.H., Kirk, M.D., Torgerson, P.R., Gibb, H.J., Hald, T., Lake, R.J., Praet, N., Bellinger, D.C., De Silva, N.R., Gargouri, N., Speybroeck, N., Cawthorne, A., Mathers, C., Stein, C., Angulo, F.J., Devleesschauwer, B., World Health Organization Foodborne Disease Burden Epidemiology Reference Group, 2015. World Health Organization global estimates and regional comparisons of the burden of foodborne disease in 2010. PLoS Med. 12 (12), e1001923. https://doi.org/10.1371/journal.pmed.1001923.

Hoffmann, S., Devleesschauwer, B., Aspinall, W., Cooke, R., Corrigan, T., Havelaar, A., Angulo, F., Gibb, H., Kirk, M., Lake, R., Speybroeck, N., Torgerson, P., Hald, T., 2017. Attribution of global foodborne disease to specific foods: findings from a World Health Organization structured expert elicitation. PLoS One 12 (9), e0183641. https://doi.org/10.1371/journal.pone.0183641.

Kärenlampi, R., Rautelin, H., Schönberg-Norio, D., Paulin, L., Hänninen, M.-L., 2007. Longitudinal study of Finnish *Campylobacter jejuni* and *C. coli* isolates from humans, using multilocus sequence typing, including comparison with epidemiological data and isolates from poultry and cattle. Appl. Environ. Microbiol. 73 (1), 148–155. https://doi.org/10.1128/AEM.01488-06.

Kenney, S.P., 2019. The current host range of hepatitis E viruses. Viruses 11 (5), 452. https://doi.org/10.3390/v11050452.

Kolwijck, E., Lutgens, S.P.M., Visser, V.X.N., Van Apeldoorn, M.J., Graham, H., Koets, A. P., Schrauwen, M.M.W.P., Reubsaet, F.A.G., Broens, E.M., Kortbeek, L.M., 2022. First case of human *Brucella canis* infection in the Netherlands. Clin. Infect. Dis. 75 (12), 2250–2252. https://doi.org/10.1093/cid/ciac425.

Koot, H., Hogema, B.M., Koot, M., Molier, M., Zaaijer, H.L., 2015. Frequent hepatitis E in the Netherlands without traveling or immunosuppression. J. Clin. Virol. 62, 38–40. https://doi.org/10.1016/j.jcv.2014.11.020.

Lazarakou, A., Mughini-Gras, L., Pijnacker, R., 2024. Global impact of COVID-19 pandemic on gastrointestinal infections: a scoping review. Foodborne Pathog. Dis., fpd.2024.0047 https://doi.org/10.1089/fpd.2024.0047.

Liu, Z., Gao, L., Wang, M., Yuan, M., Li, Z., 2024. Long ignored but making a comeback: a worldwide epidemiological evolution of human brucellosis. Emerg. Microbes Infect. 13 (1), 2290839. https://doi.org/10.1080/22221751.2023.2290839.

Mead, P.S., Slutsker, L., Dietz, V., McCaig, L.F., Bresee, J.S., Shapiro, C., Griffin, P.M., Tauxe, R.V., 1999. Food-related illness and death in the United States. Emerg. Infect. Dis. 5 (5), 607–625. https://doi.org/10.3201/eid0505.990502.

Mooij, S.H., Hogema, B.M., Tulen, A.D., Van Pelt, W., Franz, E., Zaaijer, H.L., Molier, M., Hofhuis, A., 2018. Risk factors for hepatitis E virus seropositivity in Dutch blood donors. BMC Infect. Dis. 18 (1), 173. https://doi.org/10.1186/s12879-018-3078-9.

Mughini Gras, L., Smid, J.H., Wagenaar, J.A., De Boer, A.G., Havelaar, A.H., Friesema, I. H.M., French, N.P., Busani, L., Van Pelt, W., 2012. Risk factors for campylobacteriosis of chicken, ruminant, and environmental origin: a combined case-control and source attribution analysis. PLoS One 7 (8), e42599. https://doi.org/10.1371/journal.pone.0042599.

Mughini-Gras, L., Smid, J.H., Wagenaar, J.A., Koene, M.G.J., Havelaar, A.H., Friesema, I. H.M., French, N.P., Flemming, C., Galson, J.D., Graziani, C., Busani, L., Van Pelt, W., 2013. Increased risk for *Campylobacter jejuni* and *C. coli* infection of pet origin in dog owners and evidence for genetic association between strains causing infection in humans and their pets. Epidemiol. Infect. 141 (12), 2526–2535. https://doi.org/10.1017/S0950268813000356.

Mughini-Gras, L., Smid, J., Enserink, R., Franz, E., Schouls, L., Heck, M., Van Pelt, W., 2014a. Tracing the sources of human salmonellosis: a multi-model comparison of phenotyping and genotyping methods. Infect. Genet. Evol. 28, 251–260. https://doi.org/10.1016/j.meegid.2014.10.003.

Mughini-Gras, L., Smid, J.H., Wagenaar, J.A., De Boer, A., Havelaar, A.H., Friesema, I.H. M., French, N.P., Graziani, C., Busani, L., Van Pelt, W., 2014b. Campylobacteriosis in returning travellers and potential secondary transmission of exotic strains. Epidemiol. Infect. 142 (6), 1277–1288. https://doi.org/10.1017/S0950268813002069.

Mughini-Gras, L., Penny, C., Ragimbeau, C., Schets, F.M., Blaak, H., Duim, B., Wagenaar, J.A., De Boer, A., Cauchie, H.-M., Mossong, J., Van Pelt, W., 2016. Quantifying potential sources of surface water contamination with Campylobacter jejuni and Campylobacter coli. Water Res. 101, 36–45. https://doi.org/10.1016/j.watres.2016.05.069.

Mughini-Gras, L., Kooh, P., Augustin, J.-C., David, J., Fravalo, P., Guillier, L., Jourdan-Da-Silva, N., Thébault, A., Sanaa, M., Watier, L., The Anses Working Group on Source Attribution of Foodborne Diseases, 2018a. Source attribution of foodborne diseases: potentialities, hurdles, and future expectations. Front. Microbiol. 9, 1983. https://doi.org/10.3389/fmicb.2018.01983.

Mughini-Gras, L., Van Pelt, W., Van Der Voort, M., Heck, M., Friesema, I., Franz, E., 2018b. Attribution of human infections with Shiga toxin-producing *Escherichia coli* (STEC) to livestock sources and identification of source-specific risk factors, The Netherlands (2010–2014). Zoonoses Public Health 65 (1). https://doi.org/10.1111/zph.12403.

Mughini-Gras, L., Kooh, P., Fravalo, P., Augustin, J.-C., Guillier, L., David, J., Thébault, A., Carlin, F., Leclercq, A., Jourdan-Da-Silva, N., Pavio, N., Villena, I., Sanaa, M., Watier, L., 2019. Critical orientation in the jungle of currently available methods and types of data for source attribution of foodborne diseases. Front. Microbiol. 10, 2578. https://doi.org/10.3389/fmicb.2019.02578.

Mughini-Gras, L., Pijnacker, R., Coipan, C., Mulder, A.C., Fernandes Veludo, A., de Rijk, S., van Hoek, A.H.A.M., Buij, R., Muskens, G., Koene, M., Veldman, K., Duim, B., van der Graaf-van Bloois, L., van der Weijden, C., Kuiling, S., Verbruggen, A., van der Giessen, J., Opsteegh, M., van der Voort, M., Castelijn, G.A. A., Schets, F.M., Blaak, H., Wagenaar, J.A., Zomer, A.L., Franz, E., 2021a. Sources and transmission routes of campylobacteriosis: a combined analysis of genome and exposure data. J. Infect. 82 (2), 216–226. https://doi.org/10.1016/j.jinf.2020.09.039.

Mughini-Gras, L., Chanamé Pinedo, L., Pijnacker, R., Van Den Beld, M., Wit, B., Veldman, K., Bosh, T., Franz, E., 2021b. Impact of the COVID-19 pandemic on human salmonellosis in the Netherlands. Epidemiol. Infect. 149, e254. https://doi.org/10.1017/S0950268821002557.

Mughini-Gras, L., Benincà, E., McDonald, S.A., De Jong, A., Chardon, J., Evers, E., Bonačić Marinović, A.A., 2022. A statistical modelling approach for source attribution meta-analysis of sporadic infection with foodborne pathogens. Zoonoses Public Health 69 (5), 475–486. https://doi.org/10.1111/zph.12937.

Mughini-Gras, L., Paganini, J.A., Guo, R., Coipan, C.E., Friesema, I.H.M., Van Hoek, A.H. A.M., Van Den Beld, M., Kuiling, S., Bergval, I., Wullings, B., Van Der Voort, M., Franz, E., Dallman, T.J., 2025. Source attribution of Listeria monocytogenes in the Netherlands. Int. J. Food Microbiol. 427, 110953. https://doi.org/10.1016/j.ijfoodmicro.2024.110953.

Mulder, A.C., Franz, E., De Rijk, S., Versluis, M.A.J., Coipan, C., Buij, R., Müskens, G., Koene, M., Pijnacker, R., Duim, B., Bloois, L.V.D.G., Veldman, K., Wagenaar, J.A., Zomer, A.L., Schets, F.M., Blaak, H., Mughini-Gras, L., 2020. Tracing the animal sources of surface water contamination with Campylobacter jejuni and Campylobacter coli. Water Res. 187, 116421. https://doi.org/10.1016/j.watres.2020.116421.

Mulder, A.C., Mughini-Gras, L., Van De Kassteele, J., Blanken, S.L., Pijnacker, R., Franz, E., 2024. Livestock-associated spatial risk factors for human salmonellosis and campylobacteriosis. Zoonoses Public Health 71 (8), 876–899. https://doi.org/10.1111/zph.13170.

Mullner, P., Jones, G., Noble, A., Spencer, S.E.F., Hathaway, S., French, N.P., 2009a. Source attribution of food-borne zoonoses in New Zealand: a modified Hald model. Risk Anal. 29 (7), 970–984. https://doi.org/10.1111/j.1539-6924.2009.01224.x.

Mullner, P., Spencer, S.E.F., Wilson, D.J., Jones, G., Noble, A.D., Midwinter, A.C., Collins-Emerson, J.M., Carter, P., Hathaway, S., French, N.P., 2009b. Assigning the source of human campylobacteriosis in New Zealand: a comparative genetic and epidemiological approach. Infect. Genet. Evol. 9 (6), 1311–1319. https://doi.org/10.1016/j.meegid.2009.09.003.

Nic Lochlainn, L.M., Sane, J., Schimmer, B., Mooij, S., Roelfsema, J., van Pelt, W., Kortbeek, T., 2019. Risk Factors for Sporadic Cryptosporidiosis in the Netherlands: Analysis of a 3-Year Population Based Case-Control Study Coupled With Genotyping, 2013-2016. J. Infect. Dis. 219 (7), 1121–1129. https://doi.org/10.1093/infdis/jiy634.

Nielsen, R.T., Dalby, T., Emborg, H.-D., Larsen, A.R., Petersen, A., Torpdahl, M., Hoffmann, S., Vestergaard, L.S., Valentiner-Branth, P., 2022. COVID-19 preventive measures coincided with a marked decline in other infectious diseases in Denmark, spring 2020. Epidemiol. Infect. 150, e138. https://doi.org/10.1017/S0950268822001145.

Obels, I., Mughini-Gras, L., Maas, M., Brandwagt, D., Van Den Berge, N., Notermans, D. W., Franz, E., Van Elzakker, E., Pijnacker, R., 2025. Increased incidence of human leptospirosis and the effect of temperature and precipitation, the Netherlands, 2005 to 2023. Eurosurveillance 30 (15). https://doi.org/10.2807/1560-7917.ES.2025.30.15.2400611.

Pijnacker, R., Mughini-Gras, L., Verhoef, L., Van Den Beld, M., Franz, E., Friesema, I., 2024. Impact of non-pharmaceutical interventions during the COVID-19 pandemic on pathogens transmitted via food in the Netherlands. Epidemiol. Infect. 152, e130. https://doi.org/10.1017/S0950268824000815.

Pinn-Woodcock, T., Frye, E., Guarino, C., Franklin-Guild, R., Newman, A.P., Bennett, J., Goodrich, E.L., 2023. A one-health review on brucellosis in the United States. J. Am. Vet. Med. Assoc. 261 (4), 451–462. https://doi.org/10.2460/javma.23.01.0033.

Pires, S.M., Desta, B.N., Mughini-Gras, L., Mmbaga, B.T., Fayemi, O.E., Salvador, E.M., Gobena, T., Majowicz, S.E., Hald, T., Hoejskov, P.S., Minato, Y., Devleesschauwer, B., 2021. Burden of foodborne diseases: think global, act local. Curr. Opin. Food Sci. 39, 152–159. https://doi.org/10.1016/j.cofs.2021.01.006.

Sapp, A.C., Amaya, M.P., Havelaar, A.H., Nane, G.F., 2022. Attribution of country level foodborne disease to food group and food types in three African countries: conclusions from a structured expert judgment study. PLoS Negl. Trop. Dis. 16 (9), e0010663. https://doi.org/10.1371/journal.pntd.0010663.

Strachan, N.J.C., Gormley, F.J., Rotariu, O., Ogden, I.D., Miller, G., Dunn, G.M., Sheppard, S.K., Dallas, J.F., Reid, T.M.S., Howie, H., Maiden, M.C.J., Forbes, K.J., 2009. Attribution of *Campylobacter* infections in northeast Scotland to specific sources by use of multilocus sequence typing. J. Infect. Dis. 199 (8), 1205–1208. https://doi.org/10.1086/597417.

Teunis, G., Dallman, T.J., Zając, M., Skarżyńska, M., Petrovska, L., Pista, A., Silveira, L., Clemente, L., Thépault, A., Bonifait, L., Kerouanton, A., Chemaly, M., Alvarez, J., Söderlund, R., Nielsen, E.M., Chattaway, M., Burgess, K., Byrne, W., Zomer, A.L., van den Beld, M., Hendrickx, A.P.A., Franz, E., Pires, S., Hald, T., Mughini-Gras, L., 2025. Attributable sources of the five most prevalent non-typhoidal Salmonella serovars across ten European countries. J. Infect. 91 (5), 106632. https://doi.org/10.1016/j.jinf.2025.106632.

Tulen, A.D., Vennema, H., Van Pelt, W., Franz, E., Hofhuis, A., 2019. A case-control study into risk factors for acute hepatitis E in the Netherlands, 2015–2017. J. Inf. Secur. 78 (5), 373–381. https://doi.org/10.1016/j.jinf.2019.02.001.

Van Den Berg, O.E., Stanoeva, K.R., Zonneveld, R., Hoek-van Deursen, D., Van Der Klis, F.R., Van De Kassteele, J., Franz, E., Opsteegh, M., Friesema, I.H.M., Kortbeek, L.M., 2023. Seroprevalence of *Toxoplasma gondii* and associated risk factors for infection in the Netherlands: third cross-sectional national study. Epidemiol. Infect. 151, e136. https://doi.org/10.1017/S095026882300122X.

Van Deursen, B., Hagenaars, M., Meima, A., Van Asten, L., Richardus, J.H., Fanoy, E., Voeten, H., 2022. A sharp decrease in reported non-COVID-19 notifiable infectious diseases during the first wave of the COVID-19 epidemic in the Rotterdam region, the Netherlands: a descriptive study. BMC Infect. Dis. 22 (1), 208. https://doi.org/10.1186/s12879-022-07209-5.

Van Dijk, M.A.M., Engelsma, M.Y., Visser, V.X.N., Keur, I., Holtslag, M.E., Willems, N., Meij, B.P., Willemsen, P.T.J., Wagenaar, J.A., Roest, H.I.J., Broens, E.M., 2021. Transboundary spread of *Brucella canis* through import of infected dogs, the Netherlands, November 2016–December 2018. Emerg. Infect. Dis. 27 (7), 1783–1788. https://doi.org/10.3201/eid2707.201238.

WHO Estimates of the Global Burden of Foodborne Diseases: Foodborne Disease Burden Epidemiology Reference Group 2007–2015, 2015. World Health Organization.

Wielinga, P.R., De Vries, A., Van Der Goot, T.H., Mank, T., Mars, M.H., Kortbeek, L.M., Van Der Giessen, J.W.B., 2008. Molecular epidemiology of Cryptosporidium in humans and cattle in The Netherlands. Int. J. Parasitol. 38 (7), 809–817. https://doi.org/10.1016/j.ijpara.2007.10.014.