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Food Safety Authority of Ireland

Report of the Scientific Committee
of the Food Safety Authority of Ireland

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Risk Ranking of Microbiological Hazards in Food (2015–2019)



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Abbreviations

Acronym	Definition
AGI	acute gastrointestinal illness
BCoDE	Burden of Communicable Disease in Europe
BIOHAZ	Panel on Biological Hazards
CDC	Centers for Disease Control and Prevention
CFR	case fatality rate
CIDR	Computerised Infectious Disease Reporting
COI	cost of illness
CSO	Central Statistics Office
DALY	disability-adjusted life year
DPO	Data Protection Officer
DW	disability weight
ECDC	European Centres for Disease Prevention and Control
EFSA	European Food Safety Authority
ESRD	end-stage renal disease
EU	European Union
FAO	Food and Agriculture Organization of the United Nations
FBD	foodborne disease
FDA	Food and Drug Administration
FSA	Food Standards Agency
FSAI	Food Safety Authority of Ireland
GBS	Guillain-Barré syndrome
GP	general practitioner
HAV	hepatitis A virus
HEV	hepatitis E virus
HPSC	Health Protection Surveillance Centre of the Health Service Executive
HUS	haemolytic uraemic syndrome
IBTS	Irish Blood Transfusion Service

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IID	infectious intestinal disease
MF	multiplication factor
QALY	quality-adjusted life year
ReA	reactive arthritis
RfA	Request for Advice
STEC	Shiga toxin-producing <i>Escherichia coli</i>
Spp.	Species
TESSy	The European Surveillance System
UA	under-ascertainment
UE	underestimation
UI	uncertainty interval
UR	underreporting
VTEC	verotoxigenic <i>Escherichia coli</i>
WG	working group
WHO	World Health Organization
YLD	years lived with a disability
YLL	years of life lost

Executive summary

Microbiological food safety risks encompass a broad spectrum of pathogens that may contaminate different food products at various points across the food chain. When contaminated foods are consumed, these pathogens can cause illnesses that vary widely in severity and duration, depending on factors such as the type and amount of pathogen ingested, and the susceptibility of the individuals who become exposed.

Microbiological risk ranking is a process carried out in order to understand the relative public health impact posed by major microbiological hazards across the food supply chain, and to underpin a risk-based national food safety system based on risk awareness. This process enables authorities to set priorities for microbiological food safety management at a national level, and provides evidence to inform decisions on control, prevention and surveillance of microbiological foodborne illness. It can also be used to identify data, knowledge and research gaps; to facilitate the setting of targets for reductions in foodborne microbiological illness; and to assist in evaluating the effectiveness of specific interventions designed to reduce microbiological foodborne illness.

The Food Safety Authority of Ireland (FSAI) requested its Scientific Committee to: (i) advise on a risk ranking of microbiological hazards from foodborne sources in Ireland, and (ii) identify data gaps that, if filled, would enable reduced uncertainty in future risk ranking.

(i) A risk ranking of microbiological hazards from foodborne sources in Ireland

In this report, the FSAI Scientific Committee presents its first national risk ranking exercise on microbiological hazards in food. Seven hazards were selected for inclusion in the scope of the exercise, based on a set of inclusion and exclusion criteria that have been used in previous international risk ranking studies, such as disease incidence and clinical severity.

The selected hazards included *Campylobacter* species (spp.), *Listeria monocytogenes* (*L. monocytogenes*), *Salmonella* spp., Shiga toxin-producing *Escherichia coli* (STEC)/verotoxigenic *Escherichia coli* (VTEC), hepatitis A virus (HAV), hepatitis E virus (HEV) and norovirus.

The burden of disease for each hazard was quantified in terms of disability-adjusted life years (DALYs), a metric that combines mortality and morbidity into a single measure of health loss. To generate these estimates, this study employed a top-down surveillance approach for the population of Ireland. Irish national disease incidence surveillance data (2015–2019) were obtained from the Health Protection Surveillance Centre (HPSC) of the Health Service Executive (HSE) and then adjusted for perceived underestimation (UE) (from under-ascertainment (UA) and underreporting (UR)) using multiplication factors derived from an expert consultation workshop with public health specialists. The European Centre for Disease Prevention and Control's (ECDC's)

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Burden of Communicable Disease in Europe (BCoDE) toolkit was used to simulate disease models for five of the hazards, while bespoke models built using R software were developed and used for two of the hazards not included in the BCoDE toolkit. Monte Carlo disease simulations were used to estimate total DALYs and 95% uncertainty intervals (UIs) for each hazard

An expert elicitation study using a two-round Delphi approach was conducted to estimate the proportion of total DALYs attributable to foodborne transmission, involving specialists in microbiology, public health, and related fields.

The total DALY estimates were combined with these foodborne-attribution proportions and mean foodborne DALYs with corresponding 95% UIs were calculated using Monte Carlo simulations in R software. The hazards were then ranked in descending order based on their estimated mean foodborne DALYs, as follows:

1. *Campylobacter* spp., accounting for 404.44 (95% UI: 297.73–497.42) foodborne DALYs annually
2. Norovirus, accounting for 155.51 (95% UI: 22.92–392.12) foodborne DALYs annually
3. *L. monocytogenes*, accounting for 98.11 (95% UI: 85.54–106.37) foodborne DALYs annually
4. STEC, accounting for 83.05 (95% UI: 26.47–156.65) foodborne DALYs annually
5. *Salmonella* spp., accounting for 15.02 (95% UI: 10.0–18.6) foodborne DALYs annually
6. HAV, accounting for 5.29 (95% UI: 0.35–13.04) foodborne DALYs annually
7. HEV, accounting for 1.25 (95% UI: 0.49–1.88) foodborne DALYs annually.

This risk ranking exercise provides a preliminary assessment and comparison of the burden of disease for these hazards impacting the public through the food pathway. It highlights the public health burden caused by pathogens based on a high incidence (norovirus), high severity of outcome (*L. monocytogenes*) or both (*Campylobacter* spp.).

The report presents the methods employed and results obtained in a transparent manner in order to ensure that the work can be reproduced and critically considered in the context of the data available and the assumptions employed. The estimated burden of disease associated with each hazard is expected to reflect the effectiveness of the existing food safety control measures implemented between 2015 and 2019. This information in turn can allow for risk-based prioritisation of key pathogens impacting Ireland's food safety systems which can help guide strategic decision-making.

(ii) Data gaps that, if filled, would enable a risk ranking with reduced uncertainty in the future

The risk ranking exercise focusing on microbiological hazards in food was a complex and data-intensive process, shaped by substantial methodological and contextual challenges. The analysis, based on data from 2015 to 2019, was delayed due to COVID-19 disruptions and does not capture post-2019 developments, such as emerging pathogens or enhanced surveillance capabilities. The report highlights key areas identified during this project that aim to improve the availability and utility of data in order to estimate the overall burden of disease associated with microbiological hazards, and to better assess the burden of disease attributable to the food pathway.

Estimating the total burden of disease associated with each microbiological hazard

During the initial phase of this work, certain additional hazards (e.g. *Yersinia enterocolitica*, *Toxoplasma gondii* (*T. gondii*), biogenic amines) were shortlisted for inclusion within the scope of this exercise but could not be included due to data limitations. These merit further study in future when sufficient data to support a DALY calculation are available.

Following the selection of hazards to be included in this exercise, a substantial challenge identified was the UE of foodborne disease (FBD) cases. It is well recognised that many cases of FBD go undetected due to a number of possible factors, including mild or self-limiting symptoms, limited testing, long incubation periods and surveillance system limitations. These factors mean that the true incidence of a disease is likely higher than what is reported to national surveillance systems. In order to address this gap, public health specialists provided their expert judgement to this exercise by estimating plausible UE values for each hazard, acknowledging that these estimates may be affected by potential biases, limitations in knowledge and factors not fully accounted for, such as sex and age of cases.

In order to quantify the burden of disease (i.e. DALYs) for each hazard, the BCoDE toolkit was used to simulate disease models for five hazards (*Campylobacter* spp., *L. monocytogenes*, *Salmonella* spp., STEC and HAV), while bespoke models developed using R software were employed for the remaining two hazards (norovirus and HEV). A notable limitation of these models is that they represent theoretical disease pathways rather than precise real-world patterns. Furthermore, there were literature values derived from studies conducted in other countries incorporated into these models which may not fully reflect the Irish context. Although the disease models for norovirus and hepatitis E infections were adapted using available Irish data with the aim to reflect the Irish context, some model parameters were based on data from other countries in the absence of Irish-specific information.

Estimating the proportion of burden of disease attributable to the food pathway

Attributing cases of a disease to the food pathway is challenging. Ideally, this would be informed by accurate and detailed data on reported cases of foodborne illness. In Ireland, limited surveillance data and source-attribution studies make this particularly challenging. In this exercise, a multidisciplinary team of experts provided their expertise to compensate for these gaps. As expert judgement is subjective and may potentially be influenced by biases and limitations in knowledge, three different weighting approaches were explored to assess the experts' estimates on the proportion of a disease attributable to the food pathway: equal weighting, self-allocated weighting and calibration weighting. Although each method had the potential to influence the results differently, the outcomes remained relatively consistent across all approaches, providing limited assistance in managing the uncertainty associated with these estimates.

This report identifies key limitations and opportunities for improvement in data collection and modelling with regard to FBDs in Ireland. Addressing these gaps will enhance the accuracy and reliability of future risk rankings. Despite challenges, the methodologies presented here offer a valuable contribution to Ireland's ongoing efforts to understand the national burden of FBDs.

This report outlines the methods employed, assumptions made and results obtained in a transparent manner in order to ensure reproducibility and critical evaluation in light of the available data and underlying assumptions, while recognising that future updates will be required to address remaining gaps and limitations.

Chapter 1 Background

1.1 Food safety risk ranking (microbiological)

The overarching practice of food safety risk ranking is defined by the Food and Agriculture Organization of the United Nations (FAO) as:

The systematic analysis and ordering of foodborne hazards and/or foods in terms of public health risks, based on the likelihood and severity of adverse impacts on human health in a target population. (FAO, 2020)

Microbiological risk ranking is a branch of food safety risk ranking that is carried out specifically in order to understand the relative public health impact of major microbiological hazards across the food supply chain, with the aim of underpinning a risk-based national food safety system.

Risk-based food safety systems are being implemented in a number of countries worldwide. Risk ranking allows priority setting for microbiological food safety management at a national level and can inform risk management decisions on the surveillance, prevention and control of microbiological foodborne illness. It can also be used to identify data, knowledge and research gaps. This in turn can facilitate the setting of targets for reductions across the public of foodborne diseases (FBDs) caused by microbiological hazards, as well as the assessment of the effectiveness of specific interventions designed to reduce microbiological FBDs.

1.2 Request for Advice

Ireland had not previously conducted a national microbiological risk ranking. The Food Safety Authority of Ireland (FSAI) viewed this as a valuable step to guide future activities. A Request for Advice ([Appendix 1](#)) sought the Scientific Committee's guidance on prioritising microbiological hazards and identifying data gaps in order to improve accuracy in future risk ranking exercises.

1.3 Conceptual risk ranking framework

A number of specialised agencies have generated guidance to assist national food safety authorities in ranking the public health risk posed by foodborne hazards in their countries. In 2012, the EFSA Panel on Biological Hazards (BIOHAZ) published a scientific opinion on a conceptual risk-ranking framework comprising nine stages to promote consistency, transparency, and best

practices in risk assessment (EFSA Panel on Biological Hazards, 2012). Due to the impact of data availability and time frame on the selection of a risk ranking methodology, BIOHAZ concluded that no one methodology should be considered the universal standard for risk ranking exercises. The conceptual framework put forward by BIOHAZ is summarised as follows:

1. Define the hazards to be included in the scope.
2. Select the risk metric(s) to be used.
3. Select the risk ranking approach to be used.
4. Select the type of model to be used.
5. Select the model variables to be included (input data such as incidence, etc.).
6. Collect and evaluate the data to be integrated for model variables.
7. If required, restructure the model based on data availability and revert to step 2.
8. Integrate the data by combining model inputs and formulas to produce outputs on the chosen risk metrics.
9. Present the results in a transparent manner.

Throughout this process, it is imperative there is a continuous exchange of information between risk assessors and the risk manager.

More recently, the FAO (2020) published similar guidance on a national-level ranking approach that is composed of three iterative steps, as follows:

1. Define the scope:
 - a) Define the purpose.
 - b) Select what will be ranked.
 - c) Screen foods and/or hazards for overall relevance and risk potential.
2. Develop the approach:
 - a) Select the risk ranking method.
 - b) Select the metrics for ranking risks.
 - c) Collect and evaluate the appropriateness of the data.
3. Conduct the risk ranking analysis and report the results.

1.4 Defining the purpose and scope

The first step of a risk ranking exercise is to identify the key risk management questions and goals. Typically, risk assessments focus on one hazard, whereas risk ranking considers multiple hazards. In order to identify hazards for inclusion in a risk ranking exercise, all hazards undergo an initial

screening process to determine their overall relevance and risk potential to public health. This process will typically consider the following questions:

- Has the hazard been detected in the country?
- Is it likely for the hazard to be present in food at the point of consumption?
- Can it survive and/or grow in food?
- Is there a relationship between exposure to the hazard and acute and/or chronic illness?
- Is exposure through food a significant source of illness in the population?
- Has the hazard caused outbreaks in the country?

1.5 Variability and uncertainty

Variability and uncertainty are fundamental concepts within the risk ranking framework, and assessing the implications of these elements is critical. International guidelines recommend treating variability and uncertainty as distinct factors to ensure scientific clarity (Codex Alimentarius Commission, 1999).

Variability refers to the inherent heterogeneity of values over time, space, or among different members of a population. Uncertainty, on the other hand, refers to limitations in available knowledge that affect the range and probability of possible answers to an assessment question. This uncertainty may be qualitative or quantitative and may arise from different sources, such as model uncertainty or parameter uncertainty (EFSA Scientific Committee, 2018).

Effectively communicating uncertainties and their potential impact on the risk ranking outcomes is essential for informed decision-making. In 2018, EFSA published guidance developed by its Scientific Committee on uncertainty analysis in scientific assessments, underscoring the importance of addressing this aspect in order to provide reliable information for decision-making.

1.6 Approaches to modelling the burden of disease

Once the hazards to be included in a risk ranking exercise are selected, the approach must be developed. Depending on the desired outcome and the availability/quality of data, approaches can be qualitative, semi-quantitative or quantitative. There are two main approaches when it comes to risk modelling: deterministic and stochastic. Deterministic models do not permit randomness, while stochastic models incorporate probability and randomness into their simulation.

Risk ranking can be based on either a 'top-down' surveillance approach or a 'bottom-up' prediction approach. With respect to microbiological hazards, the top-down approach attempts to ascertain the level of risk associated with the hazard based on information collected, such as disease

incidence, outbreak incidence or the prevalence of the hazard in food. Alternatively, the bottom-up approach uses predictive models to estimate the final concentration of the hazard in food at the point of consumption. The method applied should be clearly stated and reproducible. Information about the model and data sources used, assumptions, limitations, variability and uncertainties should be communicated (EFSA Panel on Biological Hazards, 2014).

In 2014, BIOHAZ prepared a scientific opinion that evaluated the performance and data requirements of existing risk ranking tools, as well as methodologies for incorporating uncertainty and variability into risk ranking models. It also developed a risk ranking toolbox to support its assessments.

BIOHAZ evaluated eight different risk ranking tools for microbiological hazards in foods and concluded that quantitative stochastic models are the most reliable for ranking microbiological risks. Among the quantitative tools that use a bottom-up approach for risk ranking, the United States Food and Drug Administration's (FDA's) FDA-iRISK system (Chen *et al.*, 2013) was identified as the most appropriate tool for meeting the needs of the EFSA BIOHAZ Panel. It also considered the European Centre for Disease Prevention and Control's (ECDC's) Burden of Communicable Disease in Europe (BCoDE) toolkit to be appropriate for implementing a top-down approach based on epidemiological data. Furthermore, BIOHAZ suggested that a combined approach employing the BCoDE toolkit alongside outputs from FDA-iRISK or other predictive microbiology tools could create a comprehensive, fit-for-purpose toolkit to support timely and transparent risk ranking.

This report identifies limitations on the risk ranking tools available online. Some of these tools did not provide an option to specify the population involved, and the outputs typically lacked a measurement of variability and uncertainty. Other challenges identified were that risk assessments are time sensitive and that, unfortunately, data of sufficient quality are often not available. BIOHAZ concluded that, where data and time constraints prevent the use of quantitative risk ranking, semi-quantitative models can be used, but the limitations of these approaches should be made clear when analysing and presenting the final results.

1.6.1 Disease outcome tree (defining health states)

Infectious diseases have diverse manifestations, which may be local (e.g. abdominal pain) or systemic (e.g. fever), and which may vary in terms of severity. Disease models are typically built to describe the disease progression respective to the incidence and adverse health effect(s) (health states) resulting from exposure to a hazard. [Figure 1](#) presents an overview of a generic disease model where each arrow connecting to various health outcomes is assigned a Greek letter representing a transition rate (i.e. a parameter representing the transition from one state of health

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to others during a specified time). These clinical outcomes will depend on a number of factors, such as the microorganism's virulence and antimicrobial susceptibility, host factors (e.g. age, immune status), and the amount of time that has elapsed since infection and since starting therapy. Defining the range of health outcomes, sequelae (long-term health effects resulting from infection) and the duration of symptoms can allow for a calculation of the estimated total burden of disease resulting from a hazard. While the disease outcome tree presented in [Figure 1](#) is relatively straightforward in terms of its components, additional factors (e.g. the provision of a stool sample by the affected individual, the prescription of medication, absence from work) can be integrated in order to create a more comprehensive disease outcome tree (Colzani *et al.*, 2017). This is frequently done in the context of cost-of-illness (COI) approaches.

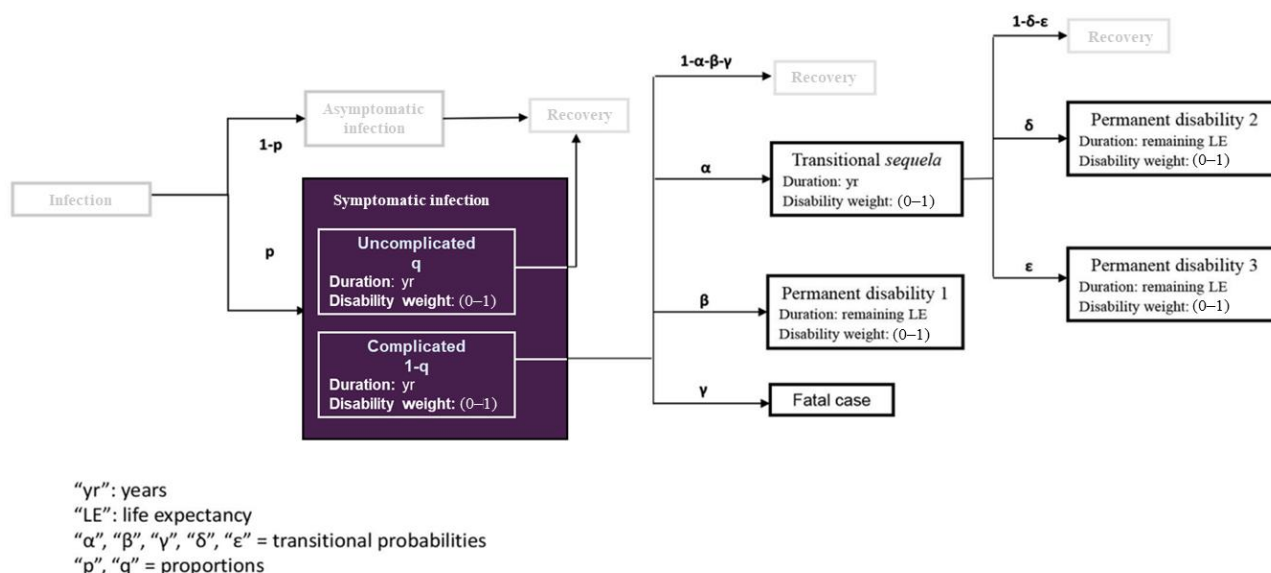


Figure 1 A disease outcome tree linking infection and all sequelae

Source: Adapted from Colzani *et al.* (2017)

1.6.2 Population characteristics

The characteristics of the population being assessed greatly influence risk ranking exercises. Identifying which groups are more vulnerable to specific hazards will better reflect the implications of a disease on public health. Characteristics for a defined population typically include such variables as age demographics, sex distribution and life expectancy. It is also possible to extend cover to other factors, such as a population's geographical distribution, health status and the prevalence of chronic conditions, etc. Incorporating population characteristics into disease models

is important for predicting how a disease may spread, guiding public health interventions and improving risk assessments.

1.6.3 Epidemiological data and underestimation

In order to monitor epidemiological data, reliable and accurate surveillance and notification systems are critical. However, for many infections, the reported number of confirmed cases is likely a significant underestimation of the true number of infections occurring in the population. The term 'iceberg phenomenon' (see [Figure 2](#)) is used to describe this situation, where a significant proportion of infections are subclinical, unreported or otherwise concealed from view, with the cases that are visible representing only the 'tip of the iceberg' to the epidemiologist. Surveillance and notification systems are typically affected by a degree of underestimation (UE). As such, there is considerable uncertainty as to the true incidence of a disease within a population, as well as its impact on morbidity and mortality rates.

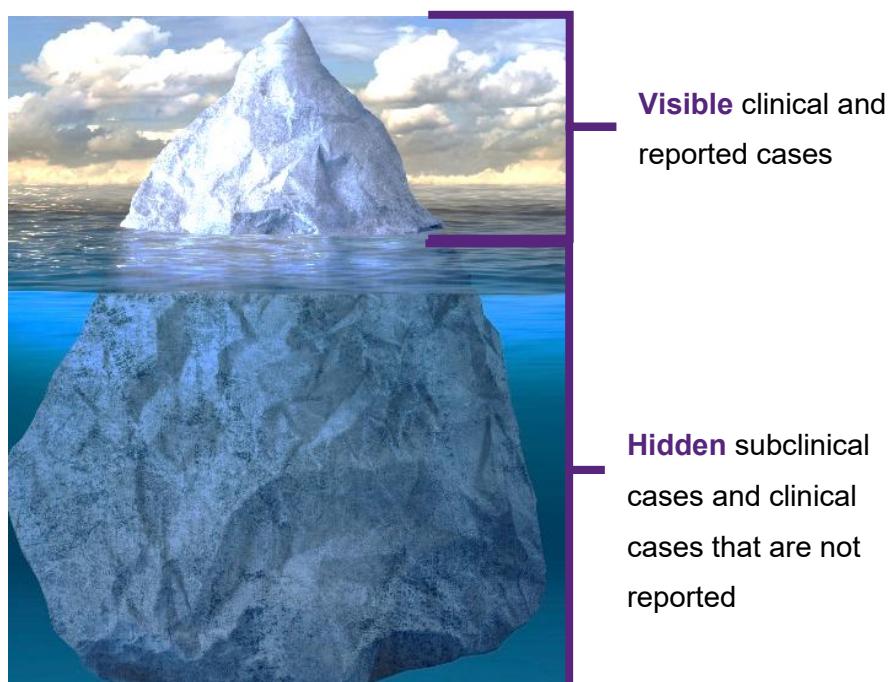


Figure 2 The iceberg phenomenon, illustrating the visible clinical and reported cases, as well as the hidden subclinical cases and clinical cases that are not reported

Several methods can be used to estimate the extent of UE associated with a disease, such as community-based studies, serological surveys, infectious intestinal disease (IID) studies, returning traveller studies and capture-recapture studies (Gibbons *et al.*, 2014), as well as extracting or extrapolating data from the scientific literature.

Mathematically, UE represents the estimated number of disease cases in a population that have not been captured by the surveillance system, for each reported case, over a specified time period. In general, UE may vary between diseases and can be attributed to a few factors, such as the following:

- Some diseases are associated with a lower frequency of serious clinical symptoms, resulting in fewer people seeking medical attention when they are infected.
- Symptomatic people who seek medical attention are not always sampled in a consistent way.
- Health services testing for different microorganisms can vary in their capacity to do so.
- Methods for detecting different microorganisms can vary in sensitivity.

In order to estimate the true incidence of a disease within a population, national surveillance data need to be corrected for UE. UE can be split into two distinct levels of under-ascertainment (UA) and underreporting (UR), as represented by the morbidity surveillance pyramid for infectious diseases provided in [Appendix 8 \(Figure 12\)](#). Correcting incidence data for UE can be achieved by either of the following two approaches:

1. Splitting the UE into UA and UR and defining two correction factors
2. Defining one correction factor that captures both the UA and UR.

Both UA and UR are defined and illustrated in the glossary of [Appendix 8](#).

1.6.4 The disability-adjusted life year metric

In public health, it is insufficient to merely count the number of individuals who become ill or succumb to disease. It is essential to assess how health conditions impact on individuals' quality of life. This understanding is crucial when comparing various diseases, establishing health priorities and/or allocating resources.

The disability-adjusted life year (DALY) is a metric developed in the 1990s as part of the Global Burden of Disease study to quantify the overall burden of disease by combining years of life lost due to premature mortality and years lived with disability. It has since been adopted by the World Health Organization (WHO) as the primary measure for assessing global disease burden.

Generally speaking, the DALY metric is a measurement of the gap between the current public health status and an ideal public health situation, where the entire population lives to an advanced age, free of disease and disability ([Figure 3](#)).

Devleesschauwer *et al.* (2014) reported a stepwise approach for calculating DALYs, emphasising the structured combination of two components: years of life lost due to premature mortality (YLL)

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and years lived with disability (YLD). The DALY metric is therefore expressed as the sum of YLL and YLD, where YLD incorporates a disability weight ranging from 0 to 1, with 0 representing perfect health and 1 representing a health state equivalent to death. Thus, 1 DALY corresponds to the loss of one year of full health.

Consequently, the higher the DALY contribution from food, the greater the impact of food on the overall disease burden within the population.



Figure 3 Schematic illustration of DALYs across the human life course, showing contributions of YLD and YLL

Source: Adapted from Planemad (2012), Wikimedia Commons, CC BY-SA 3.0.

1.7 Source attribution of FBDs

Transmission of microbiological hazards can occur through a variety of foods and other pathways (e.g. soil, water, or via direct contact with the contaminated environment or infected animals or humans). The source attribution of an FBD refers to a process of identifying and quantifying the sources that contribute to cases of foodborne illness. Attributing part of the total burden of an illness to a particular food source is challenging.

By understanding the sources of diseases, it is possible to assess the risk posed by different reservoirs and manage those risks through improved health protection measures, surveillance and control of potential disease pathways. Major transmission routes to consider may include human-to-human, animal-to-human, food-to-human, water-to-human and environment-to-human

transmission. Studies may also investigate more granular categories classifying how diseases are transmitted, such as specific food categories (e.g. percentage of FBDs transmitted due to consumption of pork), animal reservoirs (e.g. percentage of FBDs transmitted due to direct contact with pigs) or specific foods and/or risk factors (e.g. percentage of FBDs transmitted due to consumption of undercooked pork).

There are various methods of performing a source attribution study, including epidemiological approaches, microbiological approaches, quantitative risk assessments, mathematical modelling and expert elicitation procedures. Our risk ranking exercise has broadly looked at major transmission routes and utilised an expert elicitation approach to attribute the relative contribution of different sources to the total burden of disease.

1.7.1 Expert elicitation

Expert elicitation has previously helped to obtain judgements and insights into the field of food safety regarding the proportion of disease attributed to various hazards arising from food transmission (Cressey *et al.*, 2019a; Cressey *et al.*, 2019b; Cressey *et al.*, 2019c; 2005; Davidson *et al.*, 2011; Hald *et al.*, 2016; Havelaar *et al.*, 2008; Hoffmann *et al.*, 2008; 2007; Ravel *et al.*, 2010; Vally *et al.*, 2014).

An expert elicitation is a structured, systematic approach used to gather judgements from experts in a particular field. It is particularly useful in situations where empirical data are limited, uncertain or not available. Experts who participate in the elicitation are selected based on their knowledge, experience and expertise relevant to the problem being addressed. The selection process should aim to cover a broad range of expertise and perspectives. The participating experts may be requested to provide estimates of quantitative metrics (e.g. proportion, probability) or qualitative metrics (e.g. risk factors, likely sources), along with their perceived uncertainty or confidence levels, in response to defined questions. These expert judgements, as well as their respective uncertainties or confidences, are then aggregated to provide a consensus and/or possible range of outcomes. In addition, calibration methods can be explored to provide a means of putting boundaries on the final outcomes.

In certain elicitation approaches, such as the Delphi method, experts are provided with anonymised feedback on the group's responses after each round. They are then given the opportunity to reconsider and update their own estimates in subsequent rounds. This iterative process is designed to encourage convergence of expert judgements and can help reduce uncertainty in the final estimates.

While an expert elicitation assists in filling data gaps in a flexible and adaptable manner by incorporating expertise, there are various limitations to using an expert elicitation to provide data. The resulting expert opinions are subjective by nature, which may introduce variability or bias to the judgements. The quality of the elicitation depends on the selection of experts and their ability to provide reliable estimates.

1.8 Analysis and reporting of results

The results of a risk ranking exercise must be interpreted with caution, taking into consideration the bias, uncertainty and variability inherent in the metrics, as well as the data and method(s) used in the analysis. The steps, assumptions and processes used to conduct the risk ranking should be well-documented in order to ensure transparency and reproducibility. It should be noted whether local and/or regional variations of both hazards and foods consumed were accounted for. It is also imperative to explain the strengths and limitations of the approach so that decision-makers can take that into consideration. Reporting of results must be objective and include an executive summary along with the main conclusions and limitations of the risk ranking exercise. The presentation of the results should be tailored to the target audience and communicated effectively.

1.9 Prioritisation

Following the risk ranking exercise, the hazards can be prioritised in a systematic manner based on health impacts and other factors such as economic implications, food-security effects, and feasibility of controls. For example, FAO (2017) illustrates how issues like aflatoxin contamination in maize or mercury in fish may be prioritised differently once costs, practicality, and consumer acceptance are considered.

Risk prioritisation is valuable for effective risk management. The process, however, acknowledges that risk management decisions are made in an environment where factors besides public health may also need to be considered. A risk prioritisation list will thus help to inform the risk manager where to focus attention on important food safety issues (FAO, 2017).

1.10 Risk ranking studies of microbiological FBDs

The selection of microbiological hazards for inclusion in a risk ranking exercise is typically guided by considerations relevant to the specific country or region, as well as the availability and quality of data and resources. Studies assessing the global and national impact of microbiological FBDs using DALYs (measuring the loss of health), and occasionally quality-adjusted life years (QALYs)

(measuring equivalent healthy years lived), have been carried out in many countries to help improve understanding of the burden of FBDs, which may in turn help government agencies to prioritise food safety interventions. These studies generally integrate surveillance data, outbreak investigations and existing literature on long-term sequelae and source attribution models in order to estimate the DALYs or QALYs associated with specific FBDs, as well as the foodborne DALYs (i.e. the portion of the DALYs associated with a particular FBD that are attributed to the food pathway). Some research also includes economic impact assessments, using methods such as the COI indicator, which captures both direct and indirect costs associated with foodborne illnesses.

Global estimates

In 2015, the WHO published its first report assessing the global burden of FBDs (WHO, 2015). Using 2010 data on 31 hazards (bacteria, viruses, parasites and chemicals), the WHO estimated that there had been 600 million (95% uncertainty interval (UI): 420–960 million) FBDs and 420,000 (95% UI: 310,000–600,000) deaths resulting from FBDs worldwide, translating to about 33 million (95% UI: 25–45 million) DALYs in 2010. Children aged under 5 years accounted for approximately 40% of the global population infected by an FBD, despite representing only 9% of the total population. Diarrhoeal pathogens (e.g. *Campylobacter*, *Salmonella*, enterotoxigenic *Escherichia coli* (*E. coli*), norovirus) were the primary contributors to DALYs in most regions. Additionally, specific parasites (such as foodborne trematodes in East Asia) and exposure to chemicals (including aflatoxin in Africa and Asia) also resulted in substantial regional DALY burdens. The WHO study used an incidence-based DALY model, modelling disease outcomes and applying disability weights to estimate total DALYs. These estimates identified large data deficiencies in populous countries such as China, India and Russia, as well as for many hazards, emphasising the need for more national research efforts. The WHO Foodborne Disease Burden Epidemiology Reference Group (FERG) for 2021–2025 is currently updating the global burden-of-disease estimates for foodborne infections. The updated estimates will cover data from 2000 to 2021, incorporating time-trend analyses, and are scheduled for release in 2026 (WHO, 2026).

Denmark

Denmark has recently conducted assessments on the burden of FBDs. A study conducted by Pires *et al.* (2020) assessed the disease burden attributable to seven common foodborne pathogens in Denmark for the year 2017. The findings estimate that these pathogens are responsible for approximately 3,100 DALYs annually in Denmark, which has a population of approximately 5.8

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million. In terms of the burden of disease attributed to the food pathway, the primary contributor was *Campylobacter*, which was responsible for approximately 1,299 DALYs per year. *Salmonella* was the second-highest contributor, accounting for 374 DALYs. *L. monocytogenes* (196 DALYs) and *Yersinia enterocolitica* (160 DALYs) ranked third and fourth, respectively, in terms of foodborne burden. Congenital toxoplasmosis (100 DALYs) and STEC (38 DALYs) contributed smaller yet appreciable burdens. Notably, despite norovirus causing the highest number of illnesses, its DALY impact (86 DALYs) was relatively modest, ranking sixth in terms of burden of disease attributed to the food pathway.

A similar analysis for 2019, incorporating the same pathogens, also identified *Campylobacter* as the leading foodborne pathogen contributing to the burden of disease, with an estimated loss of 1,285 DALYs among the population in Denmark. *Salmonella* contributed a substantial 416 DALYs, *L. monocytogenes* accounted for 185 DALYs and *Yersinia enterocolitica* accounted for 220 DALYs, reflecting moderate burden of disease apportioned to FBDs. *Toxoplasma gondii* (*T. gondii*) and STEC contributed 88 and 153 DALYs, respectively, representing smaller yet significant burdens. Norovirus was associated with a burden of 23 DALYs, while hepatitis A virus (HAV) accounted for 4 DALYs.

Both studies employed outcome-tree models for each pathogen, capturing acute gastroenteritis and severe sequelae, with Monte Carlo simulations used to quantify uncertainty.

Japan

In Japan, the national burden of FBDs caused by *Campylobacter* species (spp.), *Salmonella* spp. and enterohaemorrhagic *E. coli* was quantified using DALYs in a comprehensive study by Kumagai *et al.* (2015). Expert consultation and statistical data on food poisoning incidents in 2011 were utilised in order to estimate the burden of disease. The study estimated that each year in Japan, foodborne illnesses resulted in 6,099 DALYs annually (95% UI: 1,651–13,687) from *Campylobacter* spp., 3,145 DALYs (95% UI: 906–6,950) from *Salmonella* spp. and 463 DALYs (95% UI: 325–606) from enterohaemorrhagic *E. coli*. These estimates were derived using a pyramid reconstruction model and were observed to be much higher than those based on routine surveillance data alone.

The Netherlands

The Netherlands was among the first countries to conduct national studies on FBDs. In their 2012 analysis, Havelaar *et al.* estimated that, in 2009, fourteen major pathogens together caused a total burden of approximately 13,500 DALYs per year among the Dutch population, corresponding to

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approximately 82 DALYs per 100,000 inhabitants. Approximately 45% of this burden (about 6,075 DALYs) was attributed to foodborne transmission. On a population level, the leading contributors to this burden were *T. gondii* (3,652 DALYs, largely due to congenital toxoplasmosis) and *Campylobacter* spp. (3,620 DALYs). These were followed by rotaviruses (2,123 DALYs), norovirus, (1,862 DALYs) and non-typhoidal *Salmonella* (1,414 DALYs). Other pathogens contributing to the burden of disease included STEC O157 (149 DALYs), *L. monocytogenes* (215 DALYs), *Bacillus cereus* (113 DALYs), *Clostridium perfringens* (538 DALYs), *Staphylococcus aureus* (769 DALYs), HAV (211 DALYs), HEV (24 DALYs), *Cryptosporidium parvum* (75 DALYs) and *Giardia lamblia* (140 DALYs). On per-case basis, perinatal listeriosis accounted for the highest burden, with 27.2 DALYs per case. This analysis applied an incidence-based DALY approach, reconstructing the full surveillance pyramid and accounting for both acute illnesses and chronic sequelae, such as Guillain-Barré syndrome (GBS) associated with *Campylobacter* infections and haemolytic uraemic syndrome (HUS) caused by *E. coli* O157, using established disability weights (DWs). Subsequent updates to the burden of FBDs in the Netherlands have been provided by Mangen *et al.* (2018; 2013), Pijnacker *et al.* (2019), Lagerweij *et al.* (2020) and Benincà *et al.* (2022; 2021).

Most recently, Benincà *et al.* (2024) reported that in 2023, the fourteen monitored pathogens collectively caused around 11,000 DALYs. *Campylobacter* spp. accounted for 2,500 DALYs, STEC for 150 DALYs, and *Salmonella* spp. for between 1,200 DALYs (based solely on human cases reported by public health laboratories) and 1,800 DALYs (based on all laboratory-confirmed human cases). Additional pathogen-specific burdens were estimated as follows: *L. monocytogenes* (330 DALYs), *B. cereus* (34 DALYs), *C. perfringens* (200 DALYs), *S. aureus* (220 DALYs), norovirus (2,400 DALYs), rotavirus (1,000 DALYs), HAV (82 DALYs), HEV (390 DALYs), *Cryptosporidium* spp. (230 DALYs), *Giardia* spp. (220 DALYs) and *T. gondii* (1,900 DALYs).

New Zealand

In New Zealand, multiple risk ranking exercises have assessed the burden of disease of foodborne pathogens using public health impact metrics. In 2004, Cressey and Lake produced an initial report intended to develop a prototype risk ranking methodology suitable for assessing food safety issues in New Zealand. Subsequently, a DALY approach was used for the first study to estimate the burden of FBDs in New Zealand (Cressey and Lake, 2007). The six diseases selected for the study included campylobacteriosis, salmonellosis, listeriosis (perinatal and acquired), infection with STEC, yersiniosis, and norovirus infection. Campylobacteriosis contributed the highest estimated burden, with an annual mean of 880 foodborne DALYs (95% UI: 586–1,174). Norovirus infection also contributed a high burden of disease, with 210 foodborne DALYs (95% UI: 51–462). Although there were fewer observed cases, listeriosis was notable for its severity, contributing a total of 215

foodborne DALYs, mainly due to life-threatening conditions associated with perinatal transmission, which accounted for 195 foodborne DALYs (95% UI: 110–290). The acquired listeriosis pathway contributed 22 foodborne DALYs (95% UI: 8–45). Following listeriosis, salmonellosis resulted in a moderate 111 DALYs (95% UI: 68–177). Yersiniosis and STEC infection had the lowest foodborne DALYs, at 52 (95% UI: 24–85) and 35 (95% UI: 24–70), respectively.

In 2009, Cressey and Lake updated the foodborne DALY estimates for the selected FBDs using revised Dutch DWs (Haagsma *et al.*, 2008), with the exception of listeriosis, which was not included in the Dutch novel disability weights study. The use of the revised DWs resulted in some variation in the overall DALY estimates but had minimal effect on the relative rankings.

These estimates were updated in 2012 to address surveillance data for the year 2011 (Cressey, 2012). The mean foodborne DALY burden of campylobacteriosis decreased to 540, largely due to improved estimates of disease incidence. For norovirus, two methodologies were applied using data from the United Kingdom's Second Study of Infectious Intestinal Disease in the Community (IID2). The first approach estimated incidence by applying IID2-derived rate ratio multipliers to New Zealand's notification data, while the second used IID2 population-based rates scaled to the New Zealand population. These methods yielded markedly different results. When population rates were applied, norovirus ranked as the highest foodborne burden, with 873 DALYs (95% UI: 675–1,083). In contrast, using rate ratios produced a substantially lower estimate of 122 DALYs (95% UI: 80–205), placing norovirus below campylobacteriosis, listeriosis, and STEC infection in relative burden. Listeriosis continued to be impactful, with 160 DALYs (95% UI: 31–305). The foodborne burden of STEC infection increased to 200 DALYs (95% UI: 1.5–783), while yersiniosis increased slightly to 62 DALYs (95% UI: 45–83). Salmonellosis contributed 67 DALYs (95% UI: 29–133) to the national FBD burden.

Cressey *et al.* (2014) revised these estimates based on surveillance data for the year 2013. The estimates reaffirmed *Campylobacter* and norovirus as leading pathogens in food. *Campylobacter* accounted for 622 foodborne DALYs, while norovirus caused between 87 (rate ratio) and 758 (population rate) DALYs. Listeriosis accounted for 179 DALYs, followed by salmonellosis at 74 DALYs, STEC at 156 DALYs and yersiniosis at 66 DALYs.

UK

The Food Standards Agency (FSA) in the UK sought to examine the impact of FBDs using both economic and health-related metrics. To quantify health losses, the FSA commissioned a study employing QALYs (Rigby *et al.*, 2017). In order to determine QALY losses, this research modelled 10 pathogens and their sequelae using decision-analytic models and surveys. The study revealed

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that campylobacteriosis, the most common foodborne infection in the UK, accounted for the highest number of QALYs lost, at 72,911, whereas *Shigella* spp. resulted in the smallest loss of QALYs among those examined, at 32. Other hazards estimated included norovirus (–49,877 QALYs), *Giardia lamblia* (–7,916 QALYs), non-typhoidal *Salmonella* (–7,023 QALYs), *L. monocytogenes* (–734 QALYs), verotoxigenic *Escherichia coli* (VTEC) O157 (–588 QALYs), *Clostridium perfringens* (–317 QALYs), HEV (–76 QALYs) and *Cryptosporidium parvum* (–63 QALYs). The FSA estimated the economic burden of foodborne illnesses at around £943.6 million annually by combining QALY-based health loss estimates with a UK public willingness-to-pay survey. This survey asked individuals how much they'd pay to avoid specific symptoms and long-term complications, allowing conversion of these values into a monetary per-QALY figure.

A more recent study assessed the burden of FBDs in the UK for the year 2018 (Daniel *et al.*, 2020). Norovirus was identified as the most impactful pathogen on the burden of disease resulting from FBDs, resulting in the loss of 256,182 QALYs among the population of the UK. Other significant contributors included Campylobacter (–72,003 QALYs), sapovirus (–29,163 QALYs), *Giardia* (–11,256 QALYs), adenovirus (–8,346 QALYs), *Salmonella* (–6,649 QALYs), rotavirus (–2,304 QALYs), astrovirus (–1,709 QALYs) and *L. monocytogenes* (–596 QALYs). Less substantial contributors to the annual burden of disease included *E. coli* O157 (–25 QALYs), *Shigella* spp. (–33 QALYs), *Cryptosporidium* (–40 QALYs) and *Clostridium perfringens* (–337 QALYs).

United States

In the United States, Hoffmann *et al.* (2012) estimated that, annually, 14 major foodborne pathogens result in a loss of approximately 61,000 QALYs. Most of this health burden (approximately 90%) is attributable to 5 pathogens: non-typhoidal *Salmonella enterica* (–17,000 QALYs per year), *T. gondii* (–11,000 QALYs per year), *Campylobacter* (–13,300 QALYs per year), *L. monocytogenes* (–9,400 QALYs per year) and norovirus (–5,000 QALYs per year). The remaining 9 pathogens included *E. coli* O157, *Clostridium perfringens*, *Staphylococcus aureus*, *Shigella* spp., *Cryptosporidium*, *Yersinia*, and others, and they accounted for approximately 10% of the total burden, or roughly 6,000 QALYs lost per year.

Hoffmann *et al.*'s methodology involved constructing disease-outcome models for each pathogen; identifying possible health states, ranging from mild gastroenteritis to severe complications such as kidney failure or reactive arthritis (ReA); and estimating the probability of each health state. Health utility weights were assigned based on EQ-5D survey data on patient-reported outcomes. The estimated QALY losses were accompanied by an economic impact assessment, approximating an annual cost of \$14 billion (ranging from \$4.4 billion to \$33.0 billion). A supplementary study by Batz

et al. (2012) utilised outbreak data and expert elicitation to attribute these health burdens to specific food categories (e.g. the study ranked poultry, produce, etc. according to their DALY or QALY impact).

1.11 Selected approach for FSAI risk ranking exercise

To conduct our national microbiological risk ranking exercise, we adopted the conceptual risk ranking framework established by the EFSA BIOHAZ in 2012.

The selection of hazards included in this analysis was determined by a Biological Safety Subcommittee working group (WG). The WG based its decisions on previously published inclusion and exclusion criteria (Kemmeren *et al.*, 2006), considering factors such as reported disease incidence and clinical severity.

The DALY was selected as the health metric to quantify the disease burden associated with each hazard. The risk-ranking methodology employed a top-down approach for the population of Ireland.

The reported incidence rates of each disease were simulated along with a MF factor to account for probable UE. Due to the absence of Irish-specific UE data, an expert consultation workshop was convened. During this workshop, five experts contributed towards generating plausible MF values to capture both UA and UR of UE for each disease.

The ECDC's BCoDE toolkit served as the primary model for disease simulation and was used for five of the diseases. Bespoke models were built in R software for the remaining two diseases, for which the toolkit did not provide models, and simulations were conducted accordingly. The outputs from these disease model simulations provided mean DALYs along with 95% UIs on the total burden of disease associated with each hazard.

To estimate the proportion of disease cases for each hazard that is attributable to the food pathway, an expert elicitation process was carried out with 13 participants using a two-round Delphi method. Monte Carlo simulations were employed to analyse the expert elicitation foodborne attribution estimates and to calculate the number of foodborne DALYs from the total burden of disease for each hazard, generating mean foodborne DALYs along with 95% UIs. These foodborne DALYs were used to generate a ranked list of hazards.

Chapter 2 Microbiological hazard selection

2.1 Introduction

As it is not possible to collect and calculate the burden of disease for all potential microbiological foodborne hazards in Ireland, a shortlist of hazards was selected for inclusion in the risk ranking exercise. The scope of the exercise included microorganisms that could be transmitted through food pathways and cause human FBD. The scope did not include antimicrobial resistance.

Transmission through food was defined as:

Transmission through food that is contaminated at source (e.g. from irrigation, faeces of food animals) or during processing and preparation. Preparation might be in any location, including abattoirs, food processing lines, kitchens and outdoor venues (domestic and commercial), etc. Food transmission includes contamination by food handlers and infections in people who have handled contaminated foods. Bottled water is also included as food.

2.2 Methods

The procedure outlined in Sections 2.2.1–2.2.4 was used to shortlist the microbiological hazards for subsequent ranking.

2.2.1 Stage 1

A comprehensive list of legally notifiable diseases and their respective causative pathogens was sourced from the Health Protection Surveillance Centre (HPSC) of the Health Service Executive (HPSC, 2018). The list was reviewed by the Scientific Committee's Biological Safety Subcommittee WG, which then selected hazards that it identified as potentially foodborne. Additionally, the WG reviewed the foodborne pathogens listed in the WHO report *Estimates of the Global Burden of Foodborne Diseases: Foodborne Disease Burden Epidemiology Reference Group 2007–2015* (WHO, 2015) and in the A–Z Index for Foodborne Illness provided by the United States Centers for Disease Control and Prevention (CDC, 2019) to identify any further foodborne hazards for consideration that were not included in the HPSC list. In total, 54 potentially important foodborne microbiological hazards were identified ([Appendix 2](#)).

2.2.2 Stage 2

The Stage 1 list was reviewed using exclusion criteria based on those used in a previous microbiological risk ranking exercise reported in the literature (Kemmeren *et al.*, 2006).

Microorganisms that met one or more of the following criteria were excluded:

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- The reported incidence of human illness in Ireland was low (fewer than 5 cases per annum in a population of 4.7 million) during the period 2014–2018.
- The infection was typically contracted outside of Ireland.
- The etiological importance of the food pathway for the hazard was not well-established.

Cases where the information for a specific exclusion criterion was unknown were recorded, and the hazard was not excluded based on that criterion. Using the above exclusion criteria, 25 hazards were eliminated ([Appendix 3](#)), and a further 2 hazards were agreed to be outside the scope of this risk ranking exercise (i.e. marine biotoxins and mycotoxins). This left 27 hazards for consideration.

2.2.3 Stage 3

The remaining 27 hazards were further reviewed based on the following criteria ([Appendix 4](#)):

- **Clinical severity:** Score of low or high potential to result in long-term chronic sequelae, hospitalisation or deaths (2014–2018)
- **Perceived human incidence:** Score of low (5–50 cases) or high (more than 50 cases). Note, that a hazard being associated with fewer than five reported cases was an exclusion criterion in Stage 2.

Hazards that scored high for both criteria were selected for inclusion. This resulted in selection of eight hazards:

- *Campylobacter* spp.
- *L. monocytogenes*
- *Salmonella* spp.
- STEC
- HAV
- HEV
- *T. gondii*
- *Yersinia* spp.

2.2.4 Stage 4

The WG had some concern that Stage 3 had resulted in the exclusion of two important hazards (norovirus and biogenic amines), both of which had scored low on clinical severity and high on perceived human incidence. Due to data and resource considerations, the WG conducted a further

review of the list of eight hazards and came to the conclusions outlined in the following subsections.

Norovirus

Despite challenges faced regarding the surveillance and UE of norovirus in Ireland, the WG was of the view that, based on the perceived incidence of norovirus in Ireland and its inclusion in other countries' microbiological risk ranking studies, norovirus should be included in the list for consideration.

Biogenic amines

The WG felt that the inclusion of biogenic amines deserved further consideration. It was noted that histamine, a biogenic amine, falls under Commission Regulation (EC) No 2073/2005 as amended, which pertains to the microbiological criteria for foodstuffs. Additionally, The European Union One Health 2021 Zoonoses Report, published by the EFSA and ECDC, highlights histamine, in combination with fish and fish products, as one of the top 10 hazard/food vehicle pairs associated with the highest number of strong evidence outbreaks in reporting European Union member states (EFSA and ECDC, 2022). However, there are limited Irish data available on biogenic amines, and they are not included in the ECDC's BCoDE toolkit.

As such, it was not feasible to include biogenic amines in the list of hazards, and it was agreed that they should be highlighted under Part (ii) of the Request for Advice (RfA) relating to identified data gaps.

***Yersinia* spp.**

The WG noted the relatively low reported incidence of yersiniosis compared with campylobacteriosis and STEC infection. Similarly, the WG was not confident that the reported incidence reflects the true incidence and severity of yersiniosis in Ireland, compared with the other bacterial diseases on the list. However, due to insufficient epidemiological data, the WG agreed to leave *Yersinia* spp. out of the exercise but agreed that it should be highlighted under Part (ii) of the RfA relating to identified data gaps.

T. gondii

While *T. gondii* was included in the selected hazards, when work began on data collection, the WG concluded that there were actually very limited incidence data on toxoplasmosis and that the available seroprevalence data were outdated.

The WG noted that the most complete data were on congenital toxoplasmosis and that data for children aged under 1 year could be used. However, calculation of its attribution to the food pathway would be very difficult in this cohort.

Consequently, the WG agreed to leave *T. gondii* out of the exercise but also agreed that it should be highlighted under Part (ii) of the RfA relating to identified data gaps.

2.3 Scope of microbiological hazards for inclusion

Based on the above decisions by the WG, the microbiological hazard selection process resulted in a final shortlist of the following seven hazards:

Bacteria

- *Campylobacter* spp.
- *L. monocytogenes*
- *Salmonella* spp.
- STEC

Viruses

- HAV
- HEV
- Norovirus.

Chapter 3 Calculating the total burden of human illness from microbiological hazards

3.1 Introduction

This stage aimed to generate estimates, along with associated uncertainties, of the burden of disease caused by each selected hazard across all sources of transmission. It involved the collection and analysis of data on the incidence, severity, and outcomes of infections, covering both acute and long-term health impacts where possible. Monte Carlo simulations were used to quantify the overall health impact of each hazard on the population in an average year.

Adjustments for UE of disease incidence were applied using multiplication factors (MFs) within disease simulations, in an attempt to provide a more accurate representation of the true burden of illness associated with each hazard. For each hazard, the total burden of disease across all sources of transmission was estimated as mean DALYs with corresponding 95% uncertainty intervals (UIs).

3.2 Methods

3.2.1 Disease model frameworks

The DALY values for campylobacteriosis, listeriosis, salmonellosis, STEC infection and hepatitis A infection were calculated using the ECDC's BCoDE toolkit, which is publicly accessible from the ECDC website (ECDC, 2019). The BCoDE toolkit is a stand-alone software application that enables the calculation of DALYs for a selection of 117 communicable diseases and 6 healthcare-associated infections. It utilises Monte Carlo simulations to analyse input parameters to deliver disease-specific results, including 95% UI.

Disease models for hepatitis E infection and norovirus infection were developed using R software (R Core Team, 2023) with input from public health specialists, as these models were not available within the BCoDE toolkit application. While these models were designed to align conceptually with the BCoDE framework, their estimates may not be fully comparable across pathogens due to differences in model structure, assumptions, and parameterisation.

Using a top-down approach, the disease models used input data for 1 year to simulate the projected incidence of the disease in the Irish population, considering the size and life expectancy of this population, stratified by sex and age (CSO 2020, 2025). Additionally, the disease incidence was adjusted by an associated factor to account for UE, capturing the under-ascertainment (UA)

resulting from the community setting, as well as the underreporting (UR) resulting from the healthcare setting.

3.2.2 Health state outcomes and severity weightings

The values used in this analysis were based on the specific severity or DWs provided in the ECDC's BCoDE toolkit as of September 2024, unless otherwise noted. Within the BCoDE toolkit, each disease model is constructed using parameters that include transition probabilities and their distributions, DWs and durations, as well as case fatality proportions by age group. Details of the outcome trees corresponding to each hazard (excluding norovirus and hepatitis E infections) are available in the BCoDE toolkit. Information regarding the inputs for the disease models employed in the BCoDE toolkit are provided in [Appendix 5](#), while the disease model framework and model inputs for norovirus infection and hepatitis E infection, which are not included in the BCoDE toolkit, were developed separately using R software and are provided in [Appendix 6](#).

3.2.3 Epidemiological data

As shown in Tables 37–43 in [Appendix 7](#), disease incidence data for each microorganism were obtained from the HPSC's Computerised Infectious Disease Reporting (CIDR) surveillance system for the years 2015–2019 (HPSC, 2022). The mean annual incidence over this 5-year period was calculated for each disease by summing the total cases across all 5 years and dividing by 5. This average was then used to inform the simulation for each age category.

Hepatitis E infection was designated as a notifiable disease in 2015. Due to limited data availability and reliability of the data for the year 2015, the average incidence of hepatitis E infection was calculated over the subsequent 4 years (2016–2019).

3.2.4 Underestimation of surveillance data

Currently, there is limited information available regarding the UE of FBD incidence in Ireland and other countries. To address this gap and develop more accurate estimates of the FBD burden in Ireland, a one-day expert consultation workshop was conducted. Public health experts reviewed compiled published data on UE estimates from countries comparable to Ireland and, to the best of their ability, identified plausible MFs for the selected diseases. This process involved assessing the likelihood of UA and UR within the current Irish surveillance systems for each disease. As outlined in Table 52 in [Appendix 8](#), the MF values to account for UE derived from expert judgment were incorporated into disease models through simulation in both the BCoDE toolkit and R software.

Further details on the methods associated with the expert consultation workshop are provided in [Appendix 8](#).

3.2.5 Population characteristics

Pre-filled values in the BCoDE toolkit for Ireland regarding age and sex demographics were available. However, these data were deemed unrepresentative of the Irish population for the years 2015–2019, during which time the case incidence data were to be modelled for each disease. Consequently, more appropriate population data were obtained from the 2016 Census. These data were utilised across all disease models in the BCoDE toolkit and R software. As detailed in Table 51 in [Appendix 9](#), the population breakdown by age group and sex was derived by accessing the official 2016 Census data from the Central Statistics Office (CSO) (2021).

3.2.6 Life expectancy data

Pre-filled values for life expectancy within Ireland were provided in the BCoDE toolkit; however, similar to the population data, these values were not considered fully representative of the Irish population for the relevant years (2015–2019). To make up for this, Irish life expectancy data for 2016 were obtained from the CSO website (CSO, 2020).

The BCoDE toolkit categorises age groups in 5-year intervals. Since CSO data provided annual life expectancy values, these data were used to calculate the mean life expectancy for each 5-year age group by averaging the annual values within that group. These data are detailed in [Appendix 10](#).

When the life expectancy for a BCoDE toolkit age group was greater than the national Irish life expectancy, the difference between the age and life expectancy beyond that point was set to zero. This prevented negative life expectancy values, which would distort DALY calculations by artificially reducing the number of years of life lost within the population and falsely implying health benefits. The same adjustment was applied in the R-based models.

3.2.7 Calculation of DALYs

For the risk ranking exercise, the disease models estimated the DALYs respective to each hazard of concern across all relevant transmission pathways. Monte Carlo simulations were iterated 100,000 times for each disease model in order to ensure the convergence of model outputs.

DALYs for a specific cause were calculated as the sum of the years of life lost (YLL) due to premature mortality from that cause and the years lived with a disability (YLD) resulting from health states associated with that disease (WHO, 2020). The basic formula for DALYs is:

$$\text{DALY}(c, s, a, t) = \text{YLL}(c, s, a, t) + \text{YLD}(c, s, a, t)$$

In this equation, c represents a given cause, s represents sex, a represents age and t represents time in years.

The YLLs for a given cause are calculated by multiplying the number of deaths from that cause by a standard life expectancy at the age at which death occurs. The basic formula for YLL is:

$$\text{YLL}(c, s, a, t) = N(c, s, a, t) \times L(s, a)$$

In this equation, $N(c, s, a, t)$ is the number of deaths due to the cause c for the given age a and sex s in year t , and $L(s, a)$ is the standard life expectancy (loss function) specifying the number of years of life lost for a given age and sex.

Following WHO recommendations, an incidence-based approach was used to calculate YLD by multiplying incident cases by the disability weight and the average duration of the disease:

$$\text{YLD}(c, s, a, t) = I(c, s, a, t) \times DW(c, s, a) \times L(c, s, a, t)$$

In this equation, $I(c, s, a, t)$ is the number of incident cases for a given cause c , age a and sex s ; $DW(c, s, a)$ is the disability weight reflecting disease severity; and $L(c, s, a, t)$ is the average duration of the condition in years until remission or death.

3.3 Results

The total DALY estimates, representing the overall burden of disease, were obtained directly from the outputs of each individual disease model, whether from the BCoDE toolkit or R software. For consistency and transparency, the mean value of the DALYs is presented alongside the 2.5th and 97.5th percentiles, reflecting the 95% UI. This format corresponds to how most of the estimates were generated within the BCoDE toolkit. The same approach was applied across all disease model outcomes, including those resulting from the disease models built using R software. This was done in order to ensure output consistency throughout the analysis.

3.3.1 Campylobacteriosis

Total burden of campylobacteriosis

This study simulated the average number of campylobacteriosis cases over a 5-year period (2015–2019), which was approximately 2,689 annually. With an MF applied to account for potential UE, the total number of cases contributing to the annual burden of disease was estimated at approximately 48,610.

The model outcomes indicate that campylobacteriosis contributes an average of 510.7 (95% UI: 451.23–568.16) DALYs annually, representing the combined 289.16 (95% UI: 236.08–341.83) DALYs resulting from YLL due to premature death and the 221.53 (95% UI: 199.77–244.29) DALYs resulting from YLD.

At the population level, campylobacteriosis results in an average of 4.65 (95% UI: 4.20–5.13) YLD and 6.07 (95% UI: 4.96–7.18) YLL, which is a total burden of 10.72 (95% UI: 9.52–11.93) DALYs per 100,000 population annually. On average, each case of campylobacteriosis contributing to the annual burden results in a loss of 0.01 DALYs.

When analysing the contribution of different health outcomes to the annual burden of campylobacteriosis, symptomatic infection has the largest contribution to the burden of disease, representing 69% of the total DALYs, equivalent to 352.68 (95% UI: 299.59–405.35) per year. ReA accounted for 23% of the burden of disease annually at 119.13 (95% UI: 98.56–141.24) DALYs. GBS represented 4% of the total DALYs, contributing 18.02 (95% UI: 14.65–21.40) DALYs per year. Additionally, permanent disability resulting from GBS added another 20.83 (95% UI: 16.77–25.04) DALYs annually, accounting for 4% of the total burden of disease. These outcomes highlight the substantial burden of symptomatic infection resulting from campylobacteriosis, with notable contributions from ReA and GBS-related disabilities.

3.3.2 Listeriosis

Total burden of listeriosis

This study simulated the average number of listeriosis cases acquired in Ireland over a 5-year period (2015–2019), which was approximately 21 cases annually. With an MF applied to account for potential UE, the total number of cases contributing to the annual burden of disease was estimated at approximately 33.

The model outcomes indicate that listeriosis contributes an average of 106.38 (95% UI: 102.40–110.37) DALYs annually, comprising 92.58 (95% UI: 91.95–93.22) DALYs due to YLL from premature mortality and 13.79 (95% UI: 9.43–18.17) DALYs due to YLD. On average, each case of listeriosis contributing to the annual burden results in a loss of 2.14 DALYs, representing the highest per-case burden among the FBDs assessed.

At the population level, listeriosis results in an average of 0.29 (95% UI: 0.20–0.39) YLD and 1.98 (95% UI: 1.96–1.99) YLL, corresponding to a total burden of 2.27 (95% UI: 2.19–2.36) DALYs per 100,000 population annually.

When analysing disease pathways separately, perinatal and acquired listeriosis contribute differently to the overall burden of disease. Perinatal listeriosis contributes an average of 16.04 (95% UI: 12.93–19.15) DALYs per year, comprising 12.45 (95% UI: 12.41–12.48) DALYs due to YLL and 3.60 (95% UI: 0.49–6.71) DALYs due to YLD. Symptomatic infection accounts for 78% of the total perinatal listeriosis burden, corresponding to 12.58 (95% UI: 12.50–12.67) DALYs annually, while permanent disability due to meningitis accounts for the remaining 22%, contributing 3.46 (95% UI: 0.35–6.57) DALYs per year.

Acquired listeriosis contributes the majority of the overall burden, with an average of 90.33 (95% UI: 88.32–92.34) DALYs annually, consisting of 80.14 DALYs due to YLL and 10.20 DALYs due to YLD. Symptomatic infection dominates the acquired listeriosis burden, accounting for 96% of total DALYs (86.93 (95% UI: 85.16–88.71) DALYs per year), while permanent disability due to meningitis contributes the remaining 4%, equivalent to 3.40 (95% UI: 2.47–4.35) DALYs annually.

3.3.3 Salmonellosis

Total burden of salmonellosis

This study simulated the average number of salmonellosis cases acquired in Ireland over a 5-year period (2015–2019), which was approximately 206 annually. With an MF applied to account for potential UE, the total number of cases contributing to the annual burden of disease was estimated at approximately 1,427.

Risk Ranking of Microbiological Hazards in Food (2015–2019)

The model outcomes indicate that salmonellosis contributes an average of 19.33 (95% UI: 18.18–20.49) DALYs annually, representing the combined 13.73 (95% UI: 12.82–14.64) DALYs resulting from YLL due to premature death and 5.59 (95% UI: 4.92–6.35) DALYs resulting from YLD.

At the population level, salmonellosis results in an average of 0.29 (95% UI: 0.27–0.31) YLL and 0.12 (95% UI: 0.10–0.13) YLD, a total burden of 0.41 (95% UI: 0.38–0.43) DALYs per 100,000 population annually. On average, each case of salmonellosis contributing to the annual burden results in a loss of 0.01 DALYs.

When analysing the contribution of different health outcomes to the annual burden of salmonellosis, symptomatic infection contributes the greatest amount to the burden of disease, representing 83% of the total, equivalent to 16.11 (95% UI: 15.23–17.04) DALYs per year. ReA accounts for the remaining 17% of the burden of disease, with 3.19 (95% UI: 2.51–3.94) DALYs annually.

3.3.4 STEC

Total burden of STEC

This study simulated the average number of STEC cases acquired in Ireland over a 5-year period (2015–2019), which was approximately 859 annually. With an MF applied to account for potential UE, the total number of cases contributing to the annual burden of disease was estimated at approximately 6,299.

The findings indicate that STEC contributes an average of 295.39 (95% UI: 285.59–285.89) DALYs annually, representing the combined 221.86 (95% UI: 213.00–230.99) DALYs resulting from YLL due to premature death and 73.55 (95% UI: 70.46–76.55) DALYs resulting from YLD.

At the population level, STEC results in an average of 4.66 (95% UI: 4.47–4.85) YLL and 1.54 (95% UI: 1.48–1.61) YLD, a total burden of 6.2 (95% UI: 6.00–6.41) DALYs per 100,000 population annually. On average, each case of STEC contributing to the annual burden results in a loss of 0.05 DALYs.

When analysing the contribution of different health outcomes to the annual burden of STEC, symptomatic infection represents 23% of the total burden of disease, equivalent to 67.93 (95% UI: 65.03–69.97) DALYs per year. The varying sequelae (i.e. HUS, end-stage renal disease and organ transplant) accounted for the largest proportion of burden of disease (77%) at 227.46 (95% UI: 218.36–237.58) DALYs annually.

3.3.5 Hepatitis A infection

Total burden of hepatitis A infection

During the 5-year period from 2015 to 2019, the average annual number of reported hepatitis A infections acquired in Ireland was approximately 30 cases. After applying an MF to account for potential UE, the total number of cases contributing to the annual disease burden was estimated at approximately 292.

The findings indicate that hepatitis A infection contributes an average of 16.64 (95% UI: 14.25–18.70) DALYs annually, representing the combined 12.77 (95% UI: 10.98–14.59) DALYs resulting from YLL due to premature death and 3.88 (95% UI: 3.03–4.91) DALYs resulting from YLD.

At the population level, hepatitis A infection results in an average of 0.27 (95% UI: 0.23–0.31) YLL and 0.08 (95% UI: 0.06–0.10) YLD, a total burden of 0.35 (95% UI: 0.30–0.39) DALYs per 100,000 population annually. On average, each case of hepatitis A infection contributing to the annual burden results in a loss of 0.06 DALYs.

3.3.6 Hepatitis E infection

Total burden of hepatitis E infection

During the 4-year period from 2016 to 2019, the average annual number of reported hepatitis E infections acquired in Ireland was approximately 37 cases. With an MF applied to account for potential UE, the total number of cases contributing to the annual disease burden was estimated at approximately 29. This lower result is due to a high proportion of infections simulated for the asymptomatic pathway and therefore not contributing to the burden of disease.

The findings indicate that hepatitis E infection contributes an average of 2.06 (95% UI: 0.10–14.76) DALYs annually, representing the combined 1.87 (95% UI: 0.00–14.53) DALYs resulting from YLL due to premature death and 0.19 (95% UI: 0.13–0.28) DALYs resulting from YLD. At the population level, hepatitis E infection results in an average of 0.038 (95% UI: 0.032–0.044) YLL and 0.004 (95% UI: 0.003–0.004) YLD, a burden of 0.61 (95% UI: 0.51–0.70) DALYs per 100,000 population annually. On average, each case contributing to the annual burden results in a loss of 0.06 DALYs.

When analysing the contribution of different health outcomes to the annual burden of HEV, moderate symptomatic infection represented approximately 5.9% of the total burden at 0.12 (95% UI: 0.06–0.21) DALYs. Severe infection resulted in 0.07 (95% UI: 0.02–0.16) DALYs, which accounted for 3.9% of DALYs towards the total burden, while fatal outcomes overwhelmingly dominated the burden at 1.87 (95% UI: 0.00–14.53) DALYs, accounting for over 90% of the annual

DALYs. This reflected the disproportionate impact of death among older adults with hepatitis E infection, even though the total number of fatal cases is small.

3.3.7 Norovirus infection

Total burden of norovirus infection

This study simulated the average number of norovirus cases in Ireland over a 5-year period (2015–2019), which was approximately 1,402 annually. With an MF applied to account for potential UE, the total number of cases contributing to the annual burden of disease was estimated at approximately 1,379,000.

The findings indicate that norovirus contributes an average of 713.18 (95% UI: 426.56–1049.09) DALYs annually, representing the combined 0.15 (95% UI: 0.00–0.71) DALYs resulting from YLL due to premature death and 713.03 (95% UI: 426.56–1049.09) DALYs resulting from YLD estimates. At the population level, norovirus results in an average of 14.98 (95% UI: 8.96–22.03) DALYs per 100,000 population annually, the sum of which results largely from YLD, while the YLL was negligible for this estimate. On average, each case of norovirus contributing to the annual burden results in a loss of 0.002 DALYs.

When analysing the contribution of different health outcomes to the annual burden of norovirus, the burden is almost entirely attributable to mild acute gastrointestinal illness (AGI), accounting for 677.02 DALYs (95% UI: 396.21–1,009.72), which represents 94.9% of the total burden. Severe AGI contributed 36.00 DALYs (95% UI: 23.75–48.88), corresponding to 5% of the total burden, reflecting its much lower incidence despite higher per-case severity. Mortality contributed minimally, with years of life lost (YLL) accounting for 0.15 DALYs (95% UI: 0.00–0.71), representing less than 0.1% of the total burden. Overall, the burden of norovirus was overwhelmingly driven by mild morbidity, with comparatively small contributions from severe morbidity and mortality.

Chapter 4 Attribution of foodborne human illness from microbiological hazards

4.1 Introduction

This stage employed an expert elicitation approach to estimate the proportion of disease incidence attributable to foodborne transmission for each selected hazard, explicitly accounting for uncertainty in these estimates. While these estimates could be generated by other means, sufficiently granular empirical data on the attribution of cases to the foodborne pathway are currently lacking. This rendered expert opinion the most suitable option for this study.

4.2 Selection of experts

The selection of experts for structured expert elicitation is typically based on various considerations, including the expected variability among the experts, the resources available for conducting the work and the time frame required to complete the process. Considering the relatively limited pool of qualified and experienced experts in Ireland within the public health, veterinary microbiology, and food safety scientific communities, a panel of at least nine experts (three from each overarching discipline) was determined to be an appropriate size for our purposes. The expert selection process was carried out using the following criteria:

- Location: The candidates should be based in Ireland.
- Evidence of expertise: The candidates should fulfil one or both of the following criteria:
 - They should have a PhD in microbiology, public health (human or veterinary) or a related discipline.
 - They should have a minimum of 10 years of professional experience in the field of food microbiology or a related discipline, specifically within Ireland.
- Field of employment: The panel should comprise representatives from the public health, veterinary microbiology, and food safety sectors, ensuring a comprehensive interdisciplinary approach.
- Impartiality: The candidates should not have any conflicts of interest.

In order to meet our participant quota, we selected a panel of 13 experts who met the criteria for this elicitation process.

4.3 Transmission routes

The disease transmission routes considered for the expert elicitation on source attribution are defined in [Table 1](#), which was adapted from Cressey *et al.* (2019). The transmission routes include water (drinking water only, excluding bottled water), animal contact, the environment (air, soil, and recreational contact with water), food (including bottled water), and human-to-human transmission.

Table 1 Transmission routes to be addressed in the expert elicitation

Transmission route	Definition
Food	Transmission through food that is contaminated at the source (e.g. from irrigation; faeces of food animals) or during processing and preparation. Preparation might be in any location, including abattoirs, food processing lines, kitchens, outdoor venues (domestic and commercial), etc. Food transmission includes contamination by food handlers and infections in people who have handled contaminated foods. Bottled water is also included in this category as food.
Water	Transmission through contaminated drinking water from any distribution system (including public and private supplies). This excludes accidental ingestion of recreational water (e.g. while swimming) and consumption of bottled water.
Environmental	Transmission through environmental matrices (soil, recreational water, etc.).
Animal contact	Transmission by direct contact with animals (farm animals, pets, animals at petting zoos, animals at livestock processing plants, etc.).
Human-to-human	Direct or indirect transmission from one infected person to another person (contaminated fomites, air, etc.).

Source: Adapted from Cressey *et al.* (2019).

The participants were asked to rank the relevance of each transmission route for each hazard in order to consider all potential pathways of disease transmission. By having the participants deliberately consider multiple transmission routes before attributing cases to the food pathway, it was hoped this would prevent them from overestimating the incidence of disease transmission resulting from food. Moreover, the different categories of ‘water’ versus ‘environmental’ were used in order to help clarify and prevent confusion about the definition of waterborne transmission, and

to assist in generating internal consistency in food attribution estimates. The denominator was for all cases of the disease where infection was acquired in Ireland (i.e. excluding travel-related cases).

4.4 Methods

4.4.1 Briefing material for participants

Briefing material was prepared and provided to the participants, along with a clear description of the problem, the parameters to be estimated and the definitions needed to ensure consistency (e.g. in the case of norovirus, food that has been contaminated by food handlers, as well as the infections in people who have handled contaminated foods, is considered foodborne in the context of the study). Examples were provided to guide completion of the questionnaire. The elicitation exercise sought to draw on individual expert knowledge. Consequently, participants were not provided with information concerning the microorganisms and diseases of interest, other than a briefing preface in the questionnaire.

4.4.2 Expert elicitation process

The elicitation followed a two-round Delphi method, adapted from the approach used by Cressey et al. (2019a, b, c, d) and similar studies (Gallagher et al., 2002; Helmer, 1967). This process enabled participants to review aggregated results from the first round and revise their estimates in the second, but with no attempt made to generate a consensus value for estimates. The specific steps involved in the expert elicitation are outlined in the following sections.

Round one: Electronic completion of the questionnaire

In round one, the participants:

- Reviewed the initial briefing document and worked example (see [Appendix 11](#)).
- Completed the self-assessment of expertise, which was used for weighting purposes (see [Appendix 11](#); approach described in Section 4.4.3).
- Completed an electronic questionnaire designed to elicit plausible transmission estimates for each disease (see [Appendix 11](#)). Each question was framed using natural frequencies (e.g. “Out of 100 cases, how many....?”). For each estimate, participants provided four values: (i) a minimum, (ii) a maximum, (iii) a most likely value, and (iv) their confidence (0–100%) that the true value lay within the stated range. Participants could opt out of providing

estimates for specific hazards or diseases if they did not consider themselves sufficiently knowledgeable to contribute.

Round two: In-person round-table discussion on round one group estimates

In round two, the participants:

- Completed the physical calibration exercise, which was used for weighting purposes (see [Appendix 11](#); approach described in Section 4.4.3).
- Participated in an independent, expert-facilitated, face-to-face chaired round-table discussion on the group's preliminary estimates. Participants were encouraged to discuss the results from the first round, particularly the estimates that differed markedly from those of the other panel members. Participants were able to update their estimates, if desired, on the elicitation questionnaire. The meeting was led by a competent individual who had no conflicts of interest.

4.4.3 Weighting schemes

In any expert elicitation, there exists the possibility that some participants will be more informed and more influential than others. This may be due to their own personal knowledge or their ability to effectively express that knowledge and its associated uncertainty. Applying different weighting schemes is a useful sensitivity test for the elicitation outputs. Three approaches were explored to determine weightings for the elicitation results based on the methods employed in an expert elicitation conducted in New Zealand (Cressey *et al.* 2019) and are discussed in the following sections.

Equal weightings

Experts' estimates were assigned the same importance on their source attribution estimates and therefore contributed equally to the aggregation process.

Self-assessed weightings

At the start of the expert elicitation questionnaire, participants were requested to provide a self-assessment of their expertise with respect to each hazard/disease.

Expertise was expressed on a five-point Likert scale using the following descriptors:

- **No response** = insufficient expertise on microorganism to provide any opinion
- **1** = low expertise: no direct experience, anecdotal knowledge only
- **2** = low-medium expertise: intermediate experience between levels 1 and 3
- **3** = medium expertise: some direct experience, wide reading
- **4** = medium-high expertise: intermediate expertise between levels 3 and 5
- **5** = high expertise: primary focus of professional work.

These self-allocated scores were then used to contribute to the aggregation process.

Performance-based weightings

An objective calibration process was carried out at the face-to-face meeting to derive performance-based weights (Cressey *et al.* 2019d). Participants were requested to fill out a calibration questionnaire ([Appendix 12](#)) and provide estimates with uncertainty for a series of questions pertinent to expertise in food attribution. These parameters have known values to the study coordinators and differed from those for which the elicitation is being conducted. The participants' performance in estimating these 'seed' variables was gauged based on the precision of their estimate and the uncertainty.

Expert weights were calculated using the Excalibur software, which is a software package for structured expert judgement elicitation based on Cooke's Classical Model (Cooke and Goossens, 2000) and was originally developed at Delft University of Technology before later maintenance by LightTwist Software (TU Delft OpenCourseWare, n.d.). Scoring rules defined within Cooke's method were used to assign weights to individual participants during the aggregation process, consistent with the use of performance-based weighting documented in similar elicitation studies such as Cressey *et al.* (2019a).

An optimisation process was employed for calculating the weights, which meant that participants who demonstrated stronger performance on the calibration questions received higher weights, while contributions from other participants were still incorporated with proportionally lower weights. Because participants were allowed to abstain from answering questions outside their expertise, some variability in the completeness of responses was expected. This made the optimisation mechanism important for ensuring that estimates reflected each participant's demonstrated performance while still allowing for all contributions to be included.

While a calibration process is an established practice, developing high-quality calibration questions remains a recognised challenge in practice; therefore, the results should be interpreted within the context of its methodological limitations.

4.4.4 Confidence estimates for elicited intervals

After round one, it became clear that some participants misunderstood how to express their confidence estimates when completing their questionnaires. To address this, the second round began with a detailed explanation provided to the group to clarify that an individual's confidence value represents the expert's judgement about the likelihood that the true value lies within the interval provided. This aligns with EFSA's guidance, which defines uncertainty expressions as statements about the probability that the real, error-free value falls within a specified range (EFSA, 2019).

For example, if an estimate spans a wide interval such as 20–70 cases, the associated confidence level should reflect the statistical uncertainty of the underlying data, rather than the proportion of the total possible range that the interval covers. If the confidence estimate is less than 50%, this communicates that the participant believes the true value likely falls outside the interval. The confidence level should normally exceed the interval's width (i.e. maximum–minimum) and should generally be above 70% for this elicitation. If unsure, participants were encouraged to widen their interval or omit from contributing their judgement for that hazard.

4.4.5 Aggregation of opinions

The four-point estimates from each participant were encoded as a program evaluation and review technique (PERT) distribution representing the participant's opinion, with the parameters being 'minimum', 'most likely' and 'maximum'. The range of the PERT distribution was adjusted so that the percentage of the distribution covering the participant's interval matched the participant's stated confidence level. An aggregate estimate of each parameter and its associated uncertainty was determined by simulating a Monte Carlo sampling of all participants' distributions from the four-point method, weighted by the methods outlined in [Section 4.4.3](#). After the elicitation, participants were offered the opportunity to review their own final distributions and compare them with the group aggregate.

4.4.6 Selection of weighting approach for foodborne DALYs

In the comparative analysis of the three expert weighting approaches applied to the elicitation (equal, self-assessed and performance-based), it was observed that all three methods produced relatively consistent outcomes. The convergence of results across these weighting strategies indicates a general robustness in the elicited data, irrespective of which specific method is used to assign weights to expert judgements.

Given this similarity in outcomes, the self-assessed weighting approach was used for the final generation of estimates for foodborne DALYs. This decision was grounded in both methodological rationale and practical relevance. Participants who rated their own expertise more highly are presumed to possess a deeper and more nuanced understanding of the hazards dealt with in the study and their transmission. By giving greater weight to these individuals' judgements, the analysis should have more reliable results due to their knowledge of specific hazards. In addition, such specialised insights might not have been fully captured through the calibration questionnaire that was used to determine the performance-based weightings. While the performance-based weighting is objective, it may undervalue expert contributions that are crucial but difficult to quantify through general test performance. Equal weighting, while simple and unbiased in nature, does not account for varying depths of knowledge among participants. Therefore, using the self-assessed expertise weighting method was both a pragmatic and a scientifically defensible choice for this context, particularly as the three weighting approaches offered overlapping narratives (95% UIs) on the food attribution of the project diseases.

4.5 Results

This section presents the outcomes derived from estimating the extent to which each burden of disease is transmitted through food. Additionally, five transmission routes were ranked based on their relative significance for each hazard.

4.5.1 Participant self-assessment of expertise

Participants in the expert elicitation were asked to provide a self-assessment of their expertise with respect to each hazard and its disease for weighting purposes. [Table 2](#) presents the results of these self-assessments, summarising the number of experts within each scoring grade, as well as the mean overall expertise across those who answered questions on each hazard. The mean value excludes those who chose to opt out of answering questions on a hazard due to their declared lack of expertise. These self-allocated scores with regard to each hazard contributed to the aggregation process as outlined in [Section 4.4.3](#).

4.5.2 Ranking of transmission routes

The mean rank position for each of the five transmission routes (i.e. animal contact, environment, food, human to human, and water) with respect to each hazard is presented in [Table 3](#). Ratings were weighted according to the equal, self-assessed and performance-based weighting schemes.

The ranking system is such that the mean rank positions close to 5.0 indicate a high level of consensus that a particular transmission route is the main contributor to the total number cases. Conversely, a mean rank position close to 1.0 indicates consensus that a particular transmission route is the lowest contributor to total cases.

4.5.3 FBD transmission estimates based on weighting schemes

An aggregate of the mean FBD transmission estimates, along with the respective 95% UIs, based on the equal, self-assessed and performance-based weighting schemes employed, are presented in [Table 4](#). For each FBD, [Appendix 13](#) presents: (i) the individual and aggregate attribution estimates with 95% UIs for food pathway cases (Figures 13, 15, 17, 19, 21, 23 and 25), and (ii) the combined distribution of estimates for the attribution of cases to food pathways (Figures 14, 16, 18, 20, 22, 24 and 26).

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Table 2** The participants' (n=13) self-rated expertise for each hazard on a five-point scale, showing the number of experts in each category and the mean expertise score for each hazard

Microbiological hazard	Number of experts in expertise category ^a						Mean expertise score for each hazard ^b
	Expertise: 0	Expertise: 1	Expertise: 2	Expertise: 3	Expertise: 4	Expertise: 5	
<i>Campylobacter</i> spp.	1	0	2	3	5	2	3.6
<i>L. monocytogenes</i>	1	0	1	4	3	4	3.8
<i>Salmonella</i> spp.	1	0	0	5	3	4	3.9
STEC	1	0	1	3	3	5	4.0
HAV	6	2	0	1	1	3	3.4
HEV	6	2	0	2	1	2	3.1
Norovirus	3	3	2	2	1	2	2.7

^a The expertise categories were rated on a five-point Likert scale, with 1 indicating low expertise and 5 indicating high expertise. A score of '0' was used when the respondent chose to abstain from answering questions related to a specific microorganism, indicating that they did not consider themselves sufficiently knowledgeable in that area.

^b The denominating number of participants varies for each hazard, as follows: *Campylobacter* spp.: n=12; *L. monocytogenes*: n=12; *Salmonella* spp.: n=12; STEC: n=12; HAV: n=7; HEV: n=7; and norovirus: n=10.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Table 3** Mean rank position for each of the five transmission routes for selected hazards, averaged over the three different weighting schemes (equal, self-assessed and performance-based)

Microbiological hazard	Mean rank position ^a (equal, self-assessed, and performance-based weighting)				
	Animal contact	Environment	Food	Human-to-human	Water
<i>Campylobacter</i> spp.	(3.1, 3.0, 3.0)	(2.1, 1.9, 2.8)	(4.3, 4.3, 4.0)	(2.7, 2.7, 1.9)	(2.4, 2.4, 3.2)
<i>L. monocytogenes</i>	(2.5, 2.4, 3.4)	(2.1, 2.1, 2.3)	(4.7, 4.6, 3.8)	(3.1, 3.1, 3.5)	(1.6, 1.5, 1.4)
<i>Salmonella</i> spp.	(3.5, 3.1, 3.2)	(1.8, 1.5, 2.0)	(4.5, 4.1, 4.0)	(3.1, 2.7, 3.0)	(2.1, 1.8, 3.0)
STEC	(3.9, 4.0, 3.6)	(2.1, 2.2, 2.5)	(2.2, 2.2, 1.9)	(3.5, 3.5, 3.6)	(3.7, 3.7, 3.4)
HAV	(1.4, 1.0, 1.5)	(1.9, 1.2, 2.0)	(3.9, 3.2, 4.2)	(3.7, 3.3, 3.5)	(2.3, 1.4, 2.5)
HEV	(3.3, 2.4, 3.2)	(1.7, 1.1, 1.8)	(4.4, 3.5, 4.3)	(2.0, 1.7, 2.2)	(2.3, 1.6, 2.2)
Norovirus	(1.2, 0.8, 2.0)	(3.1, 2.6, 4.1)	(2.8, 2.5, 2.0)	(4.3, 3.9, 3.9)	(2.9, 2.5, 3.0)

^a The individual estimates of the rank position (5 = transmission route contributing the most cases, 1 = transmission route contributing the fewest cases; ties allowed) were combined as a weighted mean using either equal weighting, weighting based on self-assessed expertise, or performance-based weights.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Table 4** Aggregate of mean FBD transmission estimates based on weighting scheme and 95% UIs

Disease	Mean aggregate foodborne estimate (%) ^a and 95% UI based on weighting scheme ^b		
	Equal ^c	Self-assessed ^c	Performance-based ^c
Campylobacteriosis	75 (95% UI: 61–95)	76 (95% UI: 61–96)	72 (95% UI: 59–90)
Listeriosis	92 (95% UI: 81–99)	92 (95% UI: 81–99)	90 (95% UI: 80–99)
Salmonellosis	77 (95% UI: 50–95)	77 (95% UI: 52–96)	82 (95% UI: 64–96)
STEC infection	27 (95% UI: 10–51)	28 (95% UI: 9–53)	32 (95% UI: 12–59)
Hepatitis A infection	35 (95% UI: 6–79)	30 (95% UI: 6–79)	35 (95% UI: 6–79)
Hepatitis E infection	63 (95% UI: 23–93)	62 (95% UI: 24–92)	59 (95% UI: 22–92)
Norovirus infection	24 (95% UI: 2–50)	23 (95% UI: 2–50)	30 (95% UI: 4–52)

^a The proportion of total infections estimated to be attributed to foodborne transmission.

^b Estimates represent weighted mean aggregates across expert elicitation results, with 95% UIs derived from the corresponding aggregated uncertainty distributions. All values are rounded to whole percentages.

^c Equal, self-assessed, and performance-based weighting schemes are described in the methods.

4.5.4 Campylobacteriosis

In food safety risk ranking exercises, *Campylobacter* spp. often ranks highly as a hazard due to its high incidence of foodborne illness. It is the most common reported cause of bacterial gastroenteric infection within the European Union. While generally self-limiting, it can cause severe illness leading to hospitalisation and long-term complications like Guillain-Barré syndrome (GBS) (EFSA, 2025a).

Ranking of transmission pathways

Based on the three weighting methods, the experts' (n=12) estimates were aggregated to rank the relevance of the following transmission routes:

- **Equal:** Animal contact: 3.1; environment: 2.1; food: 4.3; human to human: 2.7; water: 2.4
- **Self-assessed:** Animal contact: 3.0; environment: 1.9; food: 4.3; human to human: 2.7; water: 2.4
- **Performance-based:** Animal contact: 3.0; environment: 2.9; food: 4.0; human to human: 1.8; water: 3.2.

Food was ranked as the most relevant transmission pathway across all weighting methods (4.3, 4.3, and 4.0). Animal contact was considered to be the second-most relevant pathway of transmission, with rankings of 3.1, 3.0 and 3.0. The remaining three pathways were ranked similarly across weighting categories, with water transmission scores of 2.4, 2.4 and 3.2; human-to-human transmission scores of 2.7, 2.7 and 1.9; and environmental transmission scores of 2.1, 1.9 and 2.8.

Attribution of campylobacteriosis cases to the food pathway

Based on the three weighting methods, the experts' (n=12) estimates were aggregated to determine the proportion of cases attributed to the food pathway as follows:

- **Equal:** 75% (95% UI: 61–95)
- **Self-assessed:** 76% (95% UI: 61–96)
- **Performance-based:** 72% (95% UI: 59–90).

It was estimated that a substantial proportion of campylobacteriosis cases (approximately 59–96%) resulted from foodborne transmission. The estimates for campylobacteriosis were consistent across all weighting methods applied, with slight reductions under the

performance-based weighting method. This suggests a broad agreement among experts regardless of the weighting method but suggests that those who performed better in the calibration questionnaire (performance-based) were slightly more conservative in their estimates.

During the discussions in the second round of expert elicitation, it was noted that data availability for reliable source attribution in Ireland is limited. Specifically, there is an absence of enhanced surveillance for campylobacteriosis, a limited number of reported outbreaks, and insufficient typing data covering the overall number of campylobacteriosis cases. Most reported human cases are in young children, often in creches, suggesting transmission from human-to-human spread or indirect food exposure. Poultry meat is regarded as the primary suspected source of transmission, although contamination of other food may also occur via soil, manure and other animals. Testing challenges in human cases were noted, as some cases are test positive on polymerase chain reaction (PCR) tests but are not detected on culture, leading to uncertainties in data quality. Outbreaks are rare and most cases appear to be sporadic, further complicating source identification. The experts highlighted that the most recent case-control study is outdated and that a new study is warranted.

Figures 13 and 14 ([Appendix 13](#)) present the individual and aggregated estimates, along with the overall distribution of the food pathway attribution data. The distribution of experts' estimates for foodborne attribution of campylobacteriosis is mostly normal, with a mean centred around 75%. A slight right skewness is observed, evidenced by a secondary small peak near 95–100%. While most experts estimate that approximately 75% of cases of campylobacteriosis are foodborne, a subset indicate the possibility of a significantly higher attribution, approaching 100%.

4.5.5 Listeriosis

L. monocytogenes typically ranks high in food safety risk ranking exercises. Although listeriosis is rare, the disease outcome is often severe, particularly for vulnerable groups such as pregnant women and their unborn children, newborns, older adults, and individuals with compromised immune systems. Listeriosis outbreaks can result in significant morbidity and mortality, necessitating strong preventative measures in high-risk ready-to-eat foods (EFSA, 2025b).

Ranking of transmission pathways

Based on the three weighting methods, the experts' (n=12) estimates were aggregated to rank the relevance of the following transmission routes:

- **Equal:** Animal contact: 2.5; environment: 2.1; food: 4.7; human to human: 3.1; water: 1.6
- **Self-assessed:** Animal contact: 2.4; environment: 2.1; food: 4.6; human to human: 3.1; water: 1.5
- **Performance-based:** Animal contact: 3.4; environment: 2.3; food: 3.8; human to human: 3.5; water: 1.4.

Food was identified as the most relevant transmission pathway across all of the weighting methods (4.7, 4.6 and 3.8). Animal contact (2.5, 2.4 and 3.4) and human-to-human transmission (3.1, 3.1 and 3.5) were also highly ranked as notable sources of transmission. Environmental transmission (2.1, 2.1 and 2.3) was considered an appreciable, but less likely source of transmission. Water, on the other hand, was regarded as the least relevant source of transmission (1.6, 1.5 and 1.4).

Attribution of listeriosis cases to the food pathway

Based on the three weighting methods, the experts' (n=12) estimates were aggregated in order to determine the proportion of cases attributed to the food pathway:

- **Equal:** 92% (95% UI: 81–99)
- **Self-assessed:** 92% (95% UI: 81–99)
- **Performance-based:** 90% (95% UI: 80–99).

A high proportion of listeriosis cases (approximately 80–99%) were estimated to result from foodborne transmission. The estimates acquired from the expert elicitation are consistently high, with relatively moderate UIs across the three weighting methods. This indicates a strong consensus that listeriosis is predominantly foodborne. A slight reduction in the estimated numbers of foodborne listeriosis was observed when performance-based weighting was applied, which suggests that highly experienced experts may consider a marginally higher likelihood of non-foodborne transmission.

During the discussions in the second round of the expert elicitation, it was noted that most cases of listeriosis are linked to high-risk, chilled, ready-to-eat foods (e.g. soft cheeses, ready-to-eat meat, smoked fish). *L. monocytogenes* has a long incubation period (an average duration of approximately 3 weeks, ranging from 3 to 70 days) (HPSC, 2025),

making it difficult to trace back to a specific food. It is commonly associated with food processing environments.

Figures 15 and 16 ([Appendix 13](#)) present the individual and aggregated estimates, along with the overall distribution of the food pathway attribution data. The distribution is skewed, with a tail to the left. There is also a notable concentration towards higher proportions, particularly a prominent peak close to 100%. Experts generally concur that listeriosis is primarily attributable to food, with the majority of estimates regarding this pathway being above 80%, although some variation exists, indicating that a smaller portion of cases may be attributable to other sources.

4.5.6 Salmonellosis

In food safety risk ranking exercises, *Salmonella* commonly has a high ranking as a foodborne pathogen in the risk ranking literature due to its association with substantial illness. Although most cases are mild, specific serotypes (e.g. *Salmonella typhimurium* or *Salmonella Dublin*) are more frequently linked to severe illness, and the presence of antimicrobial resistance may further elevate the associated risks (EFSA, 2025c). Only serotypes of *Salmonella enterica* subspecies *enterica* are considered to be attributable to food pathways (excluding *Salmonella Typhi*, *Salmonella Paratyphi* and *Salmonella choleraesuis*).

Ranking of transmission pathways

Across the three weighting methods, the experts' (n=12) estimates were aggregated to rank the relevance of the following transmission routes:

- **Equal:** Animal contact: 3.5; environment: 1.8; food: 4.5; human to human: 3.1; water: 2.1
- **Self-assessed:** Animal contact: 3.1; environment: 1.5; food: 4.1; human to human: 2.7; water: 1.8
- **Performance-based:** Animal contact: 3.2; environment: 2.0; food: 4.0; human to human: 3.0; water: 3.0.

Food was identified as the primary transmission pathway for salmonellosis across all weighting methods (4.5, 4.1 and 4.0). Contact with animals (3.5, 3.1 and 3.2), human-to-human transmission (3.1, 2.7 and 3.0) and waterborne transmission (2.1, 1.8 and 3.0) were

all identified as notable transmission sources. In contrast, the environment, with lower ratings (1.8, 1.5 and 2.0), was seen as the least relevant transmission source.

Attribution of salmonellosis cases to the food pathway

Across the three weighting methods, the experts' (n=12) estimates were aggregated in order to determine the proportion of cases of salmonellosis attributed to the food pathway:

- **Equal:** 77% (95% UI: 50–95)
- **Self-assessed:** 77% (95% UI: 52–96)
- **Performance-based:** 82% (95% UI: 64–96).

A moderate to high proportion of salmonellosis cases (approximately 50–96%) were estimated to result from foodborne transmission. The estimates derived from the equal and self-assessed weighting methods were closely aligned. The performance-based weighting approach yielded the highest estimate, with reduced uncertainty relative to the other methods. This suggests that those who performed well in the calibration exercise had more confidence in their understanding of *Salmonella*'s foodborne transmission routes.

During the discussions in the second round of the expert elicitation, it was noted that surveillance data for salmonellosis are limited. Approximately 25–30% of cases were regarded as being associated with farming families and exposure to cattle. This occupational exposure is relevant mainly for farm settings as opposed to food processing environments. The likelihood of transmission from household pets – including reptiles, bird feeders, and fish food – and pet food was briefly noted. It was highlighted that the attribution of cases of salmonellosis varies by serovar, and the current Irish surveillance systems do not differentiate risks adequately across the serovars.

Figures 17 and 18 ([Appendix 13](#)) present the individual and aggregated estimates, along with the overall distribution of the food pathway attribution data. The distribution is skewed with a tail to the left. There are also two predominant peaks lying close together at approximately 75% and 85%, with a third, smaller peak near 100%. This corresponds to the majority of experts attributing 75–85% of salmonellosis cases to food, with one expert estimating it to be closer to 100%.

4.5.7 STEC

In the risk ranking literature of microbiological hazards in food, STEC often ranks very high due to the severe, sometimes fatal, outcomes such as haemolytic uraemic syndrome (HUS).

While incidence rates for STEC may be lower than those of other pathogens, its severity and long-term health consequences make it a priority (Health Service Executive, 2022).

Ranking of transmission pathways

Across the three weighting methods, the experts' (n=12) estimates were aggregated to rank the relevance of the following transmission routes:

- **Equal:** Animal contact: 3.9; environment: 2.1; food: 2.2; human to human: 3.5; water: 3.7
- **Self-assessed:** Animal contact: 4.0; environment: 2.2; food: 2.2; human to human: 3.5; water: 3.7
- **Performance-based:** Animal contact: 3.6; environment: 2.5; food: 1.8; human to human: 3.6; water: 3.4.

Animal contact (3.9, 4.0 and 3.6), human-to-human transmission (3.5, 3.5 and 3.6) and waterborne routes (3.7, 3.7 and 3.4) were all rated as the most relevant transmission pathways for STEC. In contrast, food (2.2, 2.2 and 1.8) and environmental exposure (2.1, 2.2 and 2.5) were seen as less relevant sources of transmission.

Attribution of STEC cases to the food pathway

Across the three weighting methods, the experts' (n=12) estimates were aggregated in order to determine the proportion of cases of STEC attributed to the food pathway:

- **Equal:** 27% (95% UI: 10–51)
- **Self-assessed:** 28% (95% UI: 9–53)
- **Performance-based:** 32% (95% UI: 12–59).

A relatively low to moderate proportion of STEC cases (approximately 9–59%) were estimated to result from foodborne transmission. The estimates derived from the equal and self-assessed weighting methods were closely aligned. The performance-based weighting approach yielded the highest mean estimate of the proportion of STEC cases attributed to the food pathway, indicating that the higher-performing experts see STEC as more foodborne than the general expert pool. Nonetheless, the wide intervals across the three weighting methods indicate considerable uncertainty.

During the discussions in the second round of the expert elicitation, it was noted that people living in rural settings, especially those who use private wells or are exposed to farms,

showed a higher incidence of STEC infection. Many outbreaks have occurred in childcare facilities, where human-to-human spread was common. Although confirmed cases of foodborne transmission of STEC were considered to be infrequent in Ireland, isolated incidents were linked to foods like raw milk, onions, sprouts and burgers. The introduction of PCR testing has increased case detection in humans, but attribution to food remains limited.

Figures 19 and 20 ([Appendix 13](#)) present the individual and aggregated estimates, along with the overall distribution of the food pathway attribution data. The data distribution has a notable peak around 15%, with a broad range of estimates primarily in the 10–50% range. Variability and uncertainty are higher in the estimates attributing STEC infections to the food pathway compared with some of the other bacterial hazards.

4.5.8 Hepatitis A infection

HAV in food incurs varying levels of concern in food safety risk ranking exercises due to its potential for large-scale outbreaks, particularly resulting from contaminated food and water; however, this risk is somewhat reduced by the availability of vaccines. Still, although vaccines are available, the pathogen continues to represent a notable risk to public health, particularly in regions with inadequate sanitation (WHO, 2025).

Ranking of transmission pathways

Across the three weighting methods, the experts' (n=7) estimates were aggregated in order to rank the relevance of the following transmission routes:

- **Equal:** Animal contact: 1.4; environment: 1.9; food: 3.9; human to human: 3.7; water: 2.3
- **Self-assessed:** Animal contact: 1.0; environment: 1.2; food: 3.2; human to human: 3.3; water: 1.4
- **Performance-based:** Animal contact: 1.5; environment: 2.0; food: 4.2; human to human: 3.5; water: 2.5.

Food (3.9, 3.2 and 4.2) and human-to-human transmission (3.7, 3.3 and 3.5) were identified as the most relevant transmission pathways for HAV. Animal contact (1.4, 1.0 and 1.5), environmental transmission (1.9, 1.2 and 2.0) and water (2.3, 1.4 and 2.5) received lower rankings.

Attribution of hepatitis A cases to the food pathway

Across the three weighting methods, the experts' (n=7) estimates were aggregated in order to determine the proportion of hepatitis A cases attributed to the food pathway:

- **Equal:** 35% (95% UI: 6–79)
- **Self-assessed:** 30% (95% UI: 6–79)
- **Performance-based:** 35% (95% UI: 6–79).

A wide range of values (approximately 6–79%) was estimated for the proportion of hepatitis A infection cases resulting from foodborne transmission. All weighting methods used produced very similar estimates, indicating that there is very little difference in results regardless of the weighting method used. The UIs for this estimate are notably broad, which suggests that there was consistent uncertainty among the experts, regardless of their self-assessed expertise or their performance in the calibration questionnaire.

During the discussions in the second round of the expert elicitation, it was noted that HAV transmission is mainly human-to-human, although some foodborne outbreaks have occurred. Frozen berries and infected food handlers were key implicated sources. Shellfish and fresh produce were also identified as foods historically associated with HAV contamination.

Figures 21 and 22 ([Appendix 13](#)) present the individual and aggregated estimates, along with the overall distribution of the food pathway attribution data. The combined distribution of the experts' estimates is strongly multimodal, exhibiting four distinct peaks at approximately 10%, 20%, 50% and 75%. This pattern suggests substantial variation among experts regarding the likelihood of foodborne transmission of HAV, with different groups estimating low, medium and high proportions of food pathway attribution. The observed divergence indicates differing perspectives and/or uncertainties among the experts regarding the role of food in HAV transmission.

4.5.9 Hepatitis E infection

HEV is seldom included in food safety risk-ranking exercises. Lower awareness and detection rates mean that HEV tends to rank lower than other microbiological hazards, but it has gained increased recognition due to its potential for foodborne transmission via undercooked pork and game.

Ranking of transmission pathways

Based on the three weighting methods, the experts' (n=7) estimates were aggregated in order to rank the relevance of the following transmission routes:

- **Equal:** Animal contact: 3.3; environment: 1.7; food: 4.4; human to human: 2.0; water: 2.3
- **Self-assessed:** Animal contact: 2.4; environment: 1.1; food: 3.5; human to human: 1.7; water: 1.6
- **Performance-based:** Animal contact: 3.2; environment: 1.8; food: 4.3; human to human: 2.2; water: 2.2.

Food (4.4, 3.5 and 4.3) was consistently the highest-rated transmission route for HEV. Animal contact (3.3, 2.4 and 3.2) was moderately important. Environmental exposure (1.7, 1.1 and 1.8), human-to-human transmission (2.0, 1.7 and 2.2) and waterborne transmission (2.3, 1.6 and 2.2) were viewed as less relevant transmission routes.

Attribution of hepatitis E cases to the food pathway

Based on the three weighting methods, the experts' (n=7) estimates were aggregated in order to determine the proportion of HEV cases attributed to the food pathway:

- **Equal:** 63% (95% UI: 23–93)
- **Self-assessed:** 62% (95% UI: 24–92)
- **Performance-based:** 59% (95% UI: 22–92).

A moderate to high proportion of hepatitis E cases (approximately 22–93%) were estimated to result from foodborne transmission. The mean estimates derived from the equal and self-assessed weighting methods were closely aligned. The mean estimate decreased slightly under the performance-based weighting method. This suggests that those who performed better in the calibration questionnaire attributed fewer hepatitis E cases to foodborne transmission. However, based on the UIs, the results are consistent across all three weighting methods and align closely with each other.

During the discussions in the second round of the expert elicitation, it was noted that HEV is becoming increasingly recognised as a foodborne pathogen in Ireland, mainly associated with pork products such as raw pork meat and liver pâté. Genotype 3, which is more likely to be linked to food than water, was described as being the dominant strain of HEV in Ireland. Occupational exposure is high among workers on pig farms. While some attribution to shellfish exists, pork remains the most common food vehicle for HEV transmission.

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Figures 23 and 24 ([Appendix 13](#)) present the individual and aggregated estimates, along with the overall distribution of the food pathway attribution data. The combined distribution of the experts' estimates is multimodal, with prominent peaks around 30%, 70% and 90%. While there was a wide range of responses, these points indicate notable concentrations of estimates at these levels. This pattern reflects varying degrees of uncertainty and differing perspectives among the experts, with some considering food to be a moderate pathway for HEV, while others view it as a primary route.

4.5.10 Norovirus infection

Norovirus is a primary cause of acute gastroenteritis worldwide and usually ranks very high in food safety risk ranking exercises globally. This is due to its high incidence, ease of transmission and significant public health burden, despite the fact that the illness caused is usually mild to moderate compared with other microbiological hazards.

Ranking of transmission pathways

Across the three weighting methods, the experts' (n=10) estimates were aggregated in order to rank the relevance of the following transmission routes:

- **Equal:** Animal contact: 1.2; environment: 3.1; food: 2.8; human to human: 4.3; water: 2.9
- **Self-assessed:** Animal contact: 0.8; environment: 2.6; food: 2.5; human to human: 3.9; water: 2.5
- **Performance-based:** Animal contact: 2.0; environment: 4.1; food: 2.0; human to human: 3.9; water: 3.0.

Human-to-human transmission (4.3, 3.9 and 3.9) was deemed the most important pathway for the transmission of norovirus, followed by environmental routes (3.1, 2.6 and 4.1). Water received moderate rankings of 2.9, 2.5 and 3.0, while food was rated with scores of 2.8, 2.5 and 2.0. Animal contact (1.2, 0.8 and 2.0) was consistently deemed the least relevant source of transmission across weighting schemes.

Attribution of norovirus infection cases to the food pathway

Across the three weighting methods, the experts' (n=10) estimates were aggregated in order to determine the proportion of norovirus cases attributed to the food pathway:

Risk Ranking of Microbiological Hazards in Food (2015–2019)

- **Equal:** 24% (95% UI: 2–50)
- **Self-assessed:** 23% (95% UI: 2–50)
- **Performance-based:** 30% (95% UI: 4–52).

A low to moderate proportion of norovirus cases (approximately 2–52%) were estimated to result from foodborne transmission. While the estimates were low across all weighting methods, the performance-based weighting yielded a slightly higher attribution of cases to foodborne transmission. Overall, the experts estimate that the proportion of foodborne norovirus cases may range from as low as 2% to as high as 52%. This indicates a large degree of uncertainty.

During the discussions in the second round of the expert elicitation, it was noted that source identification for norovirus cases is particularly difficult due to its perceived high underestimation (UE) and ascertainment bias. Most reported cases of norovirus are not linked to food, but when they are, they typically involve sandwiches, berries, oysters, and poor hygiene in food service settings. Experts alluded to one notable outbreak that was linked to contaminated water. Notifications of norovirus cases originating from other countries (e.g. from China) have sometimes led to detection in oysters. It was noted that the attribution of human cases of norovirus to contaminated oysters is likely higher than what is currently captured through surveillance data.

Figures 25 and 26 ([Appendix 13](#)) present the experts' individual and aggregated estimates attributing norovirus to food pathways, along with the overall distribution of the food attribution data. The combined distribution of the estimates displays a multimodal pattern, with prominent peaks at approximately 5% and 40%. While there was some variability in the estimates, the majority tended to suggest a lower to moderate level of attribution of norovirus infection to the food pathway.

Chapter 5 Calculating the food burden of human illness from microbiological hazards

5.1 Introduction

This stage aimed to obtain estimates, along with associated uncertainties, on the proportion of incidence caused by each selected hazard as a result of foodborne transmission. These estimates are intended to facilitate a risk ranking of microbiological hazards originating from food in Ireland to support the prioritisation of work for the FSAI.

5.2 Methods

5.2.1 Calculating the foodborne disability-adjusted life years

A Monte Carlo simulation approach was used in order to estimate the number of foodborne disability-adjusted life years (DALYs) for each hazard, incorporating uncertainty in both the total burden of disease and the proportion of cases attributable to foodborne transmission. The foodborne transmission estimates, generated using the self-assessed weighting method, were combined with the overall DALY estimates in order to calculate the foodborne DALYs. Total DALYs were modelled using normal distributions, based on the UIs, while foodborne attribution proportions were modelled using beta distributions fitted to the central estimates and UIs. The simulations were iterated 100,000 times per hazard. In each iteration, a random DALY estimate was multiplied by a randomly sampled foodborne attribution proportion to generate an estimate of foodborne DALYs. Mean estimates and 95% UIs were then derived from the simulated results.

5.3 Results

The estimates on how much the burden for each disease is estimated to be transmitted through food are presented in [Table 5](#). This table provides a summary of key statistics regarding the estimated annual burden of disease associated with the seven selected hazards, presented through various indicators. These indicators include the number of notified cases per year, the estimated number of cases contributing to the annual burden, the DALYs per case, the total annual burden of disease in DALYs, the percentage of cases attributable to foodborne sources, and annual FBD burden expressed in foodborne DALYs.

5.3.1 Total burden of campylobacteriosis attributed to the food pathway

The total burden of campylobacteriosis attributed specifically to the food pathway was estimated at 404.44 DALYs per year, with a 95% UI of 297.73–497.42 ([Table 5](#)). This substantial burden highlights *Campylobacter* as a leading contributor to FBD in Ireland. The high incidence of illness compared with the other selected hazards amplifies its overall impact on public health. It is estimated that over three-quarters of the burden of disease of campylobacteriosis is linked to foodborne transmission. The mean value of DALYs indicates that foodborne campylobacteriosis in Ireland results in a loss of 404.44 healthy life years annually. The 95% UI suggests that the true burden of disease may range from approximately 297.73 to 497.42 healthy life years lost.

5.3.2 Total burden of listeriosis attributed to the food pathway

The total burden of listeriosis attributed specifically to the food pathway was estimated at 98.11 DALYs per year, with a 95% UI of 85.54–106.37 ([Table 5](#)). The mean value indicates that foodborne listeriosis in Ireland results in a loss of more than 98.11 healthy life years annually. The UI suggests that the true foodborne burden of disease may range from approximately 85.54 to 106.37 healthy life years lost. Although the number of listeriosis cases estimated as contributing to the annual burden is considered to be low relative to most of the other FBDs studied, the burden per case was the highest among the FBDs (2.14 DALYs), reflecting the severity of outcomes. Given the high severity of listeriosis, even small reductions in its incidence can help to substantially reduce the burden of FBD in Ireland.

5.3.3 Total burden of salmonellosis attributed to the food pathway

The total burden of salmonellosis attributed specifically to the food pathway was estimated at 15.02 (95% UI: 10.0–18.6) DALYs per year ([Table 5](#)). The mean value indicates that foodborne salmonellosis in Ireland results in a loss of more than 15.02 healthy life years annually. The 95% UI suggests that the true foodborne burden of disease may range from approximately 10.0 to 18.6 healthy life years lost.

5.3.4 Total burden of STEC infection attributed to the food pathway

The total burden of STEC attributed specifically to the food pathway was estimated at 83.05 (95% UI: 26.47–156.65) DALYs per year ([Table 5](#)). The mean value indicates that foodborne STEC infection in Ireland results in a loss of 83.05 healthy life years annually. The 95% UI suggests that the true foodborne burden of disease may range from approximately 26.47 to 156.65 healthy life years lost.

5.3.5 Total burden of hepatitis A infection attributed to the food pathway

The total burden of hepatitis A infection attributed specifically to the food pathway was estimated at 5.29 (95% UI: 0.35–13.04) DALYs per year ([Table 5](#)). These results were derived from food attribution estimates that were adjusted based on self-assessed expertise levels. The mean value indicates that foodborne HAV in Ireland results in a loss of 5.29 healthy life years annually. The 95% UI suggests that the true foodborne burden of disease range from approximately 0.35 to 13.04 healthy life years lost.

5.3.6 Total burden of hepatitis E infection attributed to the food pathway

The total burden of hepatitis E infection attributed specifically to the food pathway was estimated at 1.25 (95% UI: 0.49–1.88) DALYs per year ([Table 5](#)). The mean value indicates that foodborne HEV in Ireland results in a loss of 1.25 healthy life years annually. The 95% UI suggests that the true foodborne burden of disease could range from 0.49 to 1.88 healthy life years lost.

5.3.7 Total burden of norovirus infection attributed to the food pathway

The total burden of norovirus infection attributed specifically to the food pathway was estimated at 155.51 (95% UI: 22.92–392.12) DALYs per year ([Table 5](#)). The mean value indicates that foodborne norovirus in Ireland results in a loss of 155.51 healthy life years annually. The 95% UI suggests that the true foodborne burden of disease may range from approximately 22.92 to 392.12 healthy life years lost.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Table 5** Summary statistics on the estimated annual burden of disease for the seven microbiological hazards, as described by different indicators

Disease model	Notified cases per year ^a	Estimated cases contributing to annual burden ^b	DALYs per case ^c	Total annual burden (mean DALYs [95% UIs]) ^d	DALYs per 100 000 population (mean [95% UIs]) ^e	Percentage foodborne attribution (mean [95% UIs]) ^f	Foodborne burden (mean DALYs per year [95% UIs]) ^g
Campylobacteriosis	2689	48 610	0.01	510.7 [451.23–568.16]	10.72 [9.48–11.93]	76% [61–96]	404.44 [297.73–497.42]
Listeriosis	21	33	2.14	106.38 [102.40–110.37]	2.27 [2.19–2.36]	92% [81–99]	98.11 [85.54–106.37]
Salmonellosis	206	1427	0.01	19.33 [18.18–20.49]	0.41 [0.38–0.43]	77% [52–96]	15.02 [10.0–18.6]
STEC infection	859	6299	0.05	295.39 [285.81–305.43]	6.2 [6.00–6.41]	28% [9–53]	83.05 [26.47–156.65]
Hepatitis A infection	30	292	0.06	16.64 [14.65–18.66]	0.35 [0.31–0.39]	30% [6–79]	5.29 [0.35–13.04]
Hepatitis E infection	37	29	0.06	2.03 [1.98–2.13]	0.61 [0.51–0.70]	62% [24–92]	1.25 [0.49–1.88]
Norovirus infection	1402	1 379 000	0.0004	713.18 [426.56–1049.09]	14.98 [8.96–22.03]	23% [2–50]	155.51 [22.92–392.12]

^a The notified cases per year represents the average annual number of notified cases in Ireland within a specified period (4 or 5 years), based on surveillance data (HPSC, 2022).

^b The estimated number of cases contributing to the annual burden of the disease in Ireland, based on disease model simulations.

^c The DALYs per case represents the mean burden of a single case contributing to the total burden of disease.

^d The total DALY loss per year represents the cumulative annual burden of the disease (mean and 95% UIs [2.5th to 97.5th percentiles]).

^e The DALY loss per 100,000 population represents the population-standardised contribution to the annual burden of disease (mean and 95% UIs [2.5th to 97.5th percentiles]).

^f The self-assessed weighted estimates reflect the percentage attribution of the disease to foodborne transmission (mean and 95% UIs [2.5th to 97.5th percentiles]) reflecting the most likely, minimum and maximum percentage estimates.

^g The annual number of foodborne DALYs represents the annual burden of disease attributable to foodborne transmission (mean and 95% UIs [2.5th to 97.5th percentiles]).

Chapter 6 Risk ranking of microbiological hazards from food sources in Ireland

This baseline microbiological risk ranking study highlighted the diverse risk profiles associated with the seven selected microbiological hazards. The estimated burden of disease associated with each hazard is expected to reflect the effectiveness of the existing food safety control measures that were in effect between 2015 and 2019. The hazards are listed according to their estimated mean annual burden (with 95% UIs) on public health due to foodborne transmission, as follows:

1. *Campylobacter* spp., accounting for 404.44 (95% UI: 297.73–497.42) foodborne DALYs annually
2. Norovirus, accounting for 155.51 (95% UI: 22.92–392.12) foodborne DALYs annually
3. *L. monocytogenes*, accounting for 98.11 (95% UI: 85.54–106.37) foodborne DALYs annually
4. STEC, accounting for 83.05 (95% UI: 26.47–156.65) foodborne DALYs annually
5. *Salmonella* spp., accounting for 15.02 (95% UI: 10.0–18.6) foodborne DALYs annually
6. HAV, accounting for 5.29 (95% UI: 0.35–13.04) foodborne DALYs annually
7. HEV, accounting for 1.25 (95% UI: 0.49–1.88) foodborne DALYs annually.

It is important to highlight that the mean foodborne DALY results must be interpreted in the context of their respective UIs, which reflect the variability and limitations of input data.

This feature can be observed in other existing risk ranking exercises.

For example, while *Campylobacter* spp. was the pathogen with the highest mean foodborne DALYs in a year, at 404.44, the range of DALYs (297.73–497.42) overlaps with the UI for norovirus (22.92–392.12). This means that the values are not statistically distinguishable with high confidence.

The overlap means that it is plausible that the true foodborne DALY value for norovirus could be closer to, or even greater than, that of *Campylobacter* spp. As the UI for norovirus foodborne DALYs ranges from 22.92 to 392.12 DALYs, the DALY ranges for *L. monocytogenes* (85.54–106.37) and STEC (26.47–156.65) similarly overlap with its uncertainty. The wide UI range for norovirus likely reflects both the high estimated case numbers and the substantial variability and/or uncertainty in the source attribution experts' understanding of its transmission.

In contrast, although the incidence of listeriosis is relatively low, a strong consensus among experts that it is primarily foodborne in terms of its human incidence has led to a considerably narrower UI in comparison with the other FBDs. Additionally, the UI for foodborne DALYs for

Salmonella overlaps with that of HAV. The UIs for foodborne DALYs for HAV and HEV also overlap with each other.

For this reason, the risk ranking outcomes should be interpreted with caution and as indicators for risk-based prioritisation rather than definitive hierarchies, focusing on high-impact (e.g. *Campylobacter* spp.), uncertain (e.g. STEC or norovirus) or severe (e.g. *L. monocytogenes*) microbiological hazards. [Figure 4](#) presents a stacked bar chart illustrating the total and foodborne DALYs for each hazard.

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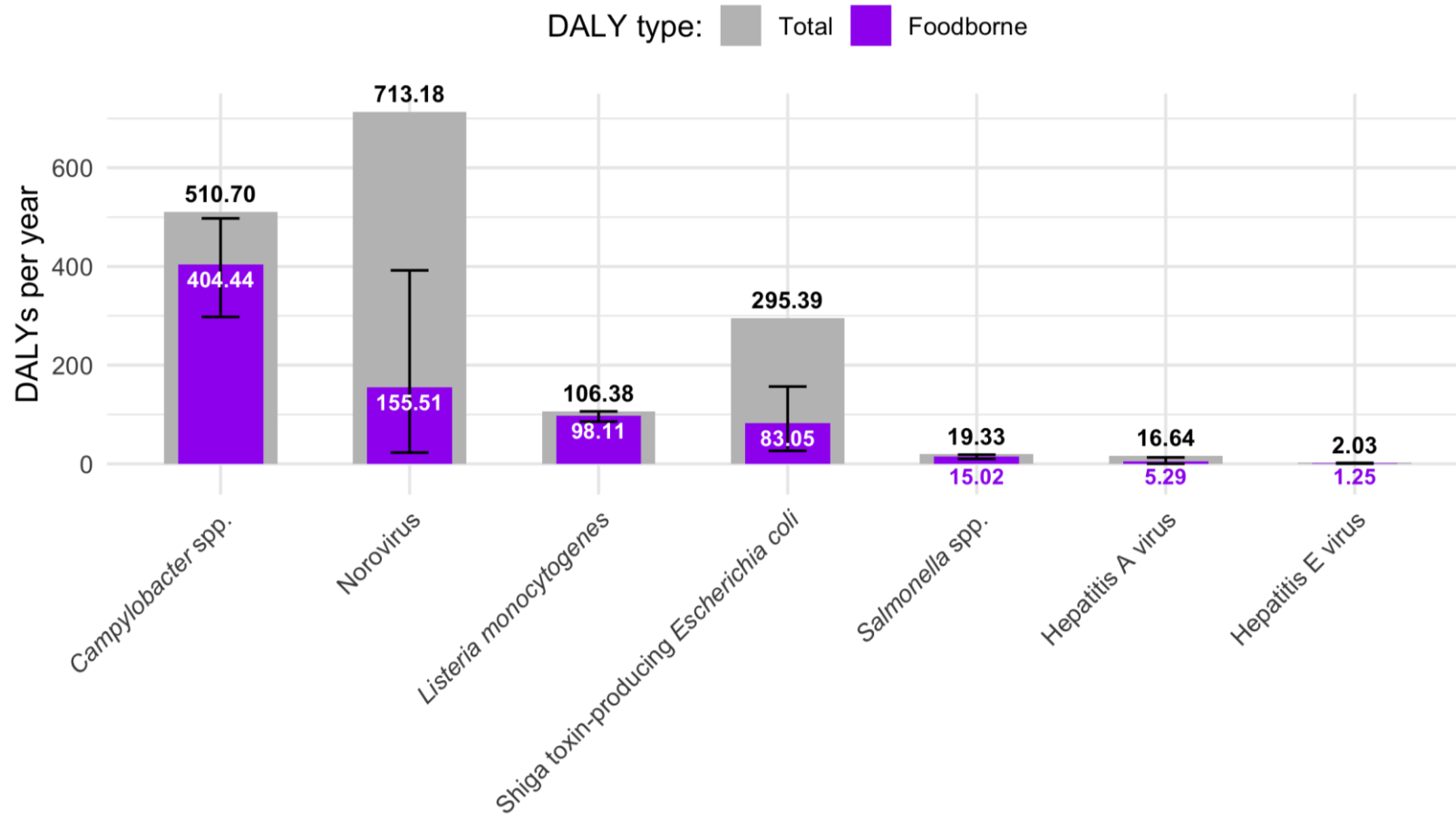


Figure 4 Stacked bar chart illustrating the total and foodborne DALYs for each hazard/pathogen annually

Note: The black error bars denote the uncertainty range (95% UIs) associated with the foodborne estimates. The labels indicate the mean point estimates for both total and foodborne DALYs, arranged in descending order from left to right for the foodborne DALYs.

Chapter 7 Data gaps and limitations

7.1 Introduction

Risk ranking exercises are beneficial for prioritising hazards, but they often face challenges arising from data gaps and limitations. These gaps can introduce varying levels of uncertainty into the results, affecting how they are interpreted and applied. Consequently, all risk management activities that rely on these outcomes must account for such constraints and recognise that the rankings are strongly influenced by the context of existing control programmes. Effective control programmes for a particular hazard reduce the incidence of human infection and illness, decrease the DALYs associated with that illness and hazard, and result in a lower ranking. Conversely, a high ranking may indicate opportunities for targeted improvements, whereas a low ranking does not necessarily imply that existing controls are excessive. Data gaps and limitations were encountered throughout this work and are identified in this report. This chapter outlines the specific challenges encountered at each stage and highlights critical areas where additional data or refined methods could enhance the reliability of future evaluations.

7.2 Burden estimation limitations

7.2.1 Hazard inclusion/exclusion

The microbiological hazard selection process faced several limitations and gaps in data. The selection process was informed by the insights of experts in the working group (WG), which may be influenced by individual experiences and potential biases.

During the microbiological hazard selection process, the inadequacy and incompleteness of disease surveillance data for a number of foodborne hazards presented challenges. This was especially relevant for biogenic amines, *Yersinia* spp., and *T. gondii*, where data limitations resulted in the WG's decision to exclude them from the exercise at stage 4, as outlined in the following subsections.

Biogenic amines

The WG felt that the inclusion of biogenic amines deserved further consideration. It was noted that histamine, a biogenic amine, falls under Commission Regulation (EC) No 2073/2005 as amended, which pertains to the microbiological criteria for foodstuffs. Additionally, The European Union One Health 2021 Zoonoses Report, published by the European Food Safety Authority (EFSA) and the European Centre for Disease Prevention and Control (ECDC), highlights histamine, in combination

with fish and fish products, as one of the top 10 hazard/food vehicle pairs associated with the highest number of strong evidence outbreaks in reporting European Union member states (EFSA and ECDC, 2022). However, there are limited Irish data available on biogenic amines, and they are not included in the ECDC's Burden of Communicable Disease in Europe (BCoDE) toolkit. As such, it was not feasible to include biogenic amines in the list of hazards, and it was agreed that they should be highlighted under Part (ii) of the Request for Advice (RfA) relating to identified data gaps.

Yersinia spp.

The WG noted the relatively low reported incidence of yersiniosis compared with campylobacteriosis and STEC infection. Similarly, the WG was not confident that the reported incidence reflects the true incidence and severity of yersiniosis in Ireland, compared with the other bacterial diseases on the list. Most clinical laboratories in Ireland do not include testing for *Yersinia* spp. in the routine test panel for people with gastrointestinal disease. Due to insufficient epidemiological data, the WG agreed to leave *Yersinia* spp. out of the exercise but also agreed that it should be highlighted under Part (ii) of the RfA relating to identified data gaps.

T. gondii

While *T. gondii* was included in the selected hazards, when work began on data collection, the WG concluded that there were actually very limited incidence data on toxoplasmosis and that the available seroprevalence data were outdated.

The WG noted that the most complete data were on congenital toxoplasmosis and that data for children aged under 1 year could be used. However, calculation of its attribution to the food pathway would be very difficult in this cohort.

Consequently, the WG agreed to leave *T. gondii* out of the exercise but also agreed that it should be highlighted under Part (ii) of the RfA relating to identified data gaps.

Across these hazards, data limitations were the primary constraint to their inclusion in the burden of disease estimates. It is recommended that these hazards be revisited through targeted One Health research that integrates data on animal, food and human health, or via alternative approaches, in order to ensure their inclusion in future assessments and to support a comprehensive evaluation of their potential risks.

7.2.2 Underestimation of disease incidence

In the context of disease modelling, several constraints are associated with utilising an expert consultation workshop approach in order to derive quantitative estimates of disease incidence UE, namely:

- Expert judgements are influenced by individual experiences and perspectives, which may introduce bias and inconsistencies to the agreed UE values.
- Due to the limited availability of data on UE reported in the literature, the estimates may be partially based on incomplete information.

In addition, it is possible that the uncertainty in these estimates could be influenced by confounding variables that were not fully explored during the workshop, as well as the decisions made regarding these variables, such as sex and age.

Sex

Sex is a variable that is thought to affect patient behaviour prior to and during medical consultations, influencing factors such as the willingness to seek healthcare, report symptoms and follow up with stool sample submissions.

Additionally, a patient's sex may influence the healthcare provider's responses during a consultation. Due to the challenges associated with quantifying the impact of sex on disease incidence data, it was assumed that there is no difference in healthcare utilisation patterns between males and females.

Age

Age is a known factor that can greatly impact on UE. Individuals can be categorised by age in years, months and even days. The WG reached a practical decision to generalise UE into three distinct age categories.

Consequently, UE related to each disease was assessed for individuals in the following age brackets: (i) those aged under 5 years, (ii) those aged 5–64 years, and (iii) those aged 65 years and over. It is important to note that variability in UE may manifest differently within and between these age groups.

Addressing these gaps may enhance the accuracy of the overall burden of disease estimates presented in this study. This could be addressed through the implementation of an epidemiological

investigation (e.g. prospective cohort study, population-based survey, capture-recapture analysis) specifically designed to evaluate the incidence and aetiology of FBDs in Ireland.

7.2.3 Absent models in the BCoDE toolkit and reliance on literature to derive disease models

In the context of disease modelling, two hazards included within the scope of our project did not have pre-existing models in the ECDC's BCoDE toolkit. As a result, these models had to be developed separately in R software, which led to inconsistencies in our approach across the different hazards. Moreover, while developing the disease models and utilising those provided in the BCoDE toolkit, we derived some data inputs from international studies. It is important to note that these studies may not fully reflect the specific epidemiological, healthcare and demographic context of Ireland. Although they serve as valuable benchmarks and comparators, there are inherent limitations in directly applying findings from different populations and healthcare settings to an Irish context.

Certain model parameters relied on assumptions due to limited data availability or insufficient understanding of specific disease dynamics. These assumptions are described in Appendices [5](#) and [6](#). While these assumptions are crucial for bridging critical data gaps and ensuring that the model operates cohesively, they do introduce a degree of uncertainty. Consequently, the outputs of the models should be interpreted with care, considering the potential discrepancies from the real-life patterns in Ireland.

It is recommended to acquire more relevant Ireland-specific data, as these would be beneficial for both refining existing disease models and developing tailored models that accurately reflect domestic trends, thereby enhancing the precision and sophistication of future risk ranking estimates.

7.3 Attribution limitations

7.3.1 Inadequate foodborne attribution data

Estimating the proportion of disease cases attributable to the food pathway presents certain challenges. Ideally, this work would rely on accurate and detailed data on the reporting of foodborne cases. However, such granular data were not available for this study, largely due to the nature of UE and the constraints of traceback and outbreak investigations, including the following:

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- Foodborne infections may not get captured by our surveillance systems, as addressed in earlier stages of this report on the task of quantifying UE. These systems typically fail to capture cases at: (i) the community level, since not all cases seek healthcare; and (ii) the healthcare level, where there can be a failure to adequately identify/report symptomatic cases that have sought medical advice.
- FBDs may be spread through routes other than food (such as through water, animals, the environment and human-to-human), making source identification difficult. Human cases of infection often involve multiple risk factors. For example, an STEC case may have documented exposure to contact with farm animals, consumption of water from a private well, contact with contaminated farm environments, and ingestion of high-risk foods such as raw milk. Without the triangulation of related cases or microbiological evidence, it is often challenging to determine the exact source of infection. As a result, cases are frequently reported without definitive information regarding whether they are foodborne.
- Tracing foodborne sources requires complex investigations, and sometimes the investigations can be inconclusive.

This limitation is particularly evident when case numbers are low, as is often the situation in Ireland. In the absence of comprehensive and precise data on FBDs, reliance on expert judgement is often necessary (Cressey *et al.*, 2019a). The resulting estimates inevitably reflect a degree of subjectivity and potential biases in the expert judgements. To assess the robustness of the attribution results to these uncertainties, we explored three different weighting approaches to view these judgements. While each weighting approach had the potential to skew the results in different ways, they produced relatively consistent outcomes across the hazards and methods.

Equal expert weightings

By treating all expert opinions as equally valuable, no single expert's view dominated in the final estimates. This approach promotes balance across diverse perspectives. However, this can dilute the influence of more accurate/knowledgeable experts, potentially leading to less precise or reliable results. In this study, all weighting methods yielded consistently similar results across different approaches, indicating that the outcomes were not identifiably skewed by dilution.

Self-assessed expert weightings

In the absence of bias, self-assessed weightings as a method of filtering the results should ideally reflect each expert's true level of knowledge and expertise in their estimates. However, results may become subjective, as experts may:

- Overestimate their expertise, which may disproportionately influence the results and potentially skew the attribution towards their opinions
- Undervalue their expertise and contribute less to the results.

In this study, all weighting methods yielded consistently similar results across different approaches, indicating that the outcomes were not identifiably skewed by subjectivity.

Performance-based expert weightings

A calibration questionnaire was employed as a means of objectively putting boundaries on the experts' estimates. The reliability of the performance-based weightings depends heavily on the quality and relevance of the calibration questions. Therefore, this approach placed greater emphasis on the estimates from experts who performed better in the questionnaire. This has the potential to skew the results if the expertise of the participants who performed best is not directly relevant to the specific source attribution work being assessed. It may, in turn, also reduce the contribution of experts whose knowledge is valuable, but whose performance on the calibration questionnaire was weaker. This is a relatively novel approach for food attribution studies. In this study, all weighting methods yielded consistently similar results across different approaches, indicating that the outcomes were not identifiably skewed by the experts' performance in the calibration questionnaire.

Overall, estimating the proportion of disease attributable to the food pathway remains a complex and uncertainty-prone task. To reduce reliance on expert judgement in future assessments, methodologies such as case–control studies, enhanced utilisation of outbreak investigation data, microbiological subtyping for source attribution, and quantitative risk assessment approaches should be further developed and applied.

To support trend monitoring and the identification of emerging risks, it is essential that this exercise be built on and conducted periodically and as part of ongoing risk assessment initiatives. The rankings should be revised as new information, data and research become available in order to ensure that the results remain relevant, accurate and representative of the current food safety environment in Ireland.

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Appendix 1 Request for Advice from the Scientific Committee

Topic title: Risk ranking of microbiological hazards

Date requested: 28 September 2018

Date accepted: 28 September 2018

Target deadline for advice: 24 months from date of acceptance

Form of advice required: Report

Background

In 2014, the EFSA Panel on Biological Hazards (BIOHAZ) adopted a scientific opinion on the development of a risk-ranking toolbox, which assessed eight different risk-ranking tools for microbiological hazards in foods. The scientific opinion concluded that quantitative stochastic models are the most reliable for risk ranking microbiological hazards, and it identified the United States Food and Drug Administration's (FDA's) FDA-iRISK tool as the most appropriate for these purposes. In addition, the Panel concluded that the European Centre for Disease Prevention and Control's (ECDC's) Burden of Communicable Disease in Europe (BCoDE) toolkit can be used in combination with the outputs of the FDA-iRISK tool, as well as those of a network of other predictive microbiology tools, databases and information sources, in order to form a fit-for-purpose toolbox that would support timely and transparent risk ranking.

The scientific opinion identified limitations on available online risk ranking tools, such as that (i) they offer no option to specify the population involved, or (ii) their outputs lack a measurement of variability and uncertainty. However, one solution to this latter limitation would be to represent outputs by means of a probability distribution. Other challenges posed are that risk assessments are time sensitive, and good-quality data are often not available. The scientific opinion concluded that where data and time constraints prevent the use of quantitative risk ranking, semi-quantitative models could be used, but the limitations of these approaches should be made clear.

In 2015, the World Health Organization (WHO) published for the first time *WHO estimates of the global burden of foodborne diseases: foodborne disease burden epidemiology reference group 2007-2015*. The report covered 31 foodborne hazards that cause a total of 32 diseases. Of the 28 microbiological hazards included, 11 were diarrhoeal disease agents (1 virus, 7 bacteria and 3 protozoa), 7 were invasive infectious disease agents (1 virus, 5 bacteria and 1 protozoon) and 10 were helminths. Together, the 31 hazards assessed caused an estimated 600 million foodborne illnesses and 420,000 deaths in 2010, with diarrhoeal disease agents being the most frequently

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reported foodborne illnesses, particularly *Campylobacter* species (spp.) and norovirus. Foodborne diarrhoeal disease agents were responsible for an estimated 230,000 deaths, particularly non-typhoidal *Salmonella enterica*. Other major causes of foodborne deaths were *Salmonella* Typhi, *Taenia solium*, hepatitis A virus and aflatoxin. The global burden of foodborne disease by the 31 hazards assessed was estimated at 33 million disability-adjusted life years (DALYs) in 2010, and 40% of this burden was in children aged under 5 years.

Question for the Scientific Committee

In order to prioritise the work of the Food Safety Authority of Ireland (FSAI), can the Scientific Committee: (i) advise the FSAI on a risk ranking of microbiological hazards from foodborne sources in Ireland, and (ii) identify data gaps which, if filled, would enable a risk ranking of these hazards with reduced uncertainty in the future?

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Appendix 2 Microbiological hazard selection (Stage 1)

Table 6 Sources for compiled hazards list (n=54) for selection in the risk ranking exercise (listed in alphabetical order)

Microbiological hazard	Source
Adenovirus	d
Aeromonas	d
Anisakidae	c
Arcobacter species (spp.)	d
Ascaris spp.	b
Astroviridae	d
Bacillus anthracis	a
Bacillus cereus	a
Biogenic amines	d
Bovine spongiform encephalopathy (variant Creutzfeldt–Jakob disease (vCJD))	a
Brucella spp.	a, b, c
Campylobacter spp.	a, b, c
Clonorchis sinensis	b
Clostridium botulinum	a, b, c
Clostridioides difficile (formerly Clostridium difficile)	a
Clostridium perfringens (type A)	a, b, c
Coxiella burnetii (Q fever)	a
Cronobacter spp.	c
Cryptosporidium spp.	a, b, c
Cyclospora cayetanensis	c
Diphyllobothrium spp.	c
Echinococcus granulosus and Echinococcus multilocularis	a, b

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Microbiological hazard	Source
<i>Echinostoma</i> spp., <i>Fasciolopsis buski</i> , <i>Heterophyes</i> spp., <i>Metagonimus</i> spp. and other foodborne intestinal trematode species	b, c
<i>Entamoeba histolytica</i>	b
Enteropathogenic, enteroinvasive and enterotoxigenic <i>Escherichia coli</i>	a, b, c
<i>Fasciola hepatica</i>	b
<i>Francisella tularensis</i>	a
<i>Giardia lamblia</i>	a, b, c
Hepatitis A	a, b, c
Hepatitis E	a
<i>Leptospira</i> spp.	a, c
<i>Listeria monocytogenes</i>	a, b, c
Marine biotoxins	c, d
<i>Mycobacterium bovis</i>	a, b
Mycotoxins	d
Norovirus	a, b, c
<i>Opisthorchis</i> spp.	b
<i>Paragonimus</i> spp.	b
Rotavirus	c
<i>Salmonella</i> spp. (other than <i>Salmonella</i> Typhi and <i>Salmonella</i> Paratyphi)	a, b, c
<i>Salmonella</i> Paratyphi	a
<i>Salmonella</i> Typhi	a, b, c
<i>Sapovirus</i>	d
Shiga toxin-producing/verotoxigenic <i>Escherichia coli</i>	a, b
<i>Shigella</i> spp.	a, b, c
<i>Staphylococcus aureus</i> (enterotoxin)	a, b, c
<i>Taenia saginata</i>	c
<i>Taenia solium</i>	b, c

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Microbiological hazard	Source
<i>Toxocara</i> spp.	d
<i>Toxoplasma gondii</i>	a, b, c
<i>Trichinella</i> spp.	a, b, c
<i>Vibrio cholerae</i>	a, b, c
<i>Vibrio</i> spp. (excluding cholera)	c
<i>Yersinia</i> spp.	a, c

a) Health Protection Surveillance Centre (2018) Notifiable Diseases and their causative pathogens specified to be Infectious Diseases under Infectious Diseases (Amendment) Regulations 2018 (S.I. No. 567 of 2018). Hazards identified as potentially foodborne were extracted from this list.

b) World Health Organization (2015) *WHO estimates of the global burden of foodborne diseases: foodborne disease burden epidemiology reference group 2007-2015*. Geneva: World Health Organization. Available at: http://www.who.int/foodsafety/publications/foodborne_disease/fergreport/en/

c) United States Centers for Disease Control and Prevention (2019) A – Z Index for Foodborne Illness. Available at: <https://www.cdc.gov/foodsafety/diseases/index.html>

d) Hazard proposed for inclusion by a member of the Biological Safety Subcommittee working group.

Appendix 3 Microbiological hazard selection (Stage 2)

Table 7 The hazards (n=27) identified and eliminated during Stage 2 of the selection process, along with the associated exclusion criteria

Microbiological hazard	Notifiable	Exclusion criteria ¹	Remarks
<i>Aeromonas</i>	No	2, 3, 4	Excluded in accordance with criteria 2, 3 and 4.
<i>Ascaris</i> species (spp.)	No	2, 3	Excluded in accordance with criteria 2 and 3.
<i>Bacillus anthracis</i>	Yes	2, 3	Excluded in accordance with criteria 2 and 3.
Bovine spongiform encephalopathy (variant Creutzfeldt–Jakob disease (vCJD))	Yes	2	Excluded in accordance with criterion 2.
<i>Brucella</i> spp.	Yes	2, 3	Excluded in accordance with criteria 2 and 3.
<i>Clonorchis sinensis</i>	No	3	Excluded in accordance with criterion 3. Currently, while this is typically contracted abroad, this hazard could present as an emerging risk as a result of an increased consumption of raw fish in Ireland (e.g. sushi).
<i>Clostridioides difficile</i> (formerly <i>Clostridium difficile</i>)	Yes	4	Excluded in accordance with criterion 4. This

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Microbiological hazard	Notifiable	Exclusion criteria ¹	Remarks
			hazard could present as an emerging risk.
<i>Coxiella burnetii</i> (Q fever)	Yes	2	Excluded in accordance with criterion 2.
<i>Cronobacter</i> spp.	No	2, 3	Excluded in accordance with criteria 2 and 3.
<i>Cyclospora cayetanensis</i>	No	3	Excluded in accordance with criterion 3.
<i>Diphyllobothrium</i> spp.	No	2, 3	Excluded in accordance with criteria 2 and 3. Freshwater tapeworms: The working group (WG) is currently unaware of any cases associated with food; however, this could potentially present as an emerging issue.
<i>Echinococcus granulosus</i> and <i>Echinococcus multilocularis</i>	No	2, 3	Excluded in accordance with criteria 2 and 3.
<i>Echinostoma</i> spp., <i>Fasciolopsis buski</i> , <i>Heterophyes</i> spp., <i>Metagonimus</i> spp. and other foodborne intestinal trematode species	No	2	Excluded in accordance with criterion 2. Pigs were mentioned as a potential source.
<i>Entamoeba histolytica</i>	No	2, 3	Excluded in accordance with criteria 2 and 3. The WG noted that it has

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Microbiological hazard	Notifiable	Exclusion criteria ¹	Remarks
			been linked to contaminated water in developing countries.
<i>Francisella tularensis</i>	Yes	2, 3	Excluded in accordance with criteria 2 and 3.
Marine biotoxins	This hazard was determined to be outside the scope of the exercise.		
Mycotoxins	This hazard was determined to be outside the scope of the exercise.		
<i>Opisthorchis spp.</i>	No	3	Excluded in accordance with criterion 3. Currently, while this is typically contracted abroad, this hazard could present as an emerging risk as a result of an increased consumption of raw fish in Ireland (e.g. sushi).
<i>Paragonimus spp.</i>	No	3	Excluded in accordance with criterion 3. Currently, while this is typically contracted abroad, this hazard could present as an emerging risk because of an increased consumption of raw fish in Ireland (e.g. sushi).

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Microbiological hazard	Notifiable	Exclusion criteria ¹	Remarks
<i>Salmonella Paratyphi</i>	Yes	3	Excluded in accordance with criterion 3.
<i>Salmonella Typhi</i>	Yes	3	Excluded in accordance with criterion 3.
<i>Shigella</i>	Yes	3	Excluded in accordance with criterion 3.
<i>Taenia saginata</i>	No	2, 3	Excluded in accordance with criteria 2 and 3.
<i>Taenia solium</i>	No	3	Excluded in accordance with criterion 3.
<i>Trichinella spp.</i>	Yes	2, 3	Excluded in accordance with criteria 2 and 3.
<i>Vibrio cholerae</i>	Yes	2, 3	Excluded in accordance with criteria 2 and 3.
<i>Vibrio spp. (excluding cholera)</i>	No	2, 3	Excluded in accordance with criteria 2 and 3. This hazard could present as an emerging risk with climate change.

¹ Exclusion criteria:

2. The reported incidence of human illness in Ireland was low (fewer than 5 cases per annum in a population of 4.7 million) in the period between 2014 and 2018.
3. The infection is typically contracted outside of Ireland.
4. The aetiological importance of the food pathway for the hazard is not well-established.

Appendix 4 Microbiological hazard selection (Stage 3)

Table 8 The outcomes from Stage 3 of the microbiological hazard selection process, where hazards (listed in alphabetical order; n=27) were reviewed considering their clinical severity and human incidence

Microbiological hazard	Clinical severity ¹	Human incidence ²	Comments (regarding incidence data)	Additional comments
Adenovirus	Low	High	Based on National Virus Reference Laboratory data	
Anisakidae	Low	Low	Based on the opinion of the working group (WG)	High prevalence of exposure in other countries based on seroprevalence, but the WG believes that incidence is low in Ireland due to the custom of cooking fish thoroughly.
Arcobacter species (spp.)	Low	Low	Based on the opinion of the WG	
Astroviridae	Low	High	Based on National Virus Reference Laboratory data	
Bacillus cereus	Low	Low	The number of notified cases is low, but underreporting is suspected.	
Biogenic amines	Low	High	Based on the opinion of the WG	According to the European Food Safety Authority (EFSA) Dashboard on foodborne outbreaks, of 69 strong evidence (fish and fish product)

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Microbiological hazard	Clinical severity ¹	Human incidence ²	Comments (regarding incidence data)	Additional comments
				outbreaks between 2018 and 2022, 24 were caused by histamine and scombrototoxin. Note: The hazard is not available in the Burden of Communicable Disease in Europe (BCoDE) toolkit.
<i>Campylobacter</i> spp.	High	High	Based on Irish notification data	
<i>Clostridium botulinum</i>	High	Low	Based on Irish notification data	
<i>Clostridium perfringens</i> (type A)	Low	High	The number of notified cases is low but underreporting (ref. infectious intestinal disease (IID) studies (in the United States and the United Kingdom)) is suspected.	
<i>Cryptosporidium</i> spp.	Low	High	Based on Irish notification data	
Enteropathogenic, enteroinvasive and enterotoxigenic <i>Escherichia coli</i>	Low	Low	Based on the opinion of the WG	
<i>Fasciola hepatica</i>	Low	Low	Based on the opinion of the WG	

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Microbiological hazard	Clinical severity ¹	Human incidence ²	Comments (regarding incidence data)	Additional comments
<i>Giardia</i>	Low	High	Based on Irish notification data	
Hepatitis A	High	High	Based on Irish notification data. The assessment indicates a low value based on notifications; however, when factoring in an element of underestimation, it is considered high.	
Hepatitis E	High	High	Based on Irish notification data	Note: Not available in the BCoDE toolkit.
<i>Leptospira spp.</i>	Low	Low	Based on Irish notification data	
<i>Listeria monocytogenes</i>	High	High	Based on Irish notification data, incidence would be low, as surveillance primarily captures invasive listeriosis (e.g. bloodstream infection). The 'high' ranking reflects the high severity of disease in vulnerable populations and the likely underestimation of non-invasive gastrointestinal infections.	Important pathogen in the context of food regulation.

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Microbiological hazard	Clinical severity ¹	Human incidence ²	Comments (regarding incidence data)	Additional comments
<i>Mycobacterium bovis</i>	High	Low	Based on Irish notification data	
Norovirus	Low	High	Based on Irish notification data	Previously included in microbiological risk ranking exercises in other countries. <i>Note: Not available in the BCoDE toolkit.</i>
Rotavirus	Low	High	Based on Irish notification data	
<i>Salmonella</i> spp. (other than <i>Salmonella</i> Typhi and <i>Salmonella</i> Paratyphi)	High	High	Based on Irish notification data	
<i>Sapovirus</i>	Low	High	Based on National Virus Reference Laboratory data	
<i>Staphylococcus aureus</i> (enterotoxin)	Low	High	Low based on Irish notification data but considered high based on underestimation	
<i>Toxocara</i> spp.	High	Low	Based on the opinion of the WG	
<i>Toxoplasma gondii</i>	High	High	Low based on Irish notification data but high based on the scientific opinion of the WG (Irish seroprevalence study (but quite old))	
Shiga toxin-producing/verotoxigenic <i>Escherichia coli</i>	High	High	Based on Irish notification data	

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Microbiological hazard	Clinical severity ¹	Human incidence ²	Comments (regarding incidence data)	Additional comments
<i>Yersinia spp.</i>	High	High	Low based on Irish notification data but potentially high based on underestimation	

¹ Clinical severity: Score of low or high, with potential to have long-term chronic sequelae, hospitalisation or deaths (2014–2018).

² Perceived human incidence: Score of low or high (low ranging from 5 to 50 cases, and high being more than 50 cases).

Note that fewer than 5 cases was an exclusion criterion in Stage 2.

Appendix 5 Summary of disease model frameworks and input data employed in the Burden of Communicable Disease in Europe toolkit

Campylobacteriosis

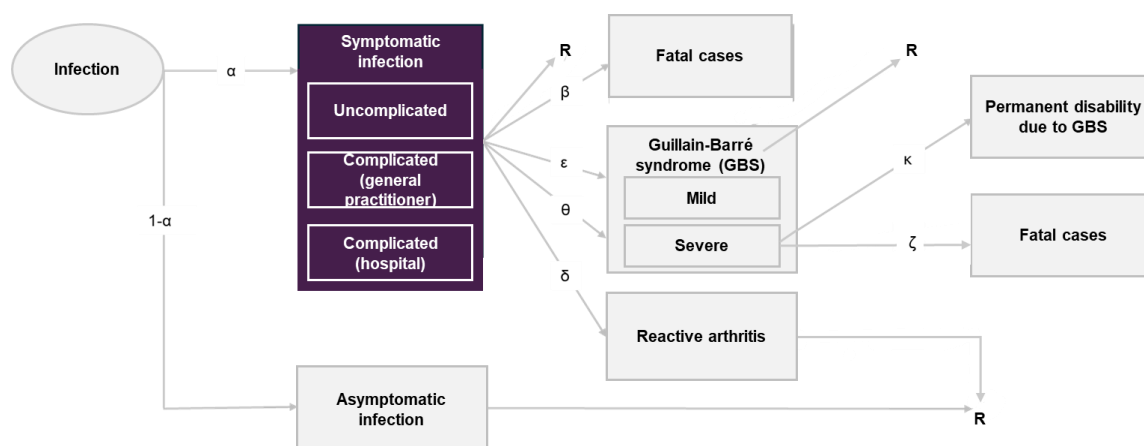


Figure 5 Disease model outcome tree for campylobacteriosis

Source: Adapted from European Centre for Disease Prevention and Control (2019)

Model input summary

Campylobacteriosis is an illness resulting from infection with *Campylobacter* bacteria. Common clinical symptoms include diarrhoea (often bloody), abdominal pain, fever, headache, nausea and vomiting. While fatalities are uncommon, they are usually limited to very young children, older adults or those with pre-existing health conditions such as immunodeficiency. Potential complications of infection include bacteraemia (presence of bacteria in the bloodstream), hepatitis, pancreatitis, and miscarriage, which are observed with varying frequency. Post-infection issues may involve reactive arthritis (ReA) (characterised by joint inflammation that can persist for several months), as well as neurological conditions such as Guillain-Barré syndrome (GBS), a rare disorder that may cause paralysis and respiratory or neurological impairments in some cases (World Health Organization, 2020). The incidence of laboratory-confirmed, non-travel-related campylobacteriosis in Ireland ([Appendix 7](#)) was corrected for its perceived relative underestimation by using the expert judgement values presented in [Appendix 8](#).

The outcome tree for campylobacteriosis

Symptomatic infection

Adapted from the European Centre for Disease Prevention and Control's (ECDC's) Burden of Communicable Disease in Europe (BCoDE) toolkit (ECDC, 2019), the average duration of illness varies depending on severity and healthcare usage, as follows (Adak *et al.*, 2002; Food Standards Agency, 2000; Mangen *et al.*, 2005; 2004):

- 3.22 days for cases that do not seek medical help
- 9.72 days for those who visit a general practitioner (GP)
- 14.39 days for hospitalised cases (parameter is abbreviated to 'hosp').

These durations were applied in the model to the respective severity categories. Approximately 47% of community cases were expected to seek medical care (Food Standards Agency, 2000).

In order to stratify symptomatic cases by severity, the following distribution was employed by the model (Kemmeren *et al.*, 2006; Kwong *et al.*, 2012):

- Mild (uncomplicated, no medical care): 76%
- Moderate (doctor visit): 23%
- Severe (hospitalised): 1%.

Case fatality risk estimates used in the model from the literature are described as follows:

- 0.001–0.05% for all cases, i.e. the total population burden including mild and non-hospitalised infection (Mead *et al.*, 1999)
- An alternative population-level estimate of 0.012–0.036% for all cases, derived from hospitalised case fatality combined with the proportion of cases hospitalised (Buzby *et al.*, 1996; Mangen *et al.*, 2004)
- Hospitalised case fatality as high as 1.3% (Mangen *et al.*, 2004).

For symptomatic infection, an overall fatality rate of 0.001–0.05% is adapted, distributed by age using The European Surveillance System (TESSy) reported deaths from 2009 to 2013, excluding aggregate-only data from Bulgaria, Greece, Portugal and Liechtenstein. Symptomatic infection can lead to the following outcomes:

- ReA:
 - There is considerable variability for the reported risk of campylobacteriosis cases progressing to ReA in the literature. The model estimates this risk at 1.7% (range: 0.73–4.4%) based on all symptomatic cases (Kemmeren *et al.*, 2006).
 - The duration of ReA is uncertain, but the average is derived to be between 1.5 months (Hannu *et al.*, 2002) and 222 days (Kemmeren *et al.*, 2006).

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- Irritable bowel syndrome:
 - Irritable bowel syndrome occurs in 8.8% (7.2–10.4%) of symptomatic cases (Haagsma *et al.*, 2010), with an estimated duration of 5 years. However, due to limited evidence and debated causality, irritable bowel syndrome is excluded from the outcome model.
- GBS:
 - The model assumes a transition probability of 0.0015–0.09% from symptomatic infection to GBS (Allos, 1997; Havelaar *et al.*, 2000a; 2000b; Ternhag *et al.*, 2008).
 - The severity distribution of GBS cases is defined as (Havelaar *et al.*, 2000a; 2000b):
 - 17% mild (age-dependent)
 - 83% severe (age-dependent).
 - Only severe GBS cases are assumed to be at risk of fatal or disabling outcomes:
 - 4.1% (2.41–6.02%) of severe cases result in death (Havelaar *et al.*, 2000a; van Koningveld, 2001)
 - 17–31% result in permanent disability, stratified by age (Havelaar *et al.*, 2000a; 2000b).

Asymptomatic infection

Typically, infection is self-limiting, and individuals recover completely without long-term effects.

Table 9 Health outcomes and transition probabilities used in the campylobacteriosis outcome tree

Health outcome (health state)	Distribution of health states in health outcome	Transition probability	Source/assumption
Symptomatic infection (Uncomplicated) (Complicated, GP) (Complicated, hosp)	76% 23% 1%		Kemmeren <i>et al.</i> , 2006; Kwong <i>et al.</i> , 2012
Fatal cases following symptomatic infection		0.001–0.05% (age-dependent; see Table 10)	Adak <i>et al.</i> , 2002; Cressey and Lake, 2007; Mangen <i>et al.</i> , 2005; Mead <i>et al.</i> , 1999; TESSy, 2009-2013

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Health outcome (health state)	Distribution of health states in health outcome	Transition probability	Source/assumption
ReA		1.7% (0.73–4.4%)	Kemmeren <i>et al.</i> , 2006
GBS (Mild) (Severe)	17% (age-dependent; see Table 11) 83% (age-dependent; see Table 12)	0.0015–0.09%	Allos, 1997; Havelaar <i>et al.</i> 2000a; 2000b; Ternhag <i>et al.</i> , 2008
Fatal cases following severe GBS		4.1% (2.41–6.02%) (age-dependent; see Table 13)	Havelaar <i>et al.</i> , 2000a; van Koningsveld, 2001 Assuming only severe cases are fatal
Permanent disability following GBS		17–31% (age-dependent; see Table 13)	Havelaar <i>et al.</i> , 2000a; 2000b Assuming only severe cases

Source: Adapted from ECDC (2019)

Table 10 Age group distribution of the case fatality rate for campylobacteriosis (0.001–0.05%)

Age groups	%
0 years	0.54
1–4 years	1.09
5–9 years	3.26
10–14 years	1.63
15–19 years	0.54
20–24 years	4.35
25–29 years	5.98

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Age groups	%
30–34 years	1.63
35–39 years	3.26
40–44 years	3.80
45–49 years	3.80
50–54 years	5.43
55–59 years	5.98
60–64 years	5.98
65–69 years	8.15
70–74 years	6.52
75–79 years	11.96
80–84 years	11.96
≥85 years	14.13
All ages	100.00

Source: Adapted from ECDC (2019)

Table 11 Age group distribution of mild GBS for campylobacteriosis

Age groups	%
0 years	0.54
1–4 years	1.09
5–9 years	3.26
10–14 years	1.63
15–19 years	0.54
20–24 years	4.35
25–29 years	5.98
30–34 years	1.63
35–39 years	3.26
40–44 years	3.80

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Age groups	%
45–49 years	3.80
50–54 years	5.43
55–59 years	5.98
60–64 years	5.98
65–69 years	8.15
70–74 years	6.52
75–79 years	11.96
80–84 years	11.96
≥85 years	14.13
All ages	100.00

Source: Adapted from ECDC (2019)

Table 12 Age group distribution of severe GBS for campylobacteriosis

Age groups	%
0 years	0.44
1–4 years	3.49
5–9 years	1.75
10–14 years	0.87
15–19 years	4.36
20–24 years	4.80
25–29 years	6.98
30–34 years	6.55
35–39 years	6.55
40–44 years	6.11
45–49 years	6.11
50–54 years	8.67
55–59 years	8.09

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Age groups	%
60–64 years	6.93
65–69 years	9.24
70–74 years	8.67
75–79 years	6.93
80–84 years	1.16
≥85 years	2.31
Total	100.00

Source: Adapted from ECDC (2019)

Table 13 Age group distribution of permanent GBS and case fatality rate for campylobacteriosis

Age groups	%
0 years	0.00
1–4 years	0.00
5–9 years	0.00
10–14 years	0.00
15–19 years	0.00
20–24 years	1.56
25–29 years	1.56
30–34 years	1.56
35–39 years	1.56
40–44 years	2.08
45–49 years	2.08
50–54 years	2.08
55–59 years	6.25
60–64 years	6.25
65–69 years	6.25
70–74 years	18.75

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Age groups	%
75–79 years	25.00
80–84 years	18.75
≥85 years	6.25
Total	100.00

Source: Adapted from ECDC (2019)

Table 14 Disability weights and duration for campylobacteriosis

Health outcome (health state)	Disability weight (DW) (Haagsma <i>et al.</i> , 2015)		Duration	
	DW	Label	In years	Source/assumption
Symptomatic infection (Uncomplicated) (Complicated, GP) (Complicated, hosp)	0.073 (0.061–0.092)	Diarrhoea, mild	0.009	Kemmeren <i>et al.</i> , 2006; Kwon <i>et al.</i> , 2012
	0.149 (0.12–0.182)	Diarrhoea, moderate	0.027	
	0.239 (0.202–0.285)	Diarrhoea, severe	0.039	
ReA	0.344 (0.3–0.391)	Musculoskeletal problems, generalised, moderate	0.131–0.608	Hannu <i>et al.</i> , 2002; Kemmeren <i>et al.</i> , 2006
GBS (Mild) (Severe)	0.053 (0.042–0.064)	Motor impairment, moderate	1	Havelaar <i>et al.</i> , 2000a; 2000b
	0.520 (0.465–0.581)	Spinal cord lesion at neck level (treated)	1	

Source: Adapted from ECDC (2019)

Listeriosis

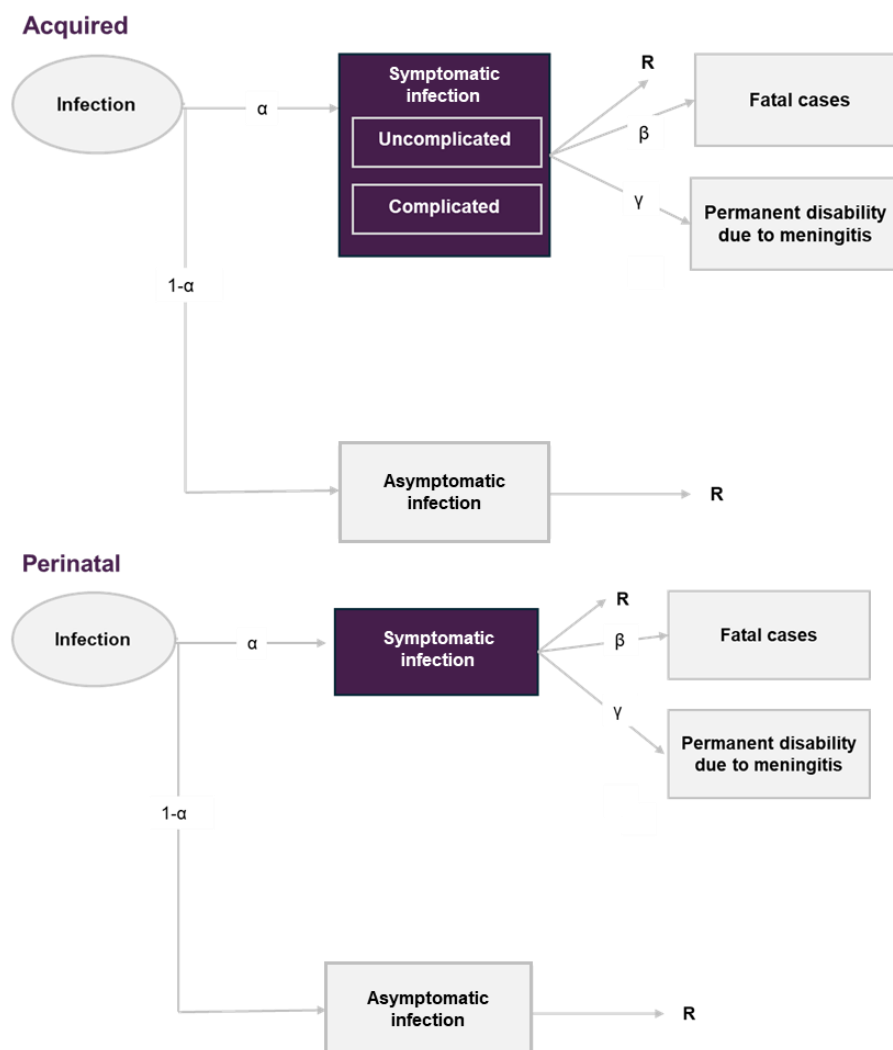


Figure 6 Disease model outcome trees for listeriosis perinatal and acquired pathways

Source: Adapted from ECDC (2019)

Model input summary

Listeriosis is a spectrum of illnesses caused by the bacteria *Listeria monocytogenes*. The disease manifests primarily in two forms: non-invasive and invasive. Non-invasive listeriosis is a mild illness predominantly affecting otherwise healthy individuals. Symptoms commonly include diarrhoea, fever, headache and muscle aches. Invasive listeriosis represents a more severe disease form, primarily affecting high-risk populations such as pregnant women (and their unborn children); cancer patients; individuals receiving treatment for human immunodeficiency virus (HIV) or organ transplantation; older adults; and young children. This form is characterised by significant symptoms, including high fever, muscle pain, sepsis and meningitis (World Health Organization,

2018a). The incidence of laboratory-confirmed, non-travel-related listeriosis in Ireland ([Appendix 7](#)) was corrected for its perceived relative underestimation using the expert judgement values presented in [Appendix 8](#).

The outcome tree for acquired listeriosis (80% of cases)

Acquired listeriosis infections may manifest with either uncomplicated or complicated symptoms or may be asymptomatic (Aouaj *et al.*, 2002).

Symptomatic infection

Symptomatic listeriosis can present with varying degrees of severity, ranging from mild illness to severe invasive disease, as outlined below:

- Complicated symptomatic infections are estimated to constitute approximately 95–97% of symptomatic cases, based on the number of reported invasive listeriosis cases (United States Centers for Disease Control and Prevention, 2014). Conversely, uncomplicated symptomatic cases are assumed to represent approximately 3–5% of cases.
- Following infection, cases may recover, result in permanent disability due to meningitis, or lead to death. Other post-infectious complications after listeriosis are rare (Haagsma *et al.*, 2009) and were omitted from this model.
- The age-specific listeriosis case fatality proportions, derived from TESSy notifications (2009–2013) and excluding Bulgaria and Lithuania, are applied to complicated cases only.

Permanent disability due to meningitis

United States Centers for Disease Control and Prevention (CDC) (2007–2012) data estimate that 13–18% of invasive symptomatic cases progress to meningitis (United States Centers for Disease Control and Prevention, 2014). Aouaj *et al.* (2002) suggested that the risk of long-term sequelae in all complicated acquired cases is 1.65–2.29%.

Asymptomatic infection

Typically, infection is self-limiting, and individuals recover completely without long-term effects.

The outcome tree for perinatal listeriosis (20% of cases)

Perinatal listeriosis presents clinical pathways affecting both the pregnant individual and the fetus or newborn (Aouaj *et al.*, 2002), and these outcomes can be summarised as follows:

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Symptomatic infection**

Symptomatic perinatal listeriosis encompasses a range of maternal and neonatal outcomes, which can be summarised as follows:

- Perinatal listeriosis affects pregnant women and their unborn children or newborns.
- Two-thirds of pregnant women with listeriosis experience prodromal flu-like symptoms (such as fever, chills and headache) 3–7 days before potential abortion or preterm labour.
- While rarely life-threatening to the mother, infection in early pregnancy can cause spontaneous abortion, and later infection may lead to stillbirth or a critically ill newborn.
- Other post-infection complications after listeriosis are rare (Haagsma *et al.*, 2009) and are omitted from this model.
- In this model, early- and late-onset cases are combined, with an overall case fatality rate of 18.71% based on TESSy data (2009–2013).

Permanent disability due to meningitis

Neonates can develop early-onset (<7 days) or late-onset (8–28 days) listeriosis. Early-onset listeriosis (acquired in utero) often results in sepsis and meningitis; late-onset listeriosis (contracted during delivery) presents typically in healthy full-term infants but has a higher risk of meningitis. Aouaj *et al.* (2002) report a 24% risk of lasting neurological disabilities in perinatal listeriosis cases.

Asymptomatic infection

Typically, infection is self-limiting, and individuals recover completely without long-term effects.

Table 15 Health outcomes and transition probabilities used in the listeriosis outcome tree

Health outcome (health state)	Distribution of health states in health outcome	Transition probability	Source/assumption
Acquired listeriosis			
Symptomatic infection (Uncomplicated)	3–5%		United States Centers for Disease Control and Prevention, 2014
(Complicated)	95–97%		
Fatal cases		Age-dependent; see Table 17	TESSy, 2009–2013

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Health outcome (health state)	Distribution of health states in health outcome	Transition probability	Source/assumption
Permanent disability following meningitis		1.65–2.29% of complicated cases	Aouaj <i>et al.</i> , 2002; United States Centers for Disease Control and Prevention, 2014
Perinatal listeriosis			
Fatal cases		18.71%	TESSy, 2009–2013
Permanent disability following meningitis		24%	Aouaj <i>et al.</i> , 2002

Source: Adapted from ECDC (2019)

Table 16 DWs and duration for listeriosis

Health outcome (health state)	DW (Haagsma <i>et al.</i> , 2015)		Duration	
	DW	Label	In years	Source/assumption
Acquired listeriosis				
Symptomatic infection (Uncomplicated) (Complicated)	0.149 (0.12–0.182) 0.655 (0.579–0.727)	Diarrhoea Moderate Intensive care unit admission	0.02–0.5	Haagsma <i>et al.</i> , 2009; Kemmeren <i>et al.</i> , 2006
Permanent disability following meningitis	0.011–0.421	From lowest to highest motor and cognitive difficulties	Remaining life expectancy	
Perinatal listeriosis				
Symptomatic infection	0.655 (0.579–0.727)	Intensive care unit admission	0.02–0.5	Haagsma <i>et al.</i> , 2009; Kemmeren <i>et al.</i> , 2006
Permanent disability due to meningitis	0.011–0.421	From lowest to highest motor and cognitive difficulties	Remaining life expectancy	

Source: Adapted from ECDC (2019)

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Table 17** Age group case fatality proportion for acquired listeriosis based on cases and deaths notified to TESSy (2009–2013)

Age groups	%
0 years	11.90
1–4 years	0.00
5–9 years	5.88
10–14 years	20.00
15–19 years	13.16
20–24 years	1.75
25–29 years	4.10
30–34 years	1.39
35–39 years	8.40
40–44 years	12.50
45–49 years	14.08
50–54 years	16.59
55–59 years	13.77
60–64 years	18.16
65–69 years	15.65
70–74 years	15.17
75–79 years	17.83
80–84 years	17.35
≥85 years	23.15
All ages	15.74

Source: Adapted from ECDC (2019)

Salmonellosis

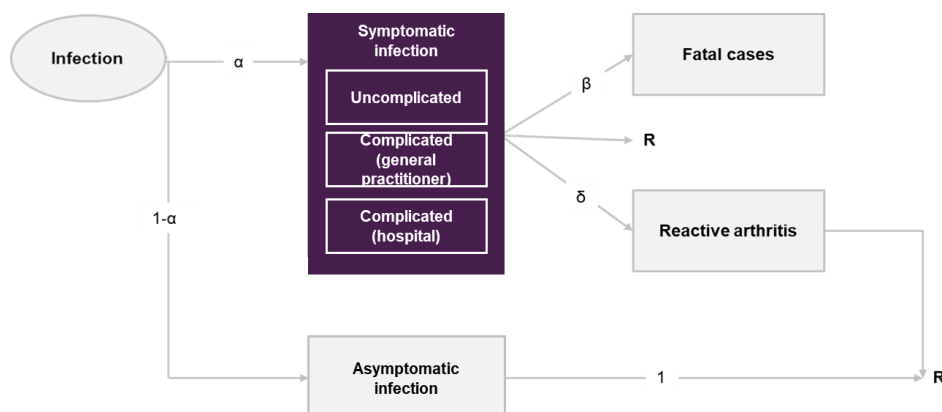


Figure 7 Disease model outcome tree for salmonellosis

Source: Adapted from ECDC (2019)

Model input summary

Salmonellosis is an illness resulting from infection with the bacteria *Salmonella*. It typically presents with an abrupt onset of fever, abdominal pain, diarrhoea, nausea and occasionally vomiting. In most cases, the symptoms are mild, and patients recover without requiring specific medical intervention. However, in certain populations, such as young children and older adults, dehydration resulting from the illness can become severe and pose substantial health risks (World Health Organization, 2018b). The incidence of laboratory-confirmed, non-travel-related salmonellosis in Ireland ([Appendix 7](#)) was corrected for its perceived relative underestimation using the expert judgement values presented in [Appendix 8](#).

The outcome tree for salmonellosis

Salmonellosis infection may present with symptoms (including uncomplicated cases, complicated cases managed with GP consultation, or complicated cases requiring hospitalisation) or remain asymptomatic.

Symptomatic infection

The following outcomes may occur among individuals with symptomatic salmonellosis:

Risk Ranking of Microbiological Hazards in Food (2015–2019)

- Among symptomatic cases, uncomplicated cases occur at a rate of 83.3%, complicated cases requiring GP attention occur at a rate of 15%, and complicated cases requiring hospitalisation occur at a rate of 1.7% (Kemmeren *et al.*, 2006; Kwong *et al.*, 2012).
- A proportion may result in fatal cases, may develop ReA or may recover.
- The estimated risk of developing ReA is approximately 1.31% among all symptomatic cases, with an average duration ranging from 1.5 to 7 months (Hannu *et al.*, 2002; Kemmeren *et al.*, 2006).

Asymptomatic infection

Typically, infection is self-limiting, and individuals recover completely without long-term effects.

Table 18 Health outcomes and transition probabilities used in the salmonellosis outcome tree

Health outcome (health state)	Distribution of health states in health outcome	Transition probability	Source/assumption
Symptomatic infection (Uncomplicated) (Complicated, GP) (Complicated, hosp)	83.3% 15% 1.7%		Kemmeren <i>et al.</i> , 2006; Kwong <i>et al.</i> , 2012
Fatal cases following symptomatic infection		0.05–0.1% (age-dependent; see Table 20)	Kemmeren <i>et al.</i> , 2006; Much <i>et al.</i> , 2007; TESSy, 2009–2013
ReA		1.31% (0.29–5.43%)	Kemmeren <i>et al.</i> , 2006

Source: Adapted from ECDC (2019)

Table 19 DWs and duration for salmonellosis

Health outcome (health state)	DW (Haagsma <i>et al.</i> , 2015)		Duration	
	DW	Label	In years	Source/assumption
Symptomatic infection (Uncomplicated) (Complicated, GP)	0.073 (0.061–0.092) 0.149 (0.12–0.182)	Diarrhoea, mild Diarrhoea, moderate	0.015 0.029	Kemmeren <i>et al.</i> , 2006

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Health outcome (health state)	DW (Haagsma <i>et al.</i> , 2015)		Duration	
	DW	Label	In years	Source/assumption
(Complicated, hosp)	0.239 (0.202–0.285)	Diarrhoea, severe	0.044	
ReA	0.344 (0.3–0.391)	Musculoskeletal problems, generalised, moderate	0.131–0.608	Hannu <i>et al.</i> , 2002

Source: Adapted from ECDC (2019)

Table 20 Age group redistribution of case fatality rate for salmonellosis (0.05–0.1%)

Age groups	%
0 years	0.69
1–4 years	1.72
5–9 years	1.38
10–14 years	0.34
15–19 years	1.03
20–24 years	0.00
25–29 years	1.72
30–34 years	0.34
35–39 years	1.03
40–44 years	0.69
45–49 years	2.07
50–54 years	3.45
55–59 years	4.14
60–64 years	5.17
65–69 years	9.31
70–74 years	12.41
75–79 years	16.55
80–84 years	18.62

Risk Ranking of Microbiological Hazards in Food (2015–2019)

≥85 years	19.31
All ages	100.00

Source: Adapted from ECDC (2019)

Shiga toxin-producing *Escherichia coli* infection

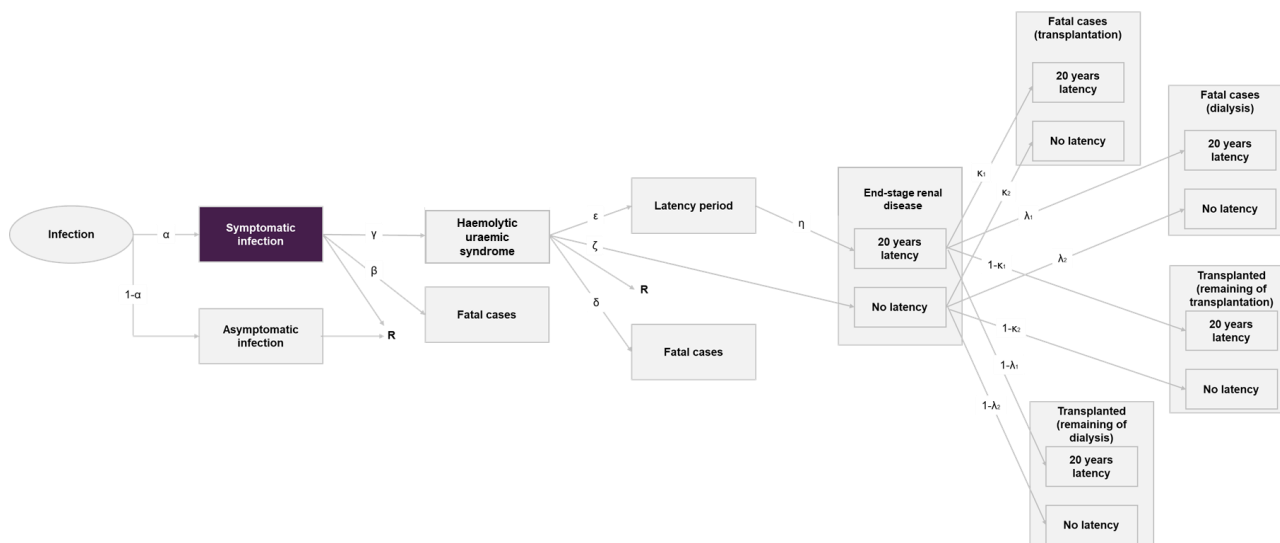


Figure 8 Disease model outcome tree for Shiga toxin-producing *Escherichia coli* infection

Source: Adapted from ECDC (2019)

Model input summary

Shiga toxin-producing *Escherichia coli* (STEC) is part of a broad group of bacteria within the *Escherichia coli* species. STEC strains produce a toxin that can lead to severe illness. Although infection can occur in individuals of all ages, young children and the elderly are at the highest risk of serious health complications. The incubation period for STEC typically ranges from 3 to 4 days following exposure. The duration of illness can extend up to 2 weeks. Some infected individuals may be asymptomatic, showing no symptoms, while others may experience symptoms such as abdominal pain or cramping, diarrhoea (which may be bloody), vomiting and sometimes fever. One potential complication is haemolytic uraemic syndrome (HUS), a serious condition resulting from toxins attacking red blood cells, which can impair kidney function. In children, HUS can lead to severe complications such as organ damage, including to the kidneys, and in some cases, it can be fatal (Health Protection Surveillance Centre, 2022). The incidence of laboratory-confirmed, non-travel-related STEC infection in Ireland ([Appendix 7](#)) was corrected for its perceived relative underestimation using the expert judgement values presented in [Appendix 8](#).

The outcome tree for STEC infection

STEC infection may present with symptoms or remain asymptomatic.

Symptomatic infection

The following outcomes may occur among individuals with symptomatic STEC infection:

- Symptomatic cases may cause acute gastroenteritis and haemorrhagic colitis, with 44.5% of cases exhibiting bloody diarrhoea (Michel *et al.*, 2000). Bloody diarrhoea persists longer, averaging 5 days, versus 3 days for non-bloody diarrhoea (Cressey and Lake, 2007; Havelaar *et al.*, 2004). These durations are modelled as a uniform distribution.
- STEC-associated mortality rates vary from 0.03% to 0.045% (Bruce-Grey-Owen Sound Health Unit, 2000; Buzby and Roberts, 2009; Havelaar *et al.*, 2004; Mead *et al.*, 1999). A uniform case-fatality proportion was assumed within this range.
- Fatal cases mainly affect older people (Bauch *et al.*, 2007). The case fatality rate of 0.03–0.045% is allocated across age groups based on TESSy-reported deaths (2009–2013) from European Union countries, excluding Bulgaria, Lithuania (aggregate data only) and Italy (sentinel surveillance with limited coverage).

HUS

The following outcomes may occur among individuals who develop HUS as a complication of STEC infection:

- HUS is characterised by rapid red blood cell destruction causing acute renal failure, often following gastrointestinal or respiratory infections.
- The risk of developing HUS after STEC infection ranges from 0.94% to 7%, with this model adopting a probability of 0.94–1.25%. It primarily affects children aged 1–5 years, with 72% of cases occurring in those aged under 15 years. Duration averages 7 days (range: 3–31 days), with 41% of cases requiring hospitalisation; hospital stays last 2–4 weeks.
- The case fatality rate is approximately 3.7%, rising to 56% in those aged over 65 years, based on outbreak data. Age-specific fatality rates are used across studies, and estimates derive from TESSy data (2009–2013), excluding Bulgaria, Italy and Lithuania.

End-stage renal disease

The following long-term outcomes may occur among individuals who progress to end-stage renal disease (ESRD) after HUS:

- ESRD the most severe stage of kidney failure, can develop shortly after or years following HUS, with an estimated 13.4% of cases progressing to ESRD (2.9% soon after HUS and 10.5% after 20 years).
- All ESRD patients undergo dialysis until transplantation.
- First-year dialysis mortality is high and varies by age, with few fatalities post-transplantation (Havelaar *et al.*, 2003). Dialysis duration until transplantation is age dependent.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Irritable bowel syndrome**

A literature review estimated that 8.8% (7.2–10.4%) of symptomatic foodborne infections may develop irritable bowel syndrome over 5 years, regardless of age or sex (Haagsma *et al.*, 2010). However, causality is debated, and other factors are influential; thus, irritable bowel syndrome is not included in the model.

Asymptomatic infection

Typically, infection is self-limiting, and individuals recover completely without long-term effects.

Table 21 Health outcomes and transition probabilities used in the STEC infection outcome tree

Health outcome (health state)	Transition probability	Source/assumption
Fatal cases following symptomatic infection	0.03–0.045% (age-dependent; see Table 23)	Buzby and Roberts, 2009; TESSy, 2009–2013
HUS	0.94–1.25% (age-dependent; see Table 24)	Cressey and Lake, 2007; Havelaar <i>et al.</i> , 2004; TESSy, 2009–2013
Latency period before ESRD	10.5%	Cressey and Lake, 2007; Havelaar <i>et al.</i> , 2004
ESRD after HUS	2.9%	Cressey and Lake, 2007; Havelaar <i>et al.</i> , 2004
ESRD after latency period	100%	
Fatal cases following HUS	Age-dependent; see Table 25	TESSy, 2009–2013
Fatal cases following ESRD	Age-dependent (see Table 26); different for dialysis and transplantation	Havelaar <i>et al.</i> , 2003
Transplanted	Remaining percentage	

Source: Adapted from ECDC (2019)

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Table 22 DWs and duration for STEC infection

Health outcome (health state)	DW (Haagsma <i>et al.</i> , 2015)		Duration	
	DW	Label	In years	Source/assumption
Symptomatic infection (gastroenteritis)	0.149 (0.12–0.182)	Diarrhoea, moderate	0.008–0.014	Cressey and Lake, 2007; Havelaar <i>et al.</i> , 2004
HUS	0.108 (0.09–0.132)	Chronic kidney disease (stage IV)	0.019 (0.008–0.085)	McPherson <i>et al.</i> , 2011
ESRD	0.487 (0.432–0.544)	ESRD, on dialysis	Age-dependent; see Table 27	Assuming that all ESRD cases are on dialysis
Transplanted	0.070 (0.057–0.088)	Generic uncomplicated disease: worry and daily medication	Remaining life expectancy	

Source: Adapted from ECDC (2019)

Table 23 Age group redistribution of case fatality proportion for STEC infection (0.03–0.045%)

Age groups	%
0 years	4.30
1–4 years	9.68
5–9 years	4.30
10–14 years	0.00
15–19 years	0.00
20–24 years	2.15
25–29 years	0.00

Risk Ranking of Microbiological Hazards in Food (2015–2019)

30–34 years	0.00
35–39 years	3.23
40–44 years	3.23
45–49 years	2.15
50–54 years	1.08
55–59 years	4.30
60–64 years	8.60
65–69 years	4.30
70–74 years	10.75
75–79 years	10.75
80–84 years	15.05
≥85 years	16.13
All ages	100.00

Source: Adapted from ECDC (2019)

Table 24 Age group redistribution of risk of developing HUS following STEC infection (0.94–1.25%)

Age groups	%
0 years	5.67
1–4 years	33.74
5–9 years	13.09
10–14 years	6.62
15–19 years	2.88
20–24 years	2.27
25–29 years	3.83
30–34 years	3.54
35–39 years	2.88
40–44 years	3.40

Risk Ranking of Microbiological Hazards in Food (2015–2019)

45–49 years	3.45
50–54 years	2.36
55–59 years	2.88
60–64 years	3.02
65–69 years	2.27
70–74 years	3.36
75–79 years	1.89
80–84 years	1.65
≥85 years	0.99
All ages	100.00

Source: Adapted from ECDC (2019)

Table 25 Age group case fatality proportion for HUS following STEC infection

Age groups	%
0 years	6.06
1–4 years	2.63
5–9 years	3.25
10–14 years	0.00
15–19 years	0.00
20–24 years	5.13
25–29 years	0.00
30–34 years	0.00
35–39 years	3.64
40–44 years	3.28
45–49 years	3.17
50–54 years	2.13
55–59 years	2.00
60–64 years	4.44

Risk Ranking of Microbiological Hazards in Food (2015–2019)

65–69 years	8.33
70–74 years	4.62
75–79 years	17.86
80–84 years	25.93
≥85 years	28.57
All ages	3.91

Source: TESSy (2009–2013); adapted from ECDC (2019)

Table 26 Case fatality proportions in the first year after starting dialysis and after renal transplantation for STEC infection

Age groups	Case fatality ratio for dialysis	Case fatality ratio for renal transplantation
0–14 years	4.1% (0.9–11.1%)	7% (2.2–16%)
15–44 years	8.7% (5.8–12.4%)	7% (2.2–16%)
45–64 years	37% (31–44%)	7% (2.2–16%)
65–74 years	65% (58–72%)	7% (2.2–16%)
≥75 years	79% (70–87%)	7% (2.2–16%)

Source: Adapted from ECDC (2019)

Table 27 Age-specific duration of dialysis for STEC infection

Age groups	Duration of dialysis (years)
0–14 years	1.7 (0.2–5.3)
15–44 years	2.5 (0.2–9.6)
45–64 years	6.7 (0.5–30)
≥65 years	5 years to remaining life expectancy

Source: Adapted from ECDC (2019)

Hepatitis A infection

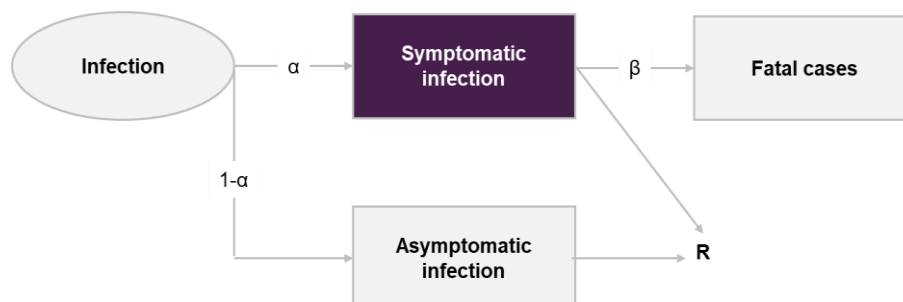


Figure 9 Disease model outcome tree for hepatitis A infection

Source: Adapted from ECDC (2019)

Model input summary

Hepatitis A infection is an acute, self-limiting liver disease caused by the hepatitis A virus (HAV). Many individuals, particularly young children, may remain asymptomatic. Generally, disease severity increases with age. The most common symptoms include fever, loss of appetite, nausea, fatigue, and abdominal discomfort, followed within a few days by jaundice. Clinical presentation can range from a mild illness lasting 1–2 weeks to a more severe condition lasting several months. In approximately 15% of cases, prolonged relapsing hepatitis may occur, lasting up to 1 year. Chronic (long-term) infection is not associated with hepatitis A infection. A small proportion of cases can develop into severe, fulminant hepatitis (Health Protection Surveillance Centre, 2017). The incidence of laboratory-confirmed, non-travel-related hepatitis A infection in Ireland ([Appendix Z](#)) was corrected for its perceived relative underestimation using the expert judgement values presented in [Appendix 8](#).

The outcome tree for hepatitis A infection

Hepatitis A infection may present with symptoms or remain asymptomatic.

Symptomatic infection

Symptomatic hepatitis A infection encompasses a range of clinical severities, with age-related differences in presentation and duration:

- Symptomatic hepatitis A infections vary by age: about 30% in children and 70–80% in adults (Ciocca, 2000; Cuthbert, 2001; Jeong and Lee, 2010). Children often experience mild, flu-like, anicteric symptoms lasting 1–2 weeks (Gingrich *et al.*, 1983), while adults

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typically show jaundice, dark urine, fatigue, loss of appetite, abdominal pain and light stools for several weeks (Koff, 1992).

- Symptom duration correlates with age: children usually recover in 1–2 weeks (Gingrich *et al.*, 1983), whereas 80% of adults are ill for up to 8 weeks (Koff, 1992). Estimates suggest that symptomatic cases last 14 days without medical help, 30 days with medical help (Haagsma *et al.*, 2009) or up to 0.3 years if hospitalised (Havelaar *et al.*, 2012). The United States CDC states that illness generally lasts less than 2 months, but 10–15% of cases have relapsing symptoms lasting up to 6 months (United States Centers for Disease Control and Prevention, 2012).
- Case fatality rates range from 0.1% to 1.0% in hospitalised cases, with recent estimates around 0.3% (Arteaga Rodriguez *et al.*, 2010; Bauch *et al.*, 2007; Fiore, 2004; Mead *et al.*, 1999). Mortality mainly affects older people (Bauch *et al.*, 2007; Jacobs *et al.*, 2004; 2000). Table 28 summarises HAV mortality rates used in cost-effectiveness analyses (Bauch *et al.*, 2007; Jacobs *et al.*, 2004; 2000).
- The case fatality proportion is estimated at 0.1–0.3%, with age-specific risks derived from TESSy data (2009–2013) but excluding Bulgaria, Lithuania, Latvia and Poland due to aggregate reporting, and Liechtenstein, which does not report data.

Risk of complications

Fulminant hepatitis is a rare complication of hepatitis A infection, with an incidence of approximately 0.011% and a liver transplantation risk of around 0.02% in young adults, increasing slightly with age. Due to its rarity, it was excluded. Rare, atypical and extra-hepatic manifestations include relapsing hepatitis, cholestasis, autoimmune and haematologic conditions, effusions, arthritis, pancreatitis, cholecystitis, neuropathies, and GBS; none were considered in the model.

Asymptomatic infection

Typically, infection is self-limiting, and individuals recover completely without long-term effects.

Table 28 Deaths among symptomatic patients per 10,000 cases, stratified by age groups, for hepatitis A infection

Age groups (in years)	Sources		
	Bauch <i>et al.</i> , 2007	Jacobs <i>et al.</i> , 2004	Jacobs <i>et al.</i> , 2000
	30		

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Age groups (in years)	Sources		
	Bauch <i>et al.</i> , 2007	Jacobs <i>et al.</i> , 2004	Jacobs <i>et al.</i> , 2000
5–14	18		
15–19	18		18 (6–30)
20–29	18	18	18 (6–30)
30–39	21	21	21 (10–32)
40–49	59	36	36 (23–49)
50–59	59	81	81 (70–92)
60–69	272	149	149 (146–152)
70–79	272	283	283 (154–310)

Source: Adapted from ECDC (2019)

Table 29 Health outcomes and transition probabilities used in the hepatitis A infection outcome tree

Health outcome (health state)	Transition probability	Source/assumption
Fatal cases	0.1–0.3% (age-dependent; see Table 31)	Bauch <i>et al.</i> , 2007; Fiore, 2004; Mead <i>et al.</i> , 1999

Source: Adapted from ECDC (2019)

Table 30 DWs and duration for hepatitis A infection

Health outcome (health state)	DW (Haagsma <i>et al.</i> , 2015)		Duration	
	DW	Label	In years	Source/assumption
Symptomatic infection	0.125 (0.104–0.152)	Infectious disease, acute episode, severe	0–9 years: 0.019–0.038 ≥10 years: 0.082 (0.038–0.5) (age-dependent; see Table 32)	Haagsma <i>et al.</i> , 2009; United States Centers for Disease Control and Prevention, 2012; age-dependent

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Source:** Adapted from ECDC (2019)**Table 31** Age group redistribution of case fatality proportion for hepatitis A infection (0.1–0.3%)

Age groups	%
0 years	0.00
1–4 years	0.00
5–9 years	0.00
10–14 years	0.00
15–19 years	0.00
20–24 years	10.00
25–29 years	0.00
30–34 years	0.00
35–39 years	0.00
40–44 years	10.00
45–49 years	0.00
50–54 years	10.00
55–59 years	20.00
60–64 years	10.00
65–69 years	0.00
70–74 years	20.00
75–79 years	20.00
80–84 years	0.00
≥85 years	0.00
All ages	100.00

Source: Adapted from ECDC (2019)

Table 32 Duration of symptomatic disease by age group for hepatitis A infection

Age groups	%
0–9 years	0.019–0.038
≥10 years	0.082 (0.038–0.5)

Source: Adapted from ECDC (2019)

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Appendix 6 Disease model frameworks and input data for hepatitis E and norovirus infections

Hepatitis E infection

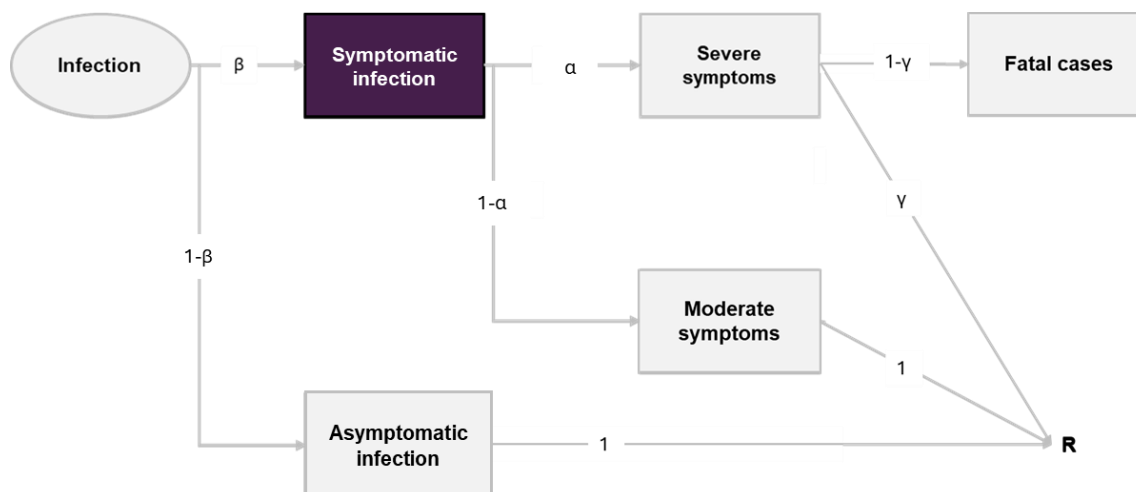


Figure 10 Disease model outcome tree for hepatitis E infection

Model input summary

Hepatitis E is an acute liver disease caused by infection with the hepatitis E virus (HEV). Multiple genotypes of HEV have been identified, with genotypes 1–4 most commonly associated with human infection and capable of causing acute viral hepatitis. Hepatitis E remains a significant public health concern worldwide (World Health Organization, 2025). Due to the largely asymptomatic nature of hepatitis E infection and substantial gaps in existing data, accurately estimating the disease burden of HEV presents significant challenges. The incidence of laboratory-confirmed, non-travel-related hepatitis E infection in Ireland ([Appendix 7](#)) was corrected for its perceived relative underestimation using the expert judgement values presented in [Appendix 8](#).

The outcome tree for hepatitis E infection

Symptomatic infection

During the expert consultation workshop, it was noted that hepatitis E infection cases documented through monitoring by the Irish Blood Transfusion Service (IBTS) indicate an approximately thirty-fold difference compared with those captured through the traditional Irish surveillance system as a notifiable disease. Based on this information, it was estimated that approximately 96.3–97.3%

(central estimate ~96.8%) of cases may be asymptomatic. This aligns with estimates suggesting that the majority of hepatitis E infections are asymptomatic, with some estimates indicating that this proportion may exceed 95% (BMJ Best Practice, 2026).

Based on this information, 2.7–3.7% of all hepatitis E infections were modelled as symptomatic cases. Symptomatic hepatitis E cases were assumed to result in mild to moderate or severe symptomatic illness. The limited proportion of cases modelled as symptomatic will result in only a small share of total infections being reflected in burden of disease estimate. This was a pragmatic modelling assumption adopted due to uncertainty regarding the extent to which asymptomatic and non-specific symptomatic hepatitis E infections translate into measurable disability within the DALY framework.

Moderate symptoms (70–90% of cases)

It was assumed that 70–90% of symptomatic hepatitis E infections would experience mild to moderate symptoms. This assumption is consistent with research indicating that most clinically apparent hepatitis E infections present with non-severe illness, particularly in Europe where genotype 3 predominates (European Centre for Disease Prevention and Control, 2017; Kumar, 2024).

Moderate symptoms of hepatitis E infection include jaundice, fever, fatigue, nausea, and abdominal pain, typically lasting 4–6 weeks (0.077–0.115 years). It was assumed that all individuals with moderate symptoms recover completely without long-term complications (Health Protection Surveillance Centre, 2023).

Severe symptoms (10–30% of cases)

It was assumed that 10–30% of cases of symptomatic hepatitis E infections would experience severe symptoms. This assumption is consistent with research indicating that a smaller percentage of symptomatic hepatitis E infection cases are reported to progress to severe manifestations of the disease, particularly among vulnerable populations (European Centre for Disease Prevention and Control, 2017; Kumar, 2024).

Severe symptoms of HEV can include life-threatening complications such as fulminant hepatitis and acute liver failure, which may require intensive medical intervention and can be fatal (WHO, 2025). For those who recover, it was assumed that the duration of severe symptoms is similar to that of moderate hepatitis E infection (0.077–0.115 years).

Among individuals experiencing severe symptoms, outcomes were assumed to differ by age group. In older adults (aged 65 years and over), outcomes may vary. While many individuals are expected to recover, a smaller proportion may experience more serious illness, which in some cases can result in mortality. Evidence indicates that severe outcomes and mortality are

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disproportionately concentrated among older individuals. The HPSC report an overall case fatality rate (CFR) for hepatitis E infection of approximately 1% (HPSC, 2023). Given that older adults may be at risk of developing more severe disease, a higher fatality estimate (10%) was applied to severe cases in individuals aged 65 years and over. This assumption is intended as a conservative estimate used within the model.

In children and healthy young adults, the CFR is generally less than 1% (European Centre for Disease Prevention and Control, 2017). In the absence of sufficient data to stratify outcomes by age, it was assumed in the model that all hepatitis E cases in individuals under 65 years result in recovery.

It is important to note that pregnant women, particularly those in the third trimester, may experience a substantially higher CFR, with estimates reaching up to 30%. This increased risk is largely attributable to a higher incidence of fulminant hepatitis in this group (Jin et al., 2016; Pallerla et al., 2020). In addition, HEV may cause chronic hepatitis in immunocompromised patients, including those who have undergone organ transplants, are receiving chemotherapy for cancer, or are living with human immunodeficiency virus (HIV) (Kumar, 2024). These higher-risk groups were not specifically targeted in the disease model but may be partially accounted for within the severe-disease outcomes.

Asymptomatic infection

As outlined above, 96.3–97.3% of all hepatitis E infections were assumed to be asymptomatic. These infections are typically self-limiting, with individuals recovering completely and no long-term health effects assumed.

Table 33 Health outcomes and transition probabilities used in the hepatitis E infection outcome tree

Stage	Health outcome (health state)	Transition probability	Source/assumption
Infection	Symptomatic	$\beta = (0.027-0.037)$	Considering the proportion of undetected hepatitis E cases captured through IBTS screening and estimates reported in the literature (BMJ Best Practice, 2026), it was estimated that 2.7–3.7% of

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Stage	Health outcome (health state)	Transition probability	Source/assumption
			infected individuals would develop symptoms.
	Asymptomatic	$1-\beta = (0.963-0.973)$	Considering the proportion of undetected hepatitis E cases captured through IBTS screening and estimates reported in the literature (BMJ Best Practice, 2026), it was estimated that asymptomatic infections occur at a rate of 96.3–97.3%.
Symptomatic infection	Moderate symptoms	$\alpha = (0.7-0.9)$	It was assumed that 70–90% of symptomatic HEV cases develop moderate, non-life-threatening symptoms.
	Severe symptoms	$1-\alpha = (0.1-0.3)$	It was assumed that 10–30% of symptomatic HEV cases develop severe symptoms, including fulminant hepatitis.
Severe symptoms	Recovery	$\gamma = (0.90-1)$ Those aged 65 years and over: 0.90 Those aged under 65 years: 1	Depending on age, 90–100% of severe HEV cases are assumed to result in recovery, informed by the low overall case fatality rates reported (European Centre for Disease Prevention and Control, 2017; HPSC, 2023)
	Fatal cases	$1-\gamma = (0-0.10)$ Those aged 65 years and over: 0.10 Those under 65 years: 0	Depending on age, 0–10% of severe HEV cases may result in fatal outcomes, reflecting the higher mortality risk in older adults and low overall case fatality rates reported (European Centre for Disease

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Stage	Health outcome (health state)	Transition probability	Source/assumption
			Prevention and Control, 2017; HPSC, 2023).
Moderate symptoms	Recovery	1	It was assumed that all HEV cases (100%) with mild to moderate symptoms recover without any fatalities.
Asymptomatic infection	Recovery	1	It was assumed that all cases (100%) of asymptomatic HEV recover without any fatalities.

Table 34 Disability weights and duration for hepatitis E infection

Health outcome (health state)	Disability weight (DW) (Haagsma <i>et al.</i> , 2015)		Duration	
	DW	Label	In years	Source/assumption
Symptomatic infection – severe symptoms	0.133 (0.088–0.189)	Severe acute HEV, temporary disability	0.077–0.115	DW is sourced from the Institute for Health Metrics and Evaluation (IHME) (2024). It was assumed that the duration of severe symptoms aligns with what is reported for the typical duration of hepatitis E infection. Duration is as reported by the HPSC (2023); however, in real life this may involve prolonged recovery.
Symptomatic infection – moderate symptoms	0.050 (0.032–0.074)	Moderate acute HEV, temporary disability	0.077–0.115	DW is sourced from the IHME (2024). Duration is as reported by the HPSC (2023).
Fatal cases	1			

Norovirus infection

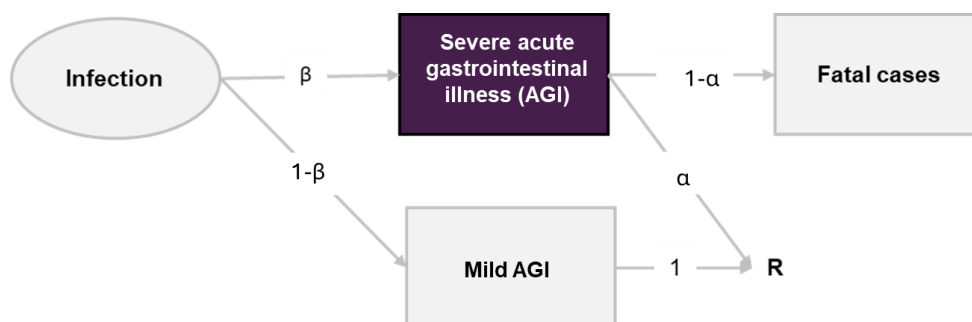


Figure 11 Disease model outcome tree for norovirus infection

Model input summary

Sequelae, or long-term health effects following infection, are not typically observed in cases of norovirus infection. Therefore, the focus of the model outcomes is solely on stages of acute gastrointestinal illness (AGI) and associated recovery or, in rare cases, may result in mortality. The incidence of laboratory-confirmed, non-travel-related norovirus infection in Ireland ([Appendix 7](#)) was corrected for its perceived relative scale of underestimation using the expert judgement values presented in [Appendix 8](#).

The outcome tree for norovirus infection

Severe AGI

It was assumed that 0.6% of all norovirus infections lead to severe AGI requiring medical care or hospitalisation (Tam and O'Brien, 2016). Individuals with severe AGI were assumed to either recover or, in rare instances, may result in mortality.

Hall et al. (2013) reported that most (90%) norovirus-associated deaths occur among individuals aged 65 years and over, at a rate of 0.20 deaths per 10,000 population. Therefore, for adults aged 65 years and over, a small proportion (0.002%) of severe AGI cases were modelled to result in a fatal outcome, while the vast majority (99.998%) were assumed to recover.

In the absence of sufficient data to stratify mortality among individuals under 65 years of age, the model assumes recovery as the sole outcome for all severe AGI cases in this group.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Mild AGI**

Given the hospitalisation rate employed in this disease model, it was assumed that majority of norovirus infections (99.4%) result in mild AGI. Mild AGI is generally self-limiting and does not require hospitalisation.

All mild norovirus-related AGI cases were assumed to recover without fatality, reflecting that mild infections are usually self-resolving. Recovery was therefore treated as the sole outcome for mild AGI across all age groups in the model.

Table 35 Health outcomes and transition probabilities used in the norovirus infection outcome tree

Stage	Health outcome (health state)	Transition probability	Source/assumption
Infection	Severe AGI	$\beta = 0.006$	The rate of severe AGI was derived from the estimated hospitalised norovirus cases (scenario 1) as a percentage of the total norovirus cases reported by Tam and O'Brien (2016).
	Mild AGI	$1-\beta = 0.994$	The rate of mild AGI was derived from the difference in estimated hospitalised norovirus cases as a percentage of the total norovirus cases reported by Tam and O'Brien (2016).
Severe AGI	Recovery	$\alpha = (0.99998-1.00)$ Those aged 65 years and over: 0.99998 Those under 65 years: 1	The 99.998% recovery rate for severe cases of AGI resulting from norovirus in those aged 65 and older is derived from Hall et al. (2013).
	Fatal cases	$1-\alpha = (0.00-0.00002)$ Those aged 65 years and over: 0.00002 Those under 65 years: 0	The mortality rate of 0.002% among severe cases of AGI resulting from norovirus in those aged 65 and older is derived from Hall et al. (2013).

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Mild AGI	Recovery	1 (100%)	It was assumed that all cases of mild AGI recover without any fatalities.
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Table 36 DWs and duration for norovirus infection

Health outcome (health state)	DW		Duration	
	DW	Label	In years	Source/assumption
Severe AGI	0.247 (0.164–0.347)	Diarrhoea, severe, temporary disability	All ages: 0.016–0.018	It was assumed that a proportion of severe AGI cases require hospitalisation. In general, the mean length of a hospital stay in Ireland was reported to range 6–6.4 days during the period 2011–2019 (Statista, 2025). DW was sourced from the IHME (2024).
Mild AGI	0.073 (0.048–0.104)	Diarrhoea, mild, temporary disability	All ages: 0.005–0.008	Duration was assumed from data reported by the Health Service Executive (2025). DW was sourced from the IHME (2024).

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Appendix 7 Epidemiological data

Epidemiological data on campylobacteriosis

Total campylobacteriosis cases reported in Ireland (2015–2019): 13,549

Travel-associated campylobacteriosis cases reported in Ireland (2015–2019): 61

Campylobacteriosis cases reported in Ireland excluding travel-associated cases (2015–2019): 13,488

Reference: Health Protection Surveillance Centre (HPSC) of the Health Service Executive (2022). *Custom extract from the Computerised Infectious Disease Reporting (CIDR) system*, prepared for the Food Safety Authority of Ireland.

Table 37 Campylobacteriosis case incidence rate over 5 years

Annual average number of cases by age group (2015–2019) ^{a, b, c}		
Age group	Females	Males
<1 year	41.8	51.4
1–4 years	163.8	231.2
5–9 years	65.0	101.2
10–14 years	27.0	64.6
15–19 years	53.8	78.2
20–24 years	86.8	96.4
25–29 years	90.2	93.8
30–34 years	78.2	74.8
35–39 years	73.0	74.6
40–44 years	63.2	71.6
45–49 years	60.6	77.6
50–54 years	66.2	73.8
55–59 years	66.6	68.0
60–64 years	54.0	68.4

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Annual average number of cases by age group (2015–2019)^{a, b, c}		
Age group	Females	Males
65–69 years	55.0	72.6
70–74 years	51.0	61.2
75–79 years	46.2	57.0
80–84 years	30.8	36.6
≥85 years	33.0	29.6
Total average incidence^{a, b, c}	1206.2	1482.6

^a Excludes travel-associated cases (n=61). The dataset includes only data from cases known to be acquired in Ireland, or where the country of infection was unknown.

^b Cases of campylobacteriosis where the sex was unknown were excluded (total: n=17).

^c Cases of campylobacteriosis in unknown age groups were excluded (females: n=12; males: n=15).

Epidemiological data on listeriosis

Total listeriosis cases reported in Ireland (2015–2019): 86

Travel-associated listeriosis cases reported in Ireland (2015–2019): 3

Listeriosis cases reported in Ireland excluding those associated with travel (2015–2019): 83

Reference: Health Protection Surveillance Centre (HPSC) of the Health Service Executive (2022). *Custom extract from the Computerised Infectious Disease Reporting (CIDR) system*, prepared for the Food Safety Authority of Ireland.

Table 38 Listeriosis case incidence rate over 5 years

Annual average number of cases by age group (2015–2019) ^a		
Age group	Females	Males
Perinatal listeriosis	3.8	0.4
<1 year	1.4	0.4
1–4 years	0.0	0.2
5–9 years	0.0	0.0
10–14 years	0.0	0.0
15–19 years	0.2	0.0
20–24 years	0.0	0.0
25–29 years	0.6	0.0
30–34 years	0.6	0.0
35–39 years	1.0	0.0
40–44 years	0.4	0.6
45–49 years	0.0	0.0
50–54 years	0.4	0.6
55–59 years	0.6	0.6
60–64 years	0.2	1.0
65–69 years	0.4	1.0

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Annual average number of cases by age group (2015–2019)^a		
70–74 years	1.2	0.4
75–79 years	0.6	1.0
80–84 years	1.0	1.2
≥85 years	0.6	0.4
Total average incidence^a	13.0	7.8

^a Excludes travel-associated cases (n=3). The dataset includes only data from cases where the infection is known to be acquired in Ireland or where the country of infection was unknown.

Epidemiological data on salmonellosis

Total salmonellosis cases reported in Ireland (2015–2019): 1,703

Travel-associated salmonellosis cases reported in Ireland (2015–2019): 671

Salmonellosis cases reported in Ireland excluding travel-associated cases (2015–2019):
1,032

Reference: Health Protection Surveillance Centre (HPSC) of the Health Service Executive (2022). *Custom extract from the Computerised Infectious Disease Reporting (CIDR) system*, prepared for the Food Safety Authority of Ireland.

Table 39 Salmonellosis case incidence rate over 5 years

Annual average number of cases by age group (2015–2019) ^{a, b}		
Age group	Females	Males
<1 year	7.0	6.6
1–4 years	11.0	18.2
5–9 years	6.2	6.6
10–14 years	3.4	4.8
15–19 years	3.8	4.6
20–24 years	6.4	7.2
25–29 years	7.6	8.6
30–34 years	8.4	5.4
35–39 years	7.8	6.4
40–44 years	4.8	4.4
45–49 years	4.8	4.6
50–54 years	3.8	5.0
55–59 years	5.0	5.6
60–64 years	2.8	4.4
65–69 years	4.2	3.8
70–74 years	3.6	3.8

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Annual average number of cases by age group (2015–2019)^{a, b}		
Age group	Females	Males
75–79 years	2.4	1.8
80–84 years	3.2	3.2
≥85 years	3.2	2.0
Total average incidence^{a, b, c}	99.4	107.0

^a Excludes travel-associated cases (n=671). The dataset includes only data from cases known to be acquired in Ireland or where the country of infection was unknown.

^b Cases of salmonellosis in unknown age groups were excluded (females: n=0; males: n=1).

Epidemiological data on Shiga toxin-producing *Escherichia coli* infection

Total Shiga toxin-producing *Escherichia coli* (STEC) cases reported in Ireland (2015–2019): 4,477

Travel-associated STEC cases reported in Ireland (2015–2019): 172

STEC cases reported in Ireland excluding travel-associated cases (2015–2019): 4,305

Reference: Health Protection Surveillance Centre (HPSC) of the Health Service Executive (2022). *Custom extract from the Computerised Infectious Disease Reporting (CIDR) system*, prepared for the Food Safety Authority of Ireland.

Table 40 STEC case incidence rate over 5 years

Annual average number of cases by age group (2015–2019) ^{a, b, c}		
Age group	Females	Males
<1 year	26.8	31.8
1–4 years	126.4	138.0
5–9 years	31.4	39.2
10–14 years	18.8	23.0
15–19 years	13.2	16.6
20–24 years	20.6	12.8
25–29 years	15.4	12.6
30–34 years	26.8	9.0
35–39 years	24.2	8.6
40–44 years	13.0	11.8
45–49 years	12.4	7.0
50–54 years	16.0	11.0
55–59 years	15.4	10.8
60–64 years	19.0	14.2
65–69 years	14.2	13.4

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Annual average number of cases by age group (2015–2019)^{a, b, c}		
Age group	Females	Males
70–74 years	15.6	12.2
75–79 years	14.6	11.4
80–84 years	13.4	12.8
≥85 years	15.8	9.8
Total average incidence^{a, b, c}	453.0	406.0

^a Excludes travel-associated cases (n=172). The dataset includes only data from cases known to be acquired in Ireland or where the country of infection was unknown.

^b Cases of STEC where the sex was unknown were excluded (total: n=5).

^c Cases of STEC in unknown age groups were excluded (females: n=4; males: n=1).

Epidemiological data on hepatitis A infection

Total hepatitis A cases reported in Ireland (2015–2019): 227

Travel-associated hepatitis A cases reported in Ireland (2015–2019): 109

Hepatitis A cases reported in Ireland excluding those associated with travel (2015–2019): 118

Reference: Health Protection Surveillance Centre (HPSC) of the Health Service Executive (2022). *Custom extract from the Computerised Infectious Disease Reporting (CIDR) system*, prepared for the Food Safety Authority of Ireland.

Table 41 Hepatitis A case incidence rate over 5 years

Annual average number of cases by age group (2015–2019) ^a		
Age group	Females	Males
<1 year	0.00	0.00
1–4 years	0.50	1.25
5–9 years	1.50	1.75
10–14 years	0.75	0.50
15–19 years	0.75	0.25
20–24 years	1.00	2.00
25–29 years	1.00	1.50
30–34 years	1.50	2.75
35–39 years	1.25	3.50
40–44 years	1.00	0.75
45–49 years	0.50	1.25
50–54 years	0.25	0.75
55–59 years	0.25	0.25
60–64 years	0.00	0.75
65–69 years	0.50	0.25
70–74 years	0.50	0.25
75–79 years	0.00	0.25

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Annual average number of cases by age group (2015–2019)^a		
Age group	Females	Males
80–84 years	0.00	0.25
≥85 years	0.00	0.00
Total average incidence^a	11.25	18.25

^a Excludes travel-associated cases (n=109). The dataset includes only data from cases known to be acquired in Ireland or where the country of infection was unknown.

Epidemiological data on hepatitis E infection

Total hepatitis E cases reported in Ireland, excluding cases captured by the Irish Blood Transfusion Service (IBTS) (2016–2019): 190

Travel-associated hepatitis E cases reported in Ireland (2016–2019): 7

Hepatitis E cases reported in Ireland excluding travel-associated cases (2016–2019): 183

Reference: Health Protection Surveillance Centre (HPSC) of the Health Service Executive (2022). *Custom extract from the Computerised Infectious Disease Reporting (CIDR) system*, prepared for the Food Safety Authority of Ireland.

Table 42 Hepatitis E case incidence rate over 4 years, excluding cases captured by the IBTS

Annual average number of cases by age group (2016–2019) ^{a, b, c}		
Age group	Females	Males
<1 years	0.0	0.0
1–4 years	0.0	0.2
5–9 years	0.0	0.0
10–14 years	0.2	0.0
15–19 years	0.2	0.0
20–24 years	0.4	1.4
25–29 years	0.8	0.4
30–34 years	0.4	0.2
35–39 years	1.2	1.8
40–44 years	1.6	1.6
45–49 years	1.2	2.4
50–54 years	1.8	3.0
55–59 years	1.4	2.2
60–64 years	1.6	2.8
65–69 years	0.6	3.2
70–74 years	1.0	2.2

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Annual average number of cases by age group (2016–2019)^{a, b, c}		
Age group	Females	Males
75–79 years	1.4	0.0
80–84 years	0.8	0.4
≥85 years	0.0	0.2
Total average incidence^{a, b, c}	14.6	22.0

^a Excludes travel-associated cases (n=7). The dataset includes only data from cases known to be acquired in Ireland or where the country of infection was unknown.

^b Cases of hepatitis E infection where the sex was unknown were excluded (total: n=1).

^c Cases of hepatitis E infection captured by the IBTS were excluded (females: n=31; males: n=69).

Note: Hepatitis E infection only became a notifiable disease in Ireland in 2015, with only three cases reported that year. Therefore, data were only used for the years 2016–2019, inclusive.

Epidemiological data on norovirus infection

Total norovirus cases reported in Ireland (2015–2019): 7,028

Travel-associated norovirus cases reported in Ireland (2015–2019): 1

Norovirus cases reported in Ireland excluding travel-associated cases (2015–2019): 7,027

Reference: Health Protection Surveillance Centre (HPSC) of the Health Service Executive (2022). *Custom extract from the Computerised Infectious Disease Reporting (CIDR) system*, prepared for the Food Safety Authority of Ireland.

Table 43 Norovirus case incidence rate over 5 years

Annual average number of cases by age group (2015–2019) ^{a, b, c}		
Age group	Females	Males
<1 year	89.2	110.8
1–4 years	124.6	136
5–9 years	14.8	27.2
10–14 years	10.4	9.6
15–19 years	8.6	11.0
20–24 years	13.0	7.6
25–29 years	15.2	12.2
30–34 years	17.6	8.0
35–39 years	19.8	12.6
40–44 years	13.4	10.8
45–49 years	8.8	12.0
50–54 years	12.0	16.4
55–59 years	17.8	19.6
60–64 years	21.2	24.8
65–69 years	24.8	32.0
70–74 years	35.6	38.8

Risk Ranking of Microbiological Hazards in Food (2015–2019)

Annual average number of cases by age group (2015–2019)^{a, b, c}		
Age group	Females	Males
75–79 years	46.8	53.2
80–84 years	72.2	58.4
≥85 years	160.4	75.0
Total average incidence^{a, b, c}	726.2	676.0

^a Excludes travel-associated cases (n=1). The dataset includes only data from cases known to be acquired in Ireland or where the country of infection was unknown.

^b Cases of norovirus where the sex was unknown were excluded (total: n=7).

^c Cases of norovirus in unknown age groups were excluded (females: n=6; males: n=3).

Appendix 8 Expert consultation workshop on underestimation

Briefing document

Background

In order to conduct a microbiological risk ranking exercise for food safety, an understanding of the true incidence of foodborne diseases (FBDs) is required. Reporting of disease incidence may be subject to under-ascertainment (UA) and underreporting (UR), which leads to a degree of uncertainty associated with the true incidence of a disease. This can vary from disease to disease. The combination of UA and UR is referred to as underestimation (UE). At present, there is limited information on the UE of infectious diseases in Ireland and most other countries.

Aim

The aim of this meeting is for the group to estimate plausible values to account for UE that may exist on the Irish surveillance of the seven FBDs included within the microbiological risk ranking exercise. The group's estimates will be based on the members' expertise and experience. This UE value is a median value, and it will be modelled as a multiplication factor (MF), capturing both elements of UA and UR.

Please refer to the definitions and [Figure 12](#) in the terminology overview to understand the terms that may be used during this workshop, and to gain a clearer understanding of the UE layers captured in an MF.

Terminology overview

Underestimation (UE): The number of infections estimated to have occurred in a population that have not been captured. UE can be broken down into the categories of under-ascertainment (UA) and underreporting (UR). The disease incidence data captured by the surveillance systems in place can be adjusted with a UE factor in order to provide a more accurate representation of the true burden of disease within a population.

Under-ascertainment (UA): Under-ascertained infections occur at the community level in individuals who do not seek healthcare and hence cannot be captured by surveillance systems, which are typically designed to capture cases who do seek healthcare. UA can be estimated as the ratio of infections in individuals who do not attend healthcare services to those who do attend.

Underreporting (UR): Underreporting occurs when a health event is not captured, despite the individual seeking healthcare, due to potential confines of the health system.

Ascertainment ratio: The ratio of the estimated number of cases of illness in the population due to specific pathogens to the number of laboratory reports in the national database for laboratory-confirmed infections.

Multiplication factor (MF): A factor used to adjust reported or observed case numbers in order to estimate the true number of infections, accounting for both under-ascertainment (UA) and under-reporting (UR).

[Figure 12](#), adapted from Gibbons *et al.* (2014), links the morbidity surveillance pyramid with a decision-tree model that illustrates how cases are progressively lost from the total infected population to the subset of reported cases. The base of the pyramid (“All infections”) corresponds to the orange box in the decision tree, while the apex (“Cases reported”) corresponds to the blue box. Using this structure, Gibbons *et al.* (2014) provide the following example for deriving MFs. First, if 55% of infected individuals who attend healthcare are reported, a UR-correction MF of 1.8 ($=100/55$) adjusts 1,000 reported cases to 1,800 true attending cases. Next, if 60% of symptomatic cases attend healthcare, a UA-correction MF of 1.7 ($=100/60$) increases this estimate to 3,000 symptomatic cases ($=1.7 \times 1,800$). If 90% of infections are symptomatic, a further MF of 1.1 ($=100/90$) yields a total of 3,300 infections ($=1.1 \times 3,000$). Combined, these components give overall MFs of 3.06 ($=1.8 \times 1.7$) for symptomatic cases and 3.4 ($=1.8 \times 1.7 \times 1.1$) for all infections.

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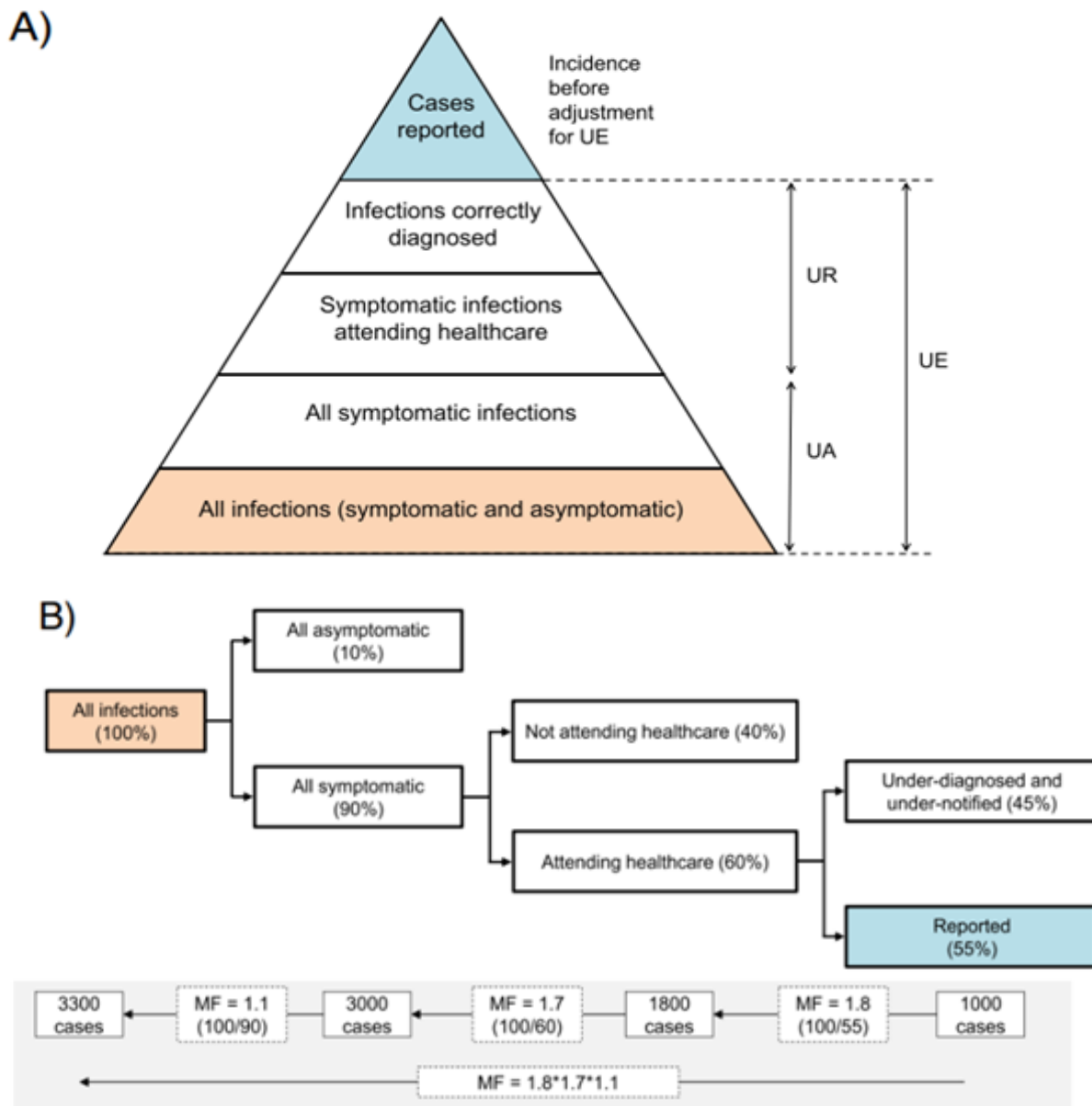


Figure 12 A) The morbidity surveillance pyramid, often used to illustrate the availability of morbidity data at each surveillance level; B) Decision tree outlining the acquisition of MFs from the morbidity surveillance pyramid

Source: Gibbons *et al.* (2014)

Expert consultation workshop

Methods

Preparation

The Food Safety Authority of Ireland (FSAI) prepared materials to provide context for this work and to facilitate discussions regarding deliverables prior to the workshop. The materials included:

- The meeting agenda
- The specific aim of the meeting and questions to be addressed
- An overview of the current understanding and issues related to the UE of diseases in Ireland
- Definitions of the relevant terms to ensure clarity and consistency
- A summary of the literature reporting UE values from studies conducted on populations comparable to Ireland (Adak *et al.*, 2002; De Jong and Ekdahl, 2006; Ekdahl and Giesecke, 2004; Haagsma *et al.*, 2013; Havelaar *et al.*, 2013; Pires *et al.*, 2020; Tam *et al.*, 2012).

Expert consultation workshop

During the expert consultation workshop, the specific aim and questions to be addressed were outlined to attendees. In addition, an overview of the current understanding and issues related to the UE of FBDs in Ireland was provided within the context of the overarching Scientific Committee project. When reviewing UE values presented in the literature for relatively comparable populations to Ireland, participants in the workshop were asked to consider how variations in surveillance systems, healthcare infrastructure, reporting practices and other differences that might exist between the countries whose values were reported could impact the scale of UE and therefore the experts' estimates. Additionally, the year in which the study from which the UE value was derived was conducted was highlighted for consideration (e.g., to account for any changes in systems or practices within a country's healthcare system since that time). Participants were encouraged to refrain from providing estimates for a specific disease or UE variable if they considered themselves not sufficiently qualified to do so. Although in practice the sex of an individual (i.e. whether they are a woman, man or nonbinary) may influence patient behaviour when it comes to seeking healthcare and likewise medical practitioners may have unconscious biases against patients based on sex, due to perceived challenges in sufficiently addressing this variable, it was assumed for the purpose of this exercise that there was no difference in UE between sexes. Variability between MFs for three age demographics was considered within each disease model. Age demographics were separated into those aged under 5 years, those aged 5–64 years and those aged 65 years and

over. MFs for each disease model were derived and agreed by the participants in the expert consultation.

Summary of expert judgements and rationale

This summary presents the expert group's reasoning for the MFs applied to account for UA and UR in disease surveillance. These MFs were derived in an attempt to correct for cases missed by routine surveillance due to clinical, behavioural and diagnostic system limitations. The values reflect considered expert judgement, not direct data measurements.

Campylobacteriosis

The rationale for the MFs presented in [Table 44](#) for campylobacteriosis reflect the group's view that case detection for campylobacteriosis varies significantly by age due to differences in the healthcare-seeking behaviour and sample submission among cohorts. Children aged under 5 years are more likely to be brought for care and tested, leading to lower UA for this demographic. Individuals aged 5–64 years tend to delay or avoid seeking healthcare services, contributing to the highest UA for this demographic. Adults aged 65 years and over have moderate engagement with healthcare services, leading to a mid-range MF. The increasing use of polymerase chain reaction (PCR) testing since 2013 also influenced the group's assumptions.

Table 44 MFs agreed by participants in the expert consultation workshop to correct for UE of campylobacteriosis cases

Age groups	MF
5 years and under	6.0
5–64 years	21.0
65 years and over	12.5

Listeriosis

The group's rationale for the MFs presented in [Table 45](#) for listeriosis was grounded in the limitations of current testing practices, which focus on blood and cerebrospinal fluid samples, missing many subclinical or atypical presentations. The group emphasised under-detection of listeriosis in neonatal cases (often recorded under maternal diagnoses) and among older adults or those receiving end-of-life care. Despite cases generally being prompted to seek healthcare due to

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the severity of listeriosis, the group agreed that surveillance is affected by an appreciable extent of UE.

Table 45 MFs agreed by participants in the expert consultation workshop to correct for UE of listeriosis cases

Age groups	MF
5 years and under	2.0
5–64 years	2.0
65 years and over	2.2

Salmonellosis

The expert group's rationale for the MFs presented in [Table 46](#) for salmonellosis reflect several key considerations. The experts judged UA for salmonellosis to be lower than that for campylobacteriosis, partly because individuals who contract a travel-related illness are more likely to seek care. The group considered that returning travellers are more likely to be tested for salmonellosis due to heightened clinical suspicion. While the group applied the same UR values as for campylobacteriosis, it acknowledged that in practice, increased clinician vigilance may slightly reduce under-detection of salmonellosis.

Table 46 MFs agreed by participants in the expert consultation workshop to correct for UE of salmonellosis cases

Age groups	MF
5 years and under	3
5–64 years	8
65 years and over	6

Shiga toxin-producing *Escherichia coli*

The expert group's rationale for the MFs presented in [Table 47](#) for Shiga toxin-producing *Escherichia coli* (STEC) reflect several key considerations. The group considered UA to be relatively low for STEC, especially in young children, due to routine outbreak testing in childcare settings. The group believed that high rates of bloody diarrhoea would prompt medical attention

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across all age groups. Inclusion of PCR-confirmed cases (including serogroups O26 and O157) enhanced detection of STEC. The group concluded that the diagnostic confirmation process rarely reversed positive findings, reducing UR.

Table 47 MFs agreed by participants in the expert consultation workshop to correct for UE of STEC cases

Age groups	MF
5 years and under	3
5–64 years	10
65 years and over	8

Hepatitis A infection

The expert group's rationale for the MFs presented in [Table 48](#) for hepatitis A infection reflects its insights on the challenges in detecting and diagnosing cases of the virus. The group attributed high UA in children to the high proportion of asymptomatic infections. Much of the cohort aged 5–64 years were considered protected from hepatitis A virus (HAV) due to receiving travel-related vaccinations, although gaps remain. Adults aged 65 years and over were considered to have natural immunity to HAV from past exposure. The likelihood of care-seeking for hepatitis A infection increases with age due to cases suffering from more pronounced symptoms as well as receiving routine liver function monitoring.

Table 48 MFs agreed by participants in the expert consultation workshop to correct for UE of hepatitis A cases

Age groups	MF
5 years and under	40.0
5–64 years	8.0
65 years and over	6.5

Hepatitis E infection

The expert group's rationale for the MFs presented in [Table 49](#) for hepatitis E infection reflects its insights on the challenges in detecting and diagnosing cases of infection with the virus. The

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experts considered UE to be particularly high for hepatitis E. Routine testing rarely includes hepatitis E, and its symptoms are often mild or non-specific. Insights from blood donor screening (e.g. the Irish Blood Transfusion Service) suggest that many infections may remain undetected within the general population. The group considered detection to be improved among older adults than the general population due to their routine healthcare engagement, although it is still limited due to low testing frequency.

Table 49 MFs agreed by participants in the expert consultation workshop to correct for UE of hepatitis E cases

Age groups	MF
5 years and under	50
5–64 years	30
65 years and over	20

Norovirus infection

The expert group's rationale for the MFs presented in [Table 50](#) for norovirus infection were based on its observations regarding the unique challenges in detecting and diagnosing norovirus. The experts agreed that most norovirus infections go undiagnosed due to the short duration of illness and lack of routine community testing. Diagnosis of norovirus typically occurs only in outbreak settings (e.g. hospitals, nursing homes), where testing is targeted and limited. The fact that norovirus often presents as a mild, self-limiting illness in the community, as well as challenges with sample collection (especially when vomiting is the primary symptom), further increase UA. The MFs reflect the consensus among the group that the vast majority of norovirus cases are missed.

Table 50 MFs agreed by participants in the expert consultation workshop to correct for UE of norovirus cases

Age groups	MF
5 years and under	1000
5–64 years	2000
65 years and over	500

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Appendix 9 Irish population breakdown by age group

Table 51 Irish population breakdown by age group for 2016.

Age	Population 2016	
	Females	Males
<1 year	30 381	31 876
1–4 years	131 403	137 855
5–9 years	174 091	181 470
10–14 years	156 098	163 378
15–19 years	147 908	154 908
20–24 years	136 052	137 584
25–29 years	152 213	145 222
30–34 years	188 796	173 179
35–39 years	198 376	191 045
40–44 years	179 978	177 482
45–49 years	163 286	162 824
50–54 years	151 723	148 212
55–59 years	136 244	133 858
60–64 years	120 158	118 698
65–69 years	106 275	104 961
70–74 years	82 771	79 501
75–79 years	61 350	54 117
80–84 years	45 841	35 196
≥85 years	44 493	23 062
Total	2 407 437	2 354 428

Source: Central Statistics Office (2021) E3001: Enumerated Population 1926 to 2016 (Number)

Appendix 10 Irish life expectancy by age group

Table 52 Mean Irish life expectancy (2016^{a, b}) by age group and sex in the Burden of Communicable Disease in Europe toolkit required format.

Age	Females	Males
<1 year	83.42	79.64
1–4 years	80.92	77.14
5–9 years	76.42	72.64
10–14 years	71.42	67.64
15–19 years	66.42	62.64
20–24 years	61.42	57.64
25–29 years	56.42	52.64
30–34 years	51.42	47.64
35–39 years	46.42	42.64
40–44 years	41.42	37.64
45–49 years	36.42	32.64
50–54 years	31.42	27.64
55–59 years	26.42	22.64
60–64 years	21.42	17.64
65–69 years	16.42	12.64
70–74 years	11.42	7.64
75–79 years	6.42	2.64
80–84 years	1.42	0.00 ^b
≥85 years	0.00 ^b	0.00 ^b

^a The most recent life expectancy data available for Ireland are from 2016.

^b Although individuals may live beyond the mean life expectancy, this value was used as a threshold for estimating years of life lost due to each disease. Values exceeding this threshold were capped at zero to prevent negative DALYs.

Source: Central Statistics Office (2020) Irish Life Tables

Appendix 11 Expert elicitation



Údarás Sábháilteachta Bia NA hÉIREANN
Food Safety AUTHORITY OF IRELAND

Expert elicitation preparation material:

Foodborne attribution of selected microbiological hazards in Ireland

December 2024 to March 2025

Identifier	
Name of panel member	
Organisational affiliation	

Data protection

The Food Safety Authority of Ireland (FSAI) will handle the contents of this questionnaire with all due care. In this survey, personal data will be processed (for example, name, personal data used to evaluate performance, etc.). This information will be held securely and will only be accessible to authorised staff members. It will be held until such time as the purpose for its collection is complete and it will be securely destroyed after this point.

By providing this information to the FSAI, you are giving your consent for us to use it for the stated purpose. If you change your mind, however, and would later like to withdraw consent, you may contact the FSAI's Data Protection Officer (DPO) at [REDACTED] to make this request. If you have any questions about this statement or about data protection generally at the FSAI, please feel free to contact the FSAI's DPO at [REDACTED].

Thank you.

Point of contact

If you have any questions in completing the questionnaire, please contact:

Name: Lisa O'Connor

Email: [REDACTED]

Phone: [REDACTED]

This document includes the following components:

Expert elicitation preparation material:

- Briefing document
- Worked example.

Expert elicitation questionnaire:

- **A.** Self-assessment of expertise for each individual microbial hazard
- **B.** Expert elicitation questionnaire for each individual microbial hazard.

BRIEFING DOCUMENT

Background

The aim of this expert elicitation is to obtain estimates, with associated uncertainties, of the proportion of incidence caused by the following microorganisms due to foodborne transmission:

- *Campylobacter* species (spp.)
- *Listeria monocytogenes* (*L. monocytogenes*)
- *Salmonella* species (spp.)
- Shiga toxin-producing *Escherichia coli* (STEC)/verotoxigenic *Escherichia coli*
- Hepatitis A virus
- Hepatitis E virus
- Norovirus.

Please note that the disease incidence for each of these diseases has been modelled with a factor to account for the potential underestimation associated with their surveillance. These estimates will facilitate a risk ranking of microbiological hazards from foodborne sources in Ireland. The outcomes will assist the prioritisation of work for the FSAI. In addition, this will allow the FSAI to identify data gaps that, if filled, would enable a risk ranking with reduced uncertainty in the future.

What are we requesting you to do?

We are requesting that you participate in an expert elicitation, conducted using a two-round Delphi method, which involves the activities outlined below.

Round one: Electronic completion of questionnaire

During the first round, you will complete the following tasks electronically.

- Review the initial briefing document and worked example.
- Complete the electronic self-assessment of expertise, which is used for weighting purposes.
- Complete the electronic questionnaire to attribute plausible transmission estimates for each disease. Refer to [Table 53](#) for definitions of all transmission routes.

Round two: In-person meeting at the FSAI and review of round one estimates

During the second round, you will take part in the following in-person activities at the FSAI.

- Complete the paper-based calibration questionnaire, which is used for weighting purposes.
- Participate in the expert-facilitated face-to-face group discussion on the preliminary estimates.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Table 53** Definitions of the transmission routes for microorganisms

Transmission route	Definition
Food	Transmission through food that is contaminated at source (e.g. from irrigation; faeces of food animals) or during processing and preparation. Preparation might occur in any location, including abattoirs, food processing lines, kitchens, outdoor venues (domestic and commercial), etc. Food transmission includes contamination by food handlers and infections in people who have handled contaminated foods. Bottled water is also included in the category of food.
Water	Transmission through contaminated drinking water from any distribution system (including public and private supplies). This excludes accidental ingestion of recreational water (e.g. while swimming) and consumption of bottled water.
Environmental	Transmission through environmental matrices (soil, recreational water, etc.).
Animal contact	Transmission by direct contact with animals (farm animals, pets, animals at petting zoos, at livestock processing plants, etc.).
Human-to-human	Direct or indirect transmission from one infected person to another person (contaminated fomites, air, etc.).

Source: Adapted from Cressey *et al.* (2019)

WORKED EXAMPLE

A. Self-assessment of expertise in relation to selected microorganisms

For each microorganism listed below, what level of expertise would you describe yourself as having with respect to the microorganism/disease associated with foodborne transmission?

For each microorganism listed below, please indicate your opinion of your level of expertise by selecting a score from one of the five defined scale point descriptors to the right of the microorganism's name. The scale ranges from 1 (least expertise) to 5 (most expertise). Participants are offered the opportunity to refrain from answering questions on specific microorganisms if they feel that their level of expertise is negligible (descriptor level 0).

Please note that this worked example does not relate to any specific microorganism(s).

Descriptors for expertise levels:

0 = insufficient expertise on microorganism to provide any opinion (opting out)

1 = low expertise: no direct experience, anecdotal knowledge only

2 = low-medium expertise: intermediate experience between levels 1 and 3

3 = medium expertise: some direct experience, wide reading

4 = medium-high expertise: intermediate expertise between levels 3 and 5

5 = high expertise: primary focus of professional work

Indicate your level of expertise by placing a value beside each microorganism that you feel most accurately reflects your level of expertise:

Microorganism	Expertise
Microorganism A	4
Microorganism B	3
Microorganism C	0 (i.e. the participant has indicated that they have insufficient expertise with regard to microorganism C and therefore will opt out of providing responses for this hazard)

B. Expert elicitation questionnaire in relation to selected microorganisms

Microorganism A

There are many species of microorganism A, but the evidence in Ireland suggests that two species (serotypes A1 and A2) are of major significance to public health. Other species have occasionally been reported as causing human illness, but their significance in Ireland is unknown/limited, as different isolation methods are required.

i. Estimated ranking of all transmission routes

Using the definitions on transmission routes in the briefing document ([Table 53](#)) please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	4=
Environment	2
Food	1
Human-to-human	4=
Water	5

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by **microorganism A** occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	55
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	38
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	75

Risk Ranking of Microbiological Hazards in Food (2015–2019)

How confident are you (**0–100%**) that the interval you have defined (minimum–maximum) will contain the true value?

90%



Údarás Sábháilteachta Bia NA hÉIREANN
Food Safety AUTHORITY OF IRELAND

**Expert elicitation questionnaire:
Foodborne attribution of selected microbiological hazards in
Ireland**

December 2024 to March 2025

A. Self-assessment of expertise in relation to selected microorganisms

For each microorganism listed below, what level of expertise would you describe yourself as having with respect to the microorganism/disease associated with foodborne transmission?

For each microorganism listed below, please indicate your opinion of your level of expertise by selecting a score from one of the five defined scale point descriptors to the right of the microorganism's name. The scale ranges from 1 (least expertise) to 5 (most expertise). Participants are offered the opportunity to refrain from answering questions on specific microorganisms if they feel that their level of expertise is negligible (descriptor level 0).

Descriptors for expertise levels:

0 = insufficient expertise on microorganism to provide any opinion (opting out)

1 = low expertise: no direct experience, anecdotal knowledge only

2 = low-medium expertise: intermediate experience between levels 1 and 3

3 = medium expertise: some direct experience, wide reading

4 = medium-high expertise: intermediate expertise between levels 3 and 5

5 = high expertise: primary focus of professional work

Indicate your level of expertise by placing a value beside each microorganism that you feel most accurately reflects your level of expertise:

Microorganism	Expertise
<i>Campylobacter</i> spp.	
<i>L. monocytogenes</i>	
<i>Salmonella</i> spp.	
STEC	
Hepatitis A virus	
Hepatitis E virus	
Norovirus	

B. Expert elicitation questionnaire in relation to selected microorganisms

Campylobacter spp.

There are many species of *Campylobacter*, but the evidence in Ireland suggests that two species (*Campylobacter jejuni* and *Campylobacter coli*) are of major significance to public health. Other species, such as *Campylobacter upsaliensis*, *Campylobacter fetus*, *Campylobacter hyointestinalis* and *Campylobacter lari*, have occasionally been reported as causing human illness, but their significance in Ireland is unknown/limited, as different isolation methods are required for these organisms. All *Campylobacter* species should be considered in your estimates.

i. Estimated ranking of all transmission routes

Using the definitions on transmission routes in the briefing document ([Table 53](#)), please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	
Environment	
Food	
Human-to-human	
Water	

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by *Campylobacter* spp. occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	

Risk Ranking of Microbiological Hazards in Food (2015–2019)

How confident are you (0–100%) that the interval you have defined (minimum–maximum) will contain the true value?

Listeria monocytogenes

L. monocytogenes is the most important *Listeria* species with respect to human health. Two forms of disease caused by this microorganism are now recognised: a serious invasive disease and a non-invasive gastroenteritis. While the invasive form of the disease is uncommon, the clinical consequences are often serious. Only *L. monocytogenes* (and both forms of disease) should be considered in your estimates.

i. Estimated ranking of all transmission routes

Using the definitions on transmission routes in the briefing document ([Table 53](#)), please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	
Environment	
Food	
Human-to-human	
Water	

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by *L. monocytogenes* occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	
How confident are you (0–100%) that the interval you have defined (minimum–maximum) will contain the true value?	

Risk Ranking of Microbiological Hazards in Food (2015–2019)**Salmonella spp.**

This group of bacteria is composed of two species: *Salmonella enterica*, which is divided into six subspecies (*enterica*, *salamae*, *arizonae*, *diarizonae*, *houtenae* and *indica*), and *Salmonella bongori*. Most pathogenic isolates from humans belong to subspecies I: *Salmonella enterica* subspecies *enterica*. Only serotypes of *Salmonella enterica* subspecies *enterica* should be considered in your estimates (excluding *Salmonella* Typhi, *Salmonella* Paratyphi and *Salmonella choleraesuis*).

i. Estimated ranking of all transmission routes

Using the definitions on transmission routes in the briefing document ([Table 53](#)), please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	
Environment	
Food	
Human-to-human	
Water	

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by *Salmonella* spp. occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	
How confident are you (0–100%) that the interval you have defined (minimum–maximum) will contain the true value?	

Risk Ranking of Microbiological Hazards in Food (2015–2019)**STEC**

STEC, also known as verotoxigenic *Escherichia coli* (VTEC), is defined by the presence of one or both Shiga toxin genes: Stx1 and Stx2. While the most commonly reported STEC serogroups in Ireland are O157 and O26, all STEC serogroups should be considered in your estimates.

i. Estimated ranking of all transmission routes

Using the definitions on transmission routes in the briefing document ([Table 53](#)), please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	
Environment	
Food	
Human-to-human	
Water	

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by **STEC** occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	
How confident are you (0–100%) that the interval you have defined (minimum–maximum) will contain the true value?	

Norovirus

Norovirus causes gastrointestinal illness in humans. They belong to a group of viruses called caliciviruses. The surveillance of norovirus in Ireland includes data captured both from the

Risk Ranking of Microbiological Hazards in Food (2015–2019)

community setting (e.g. primary care facilities) and the healthcare setting (e.g. hospitals and long-term care facilities). Please consider both symptomatic and asymptomatic disease in your estimates.

i. Estimated ranking of all transmission routes

Using the definitions on transmission routes in the briefing document ([Table 53](#)), please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	
Environment	
Food	
Human-to-human	
Water	

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by **norovirus** occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	
How confident are you (0–100%) that the interval you have defined (minimum–maximum) will contain the true value?	

Hepatitis A virus

Hepatitis A infection is an acute disease of the liver caused by the hepatitis A virus (HAV). HAV occurs sporadically and in epidemics worldwide, with a tendency for cyclic recurrences. Please consider both symptomatic and asymptomatic disease in your estimates.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**i. Estimated ranking of all transmission routes**

Using the definitions on transmission routes in the briefing document ([Table 53](#)), please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	
Environment	
Food	
Human-to-human	
Water	

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by **HAV** occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	
How confident are you (0–100%) that the interval you have defined (minimum–maximum) will contain the true value?	

Hepatitis E virus

Hepatitis E infection is a disease of the liver caused by hepatitis E virus (HEV). Asymptomatic infections are often captured through the Irish Blood Transfusion Service. Please consider both symptomatic and asymptomatic disease in your estimates.

Risk Ranking of Microbiological Hazards in Food (2015–2019)**i. Estimated ranking of all transmission routes**

Using the definitions on transmission routes in the briefing document ([Table 53](#)), please rank the transmission routes with respect to their contribution to 100 cases (5 = the most cases, 1 = the fewest cases). If you believe that two transmission routes contribute equally to the disease burden, place the same ranking number and a '=' symbol next to those two transmission routes. For example, if you believe that two routes equally account for the second-highest number of cases, then your rankings will be 5, 4=, 4=, 2 and 1.

Transmission route for human infection	Ranking (1–5)
Animal contact	
Environment	
Food	
Human-to-human	
Water	

ii. Estimated proportion attributable to foodborne transmission

For **100** cases of disease due to infection by **HEV** occurring during the years 2015–2019 (excluding travel-related cases):

Question	Response
What do you think is the most likely number of cases that may be due to foodborne transmission (most likely)?	
What do you think is the lowest number of cases that may be due to foodborne transmission (minimum)?	
What do you think is the highest number of cases that may be due to foodborne transmission (maximum)?	
How confident are you (0–100%) that the interval you have defined (minimum–maximum) will contain the true value?	

References

Cressey PJ, Lake RJ, Thornley C and Campbell D (2019) Expert elicitation for estimation of the proportion foodborne for selected microbiological pathogens in New Zealand. *Foodborne Pathogens and Disease*, 16(8): 543–549.

Appendix 12 Performance-based calibration exercise



Údarás Sábháilteachta Bia NA hÉIREANN
Food Safety AUTHORITY OF IRELAND

Expert elicitation performance-based calibration exercise

March 2025

Questionnaire identifier	
Name of panel member	
Organisational affiliation	

Data protection

The Food Safety Authority of Ireland (FSAI) will handle the contents of this questionnaire with all due care. In this survey, personal data will be processed (for example, name, personal data used to evaluate performance, etc.). This information will be held securely and will only be accessible to authorised staff members. It will be held until such time as the purpose for its collection is complete and it will be securely destroyed after this point.

By providing this information to the FSAI, you are giving your consent for us to use it for the stated purpose. If you change your mind, however, and would later like to withdraw consent, you may contact the FSAI's Data Protection Officer (DPO) at [REDACTED] to make this request. If you have any questions about this statement or about data protection generally at the FSAI, please feel free to contact the FSAI's DPO at [REDACTED].

Thank you.

Background

In order to explore a variety of means of analysing the outcomes of the expert elicitation, this study will assess how participant weighting approaches may impact on the resulting food attribution estimates.

The three weighting methods being employed are:

- 1. Self-assessed weightings:** Experts assign weight to their estimates based on their own expertise and confidence.
- 2. Equal weightings:** All estimates from experts are treated with equal importance.
- 3. Calibration weightings:** Expert weightings are adjusted based on the accuracy of answering a calibration questionnaire.

A participant's performance on the expert elicitation questions (i.e. the variables of interest) can be evaluated based on how well they performed on a set of calibration questions, termed 'seed' variables. This is based on the classical paradigm of a structured expert elicitation according to Cooke and Goossens (2000), which was carried out by Cressey *et al.* (2019) for a source attribution study in New Zealand.

The calibration questions presented in this questionnaire are used in order to assess relevant knowledge on the source attribution for diseases in Ireland. The estimates obtained from experts for the variables of interest will be calibrated by using the experts' performance for these 'seed' variables.

The experts' performance will be partially determined by accurate parameter estimates (calibration) and the confidence inferred from the lowest and highest estimate intervals (information).

Please note that the FSAI does not view your result as a personal reflection of expertise, and your results will be anonymised.

What are we asking you to do?

Please provide your best estimate (i.e. most likely answer), as well as the minimum and maximum values you would consider plausible, in response to the set of calibration questions presented in this questionnaire.

Risk Ranking of Microbiological Hazards in Food (2015–2019)

1. In 2022, what percentage of the norovirus cases notified in Ireland (n=990) were linked to outbreaks?

Question	Estimate (%)
Most likely	
Maximum	
Minimum	

2. In a survey of the general population conducted over a 12-month period during 2000 and 2001, what do you think was the percentage of respondents (n=9,903) who reported having experienced diarrhoea in the 4 weeks prior to their interview?

Question	Estimate (%)
Most likely	
Maximum	
Minimum	

3. From environmental testing of the 380 Private Group Schemes* supplied in Ireland in 2022, what percentage of schemes do you think were found to have *Escherichia coli* contamination?

* Private Group Schemes (set up by community groups) source, treat and distribute drinking water to their scheme members. There are around 380 Private Group Schemes serving almost 200,000 people in Ireland.

Question	Estimate (%)
Most likely	
Maximum	
Minimum	

Risk Ranking of Microbiological Hazards in Food (2015–2019)

4. In 2019, a consumer behaviour survey evaluated the practices of Irish consumers with regard to frozen breaded chicken. What percentage of respondents do you think stated that they always follow cooking instructions for frozen breaded chicken?

Question	Estimate (%)
Most likely	
Maximum	
Minimum	

5. In 2022, the FSAI national microbiological survey assessed the prevalence of *Salmonella* species in non-ready-to-eat coated (e.g. breaded or battered) chicken products (n=382). What percentage of samples do you think tested positive for *Salmonella* species?

Question	Estimate (%)
Most likely	
Maximum	
Minimum	

References

- Cooke RM and Goossens LHJ (2000) Procedures guide for structural expert judgement in accident consequence modelling. *Radiation Protection Dosimetry*, 90(3): 303–309.
- Cressey PJ, Lake RJ, Thornley C and Campbell D (2019a) Expert elicitation for estimation of the proportion foodborne for selected microbiological pathogens in New Zealand. *Foodborne Pathogens and Disease*, 16(8): 543–549.

Appendix 13 Expert elicitation estimates

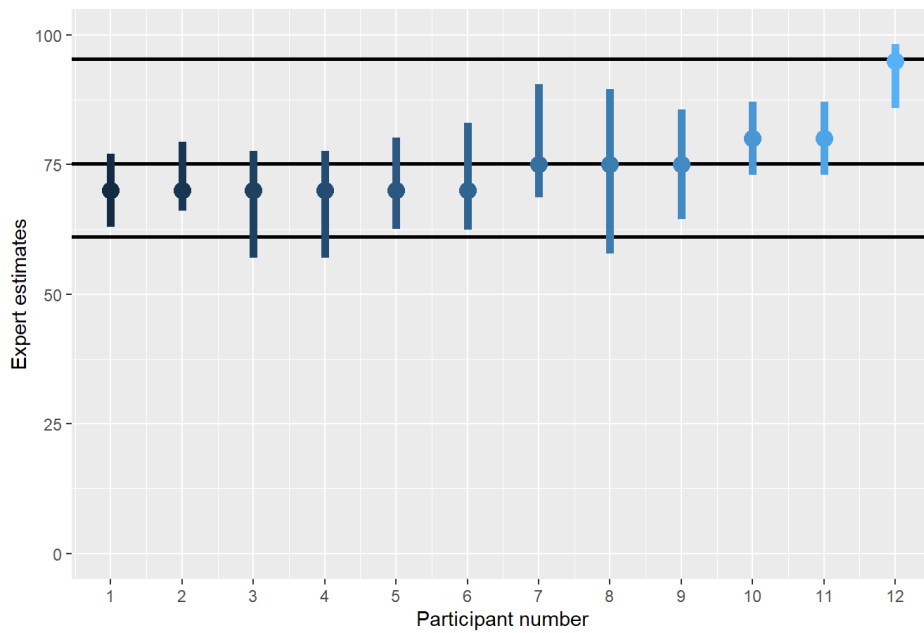


Figure 13 Individual and aggregate expert estimates with 95% uncertainty intervals for attributing campylobacteriosis cases to the food pathway

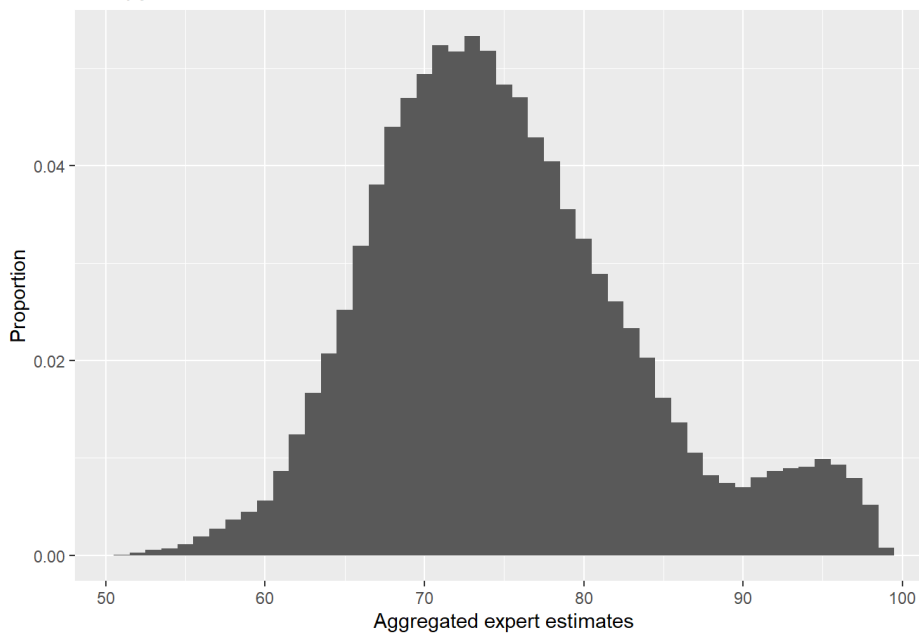


Figure 14 Combined distribution of expert estimates regarding the attribution of campylobacteriosis cases to the food pathway (n=100,000 iterations)

Risk Ranking of Microbiological Hazards in Food (2015–2019)

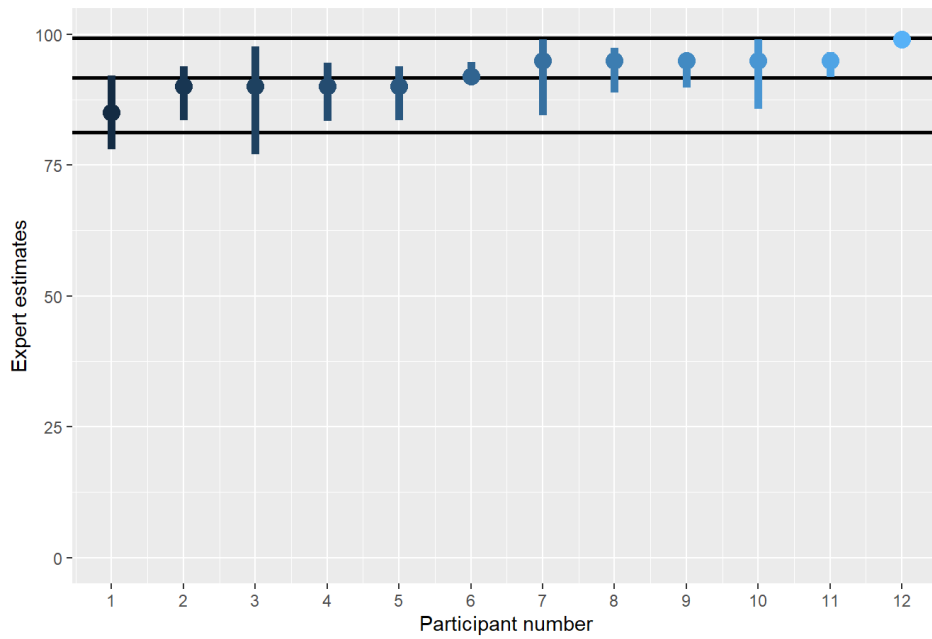


Figure 15 Individual and aggregate expert estimates with 95% uncertainty intervals for attributing listeriosis cases to the food pathway

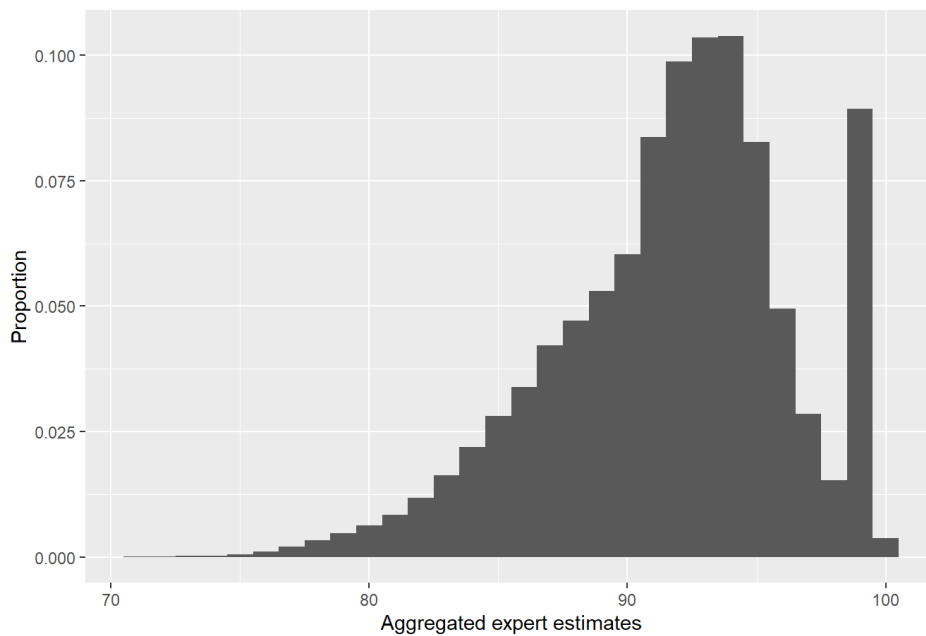


Figure 16 Combined distribution of expert estimates regarding the attribution of listeriosis cases to the food pathway (n=100,000 iterations)

Risk Ranking of Microbiological Hazards in Food (2015–2019)

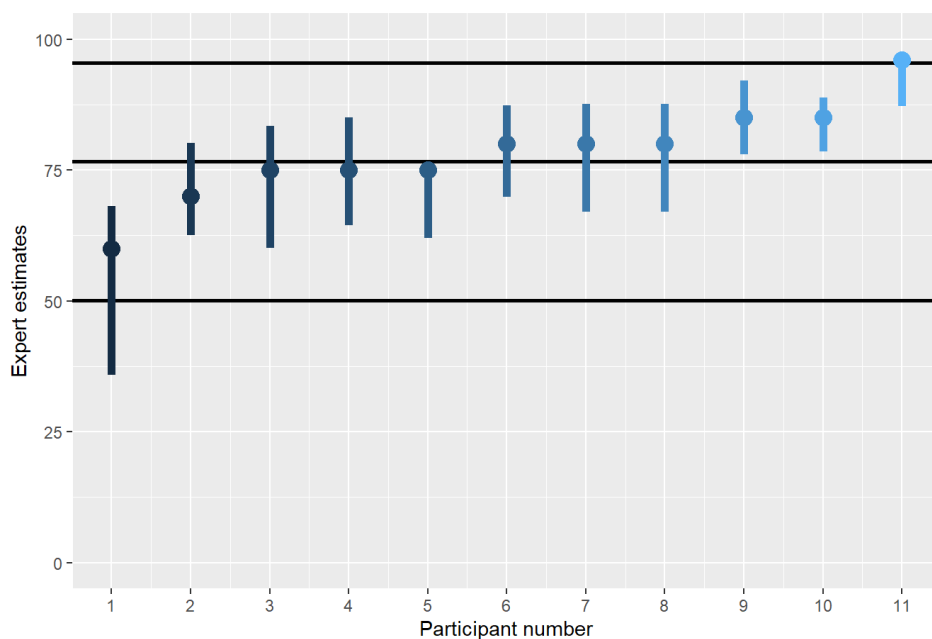


Figure 17 Individual and aggregate expert estimates with 95% uncertainty intervals for attributing salmonellosis cases to the food pathway

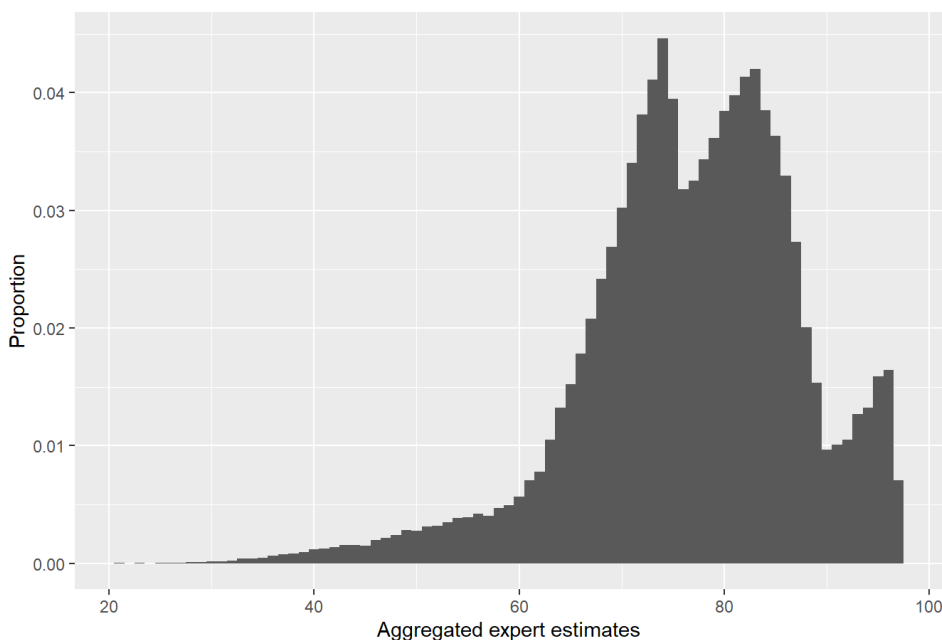


Figure 18 Combined distribution of expert estimates regarding the attribution of salmonellosis cases to the food pathway (n=100,000 iterations)

Risk Ranking of Microbiological Hazards in Food (2015–2019)

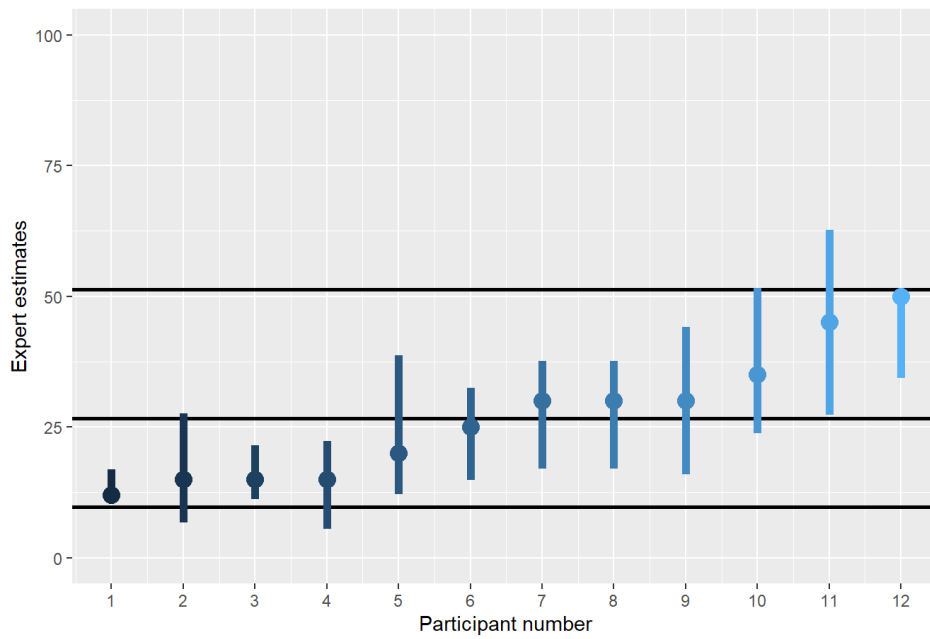


Figure 19 Individual and aggregate expert estimates with 95% uncertainty intervals for attributing Shiga toxin-producing *Escherichia coli* infection cases to the food pathway

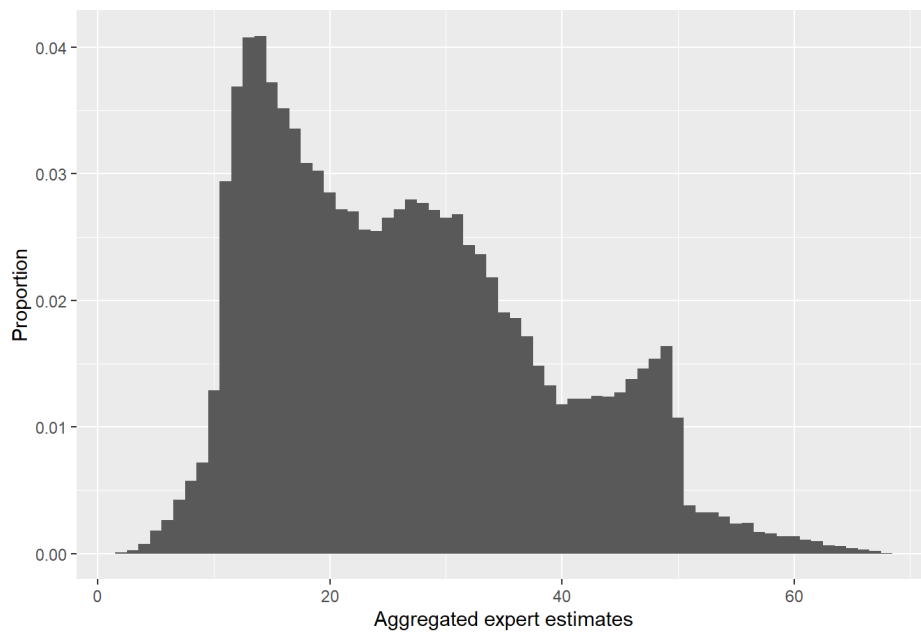


Figure 20 Combined distribution of expert estimates regarding the attribution of Shiga toxin-producing *Escherichia coli* infection cases to the food pathway (n=100,000 iterations)

Risk Ranking of Microbiological Hazards in Food (2015–2019)

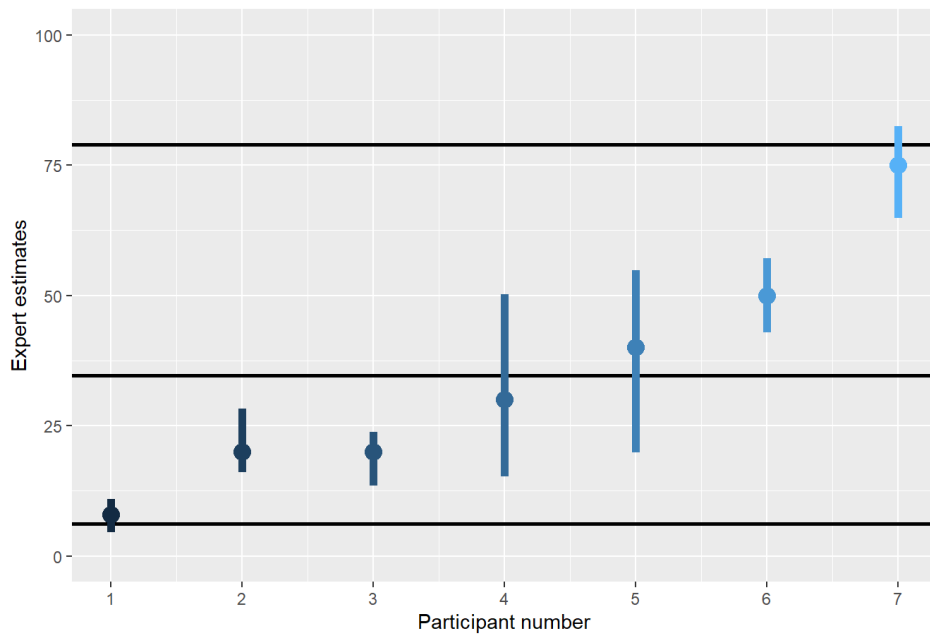


Figure 21 Individual and aggregate expert estimates with 95% uncertainty intervals for attributing hepatitis A cases to the food pathway

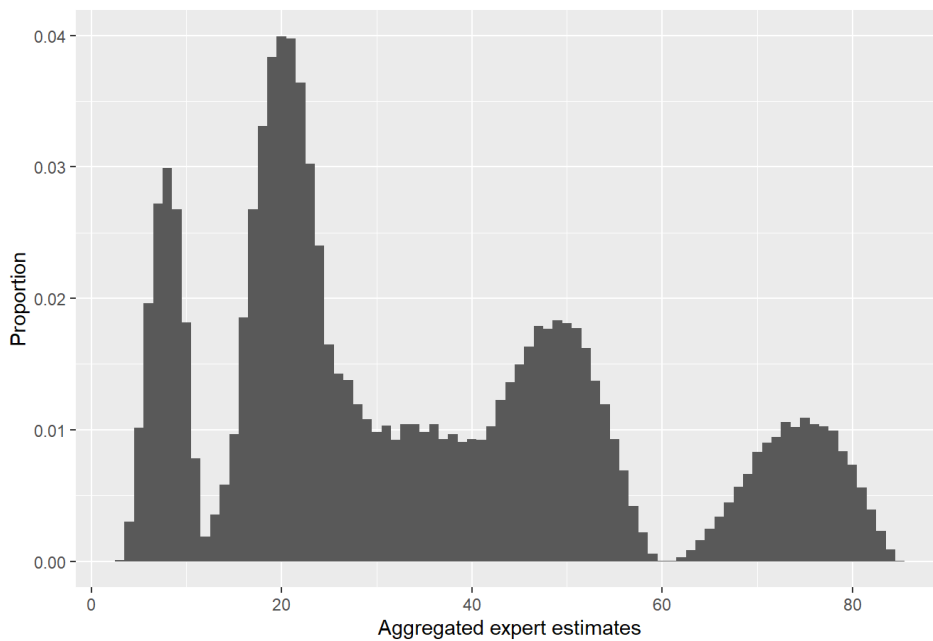


Figure 22 Combined distribution of expert estimates regarding the attribution of hepatitis A cases to the food pathway (n=100,000 iterations)

Risk Ranking of Microbiological Hazards in Food (2015–2019)

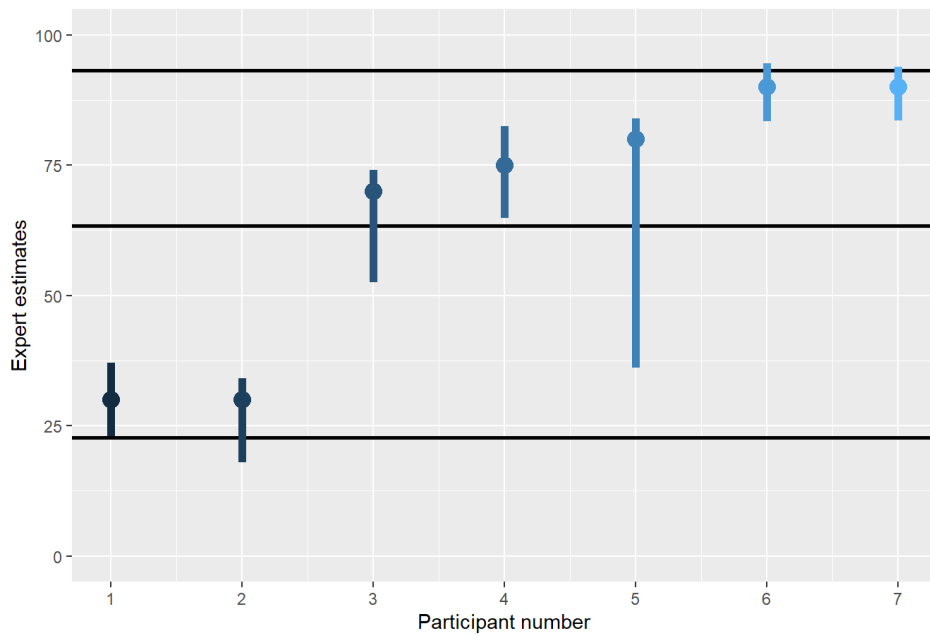


Figure 23 Individual and aggregate expert estimates with 95% uncertainty intervals for attributing hepatitis E cases to the food pathway

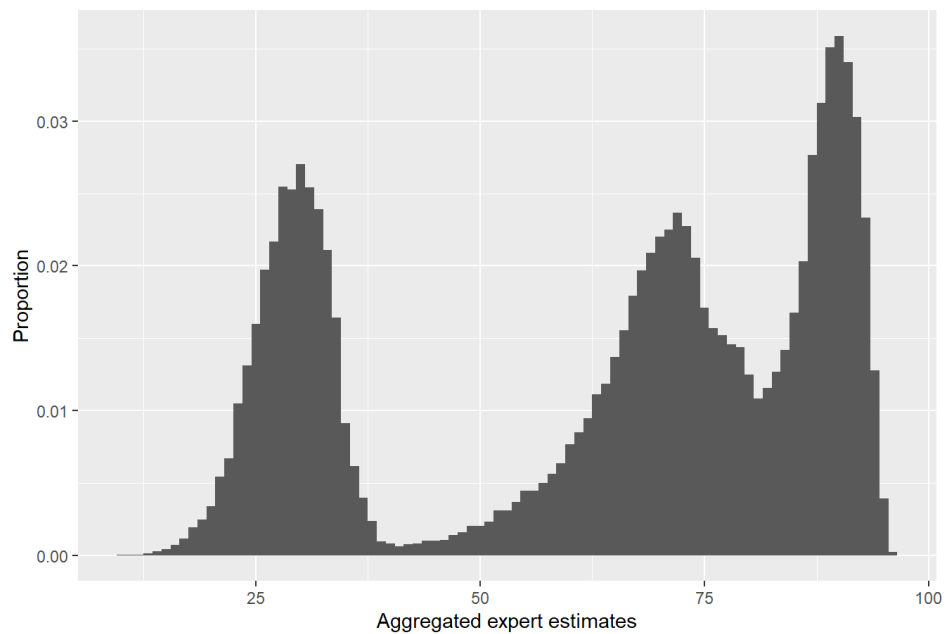


Figure 24 Combined distribution of expert estimates regarding the attribution of hepatitis E cases to the food pathway (n=100,000 iterations)

Risk Ranking of Microbiological Hazards in Food (2015–2019)

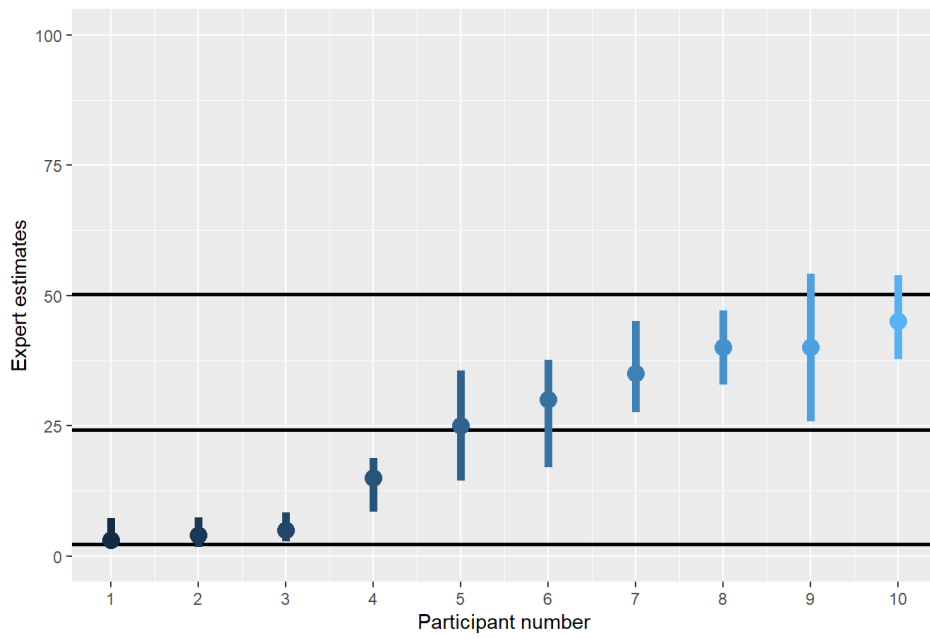


Figure 25 Individual and aggregate expert estimates with 95% uncertainty intervals for attributing norovirus infection cases to the food pathway

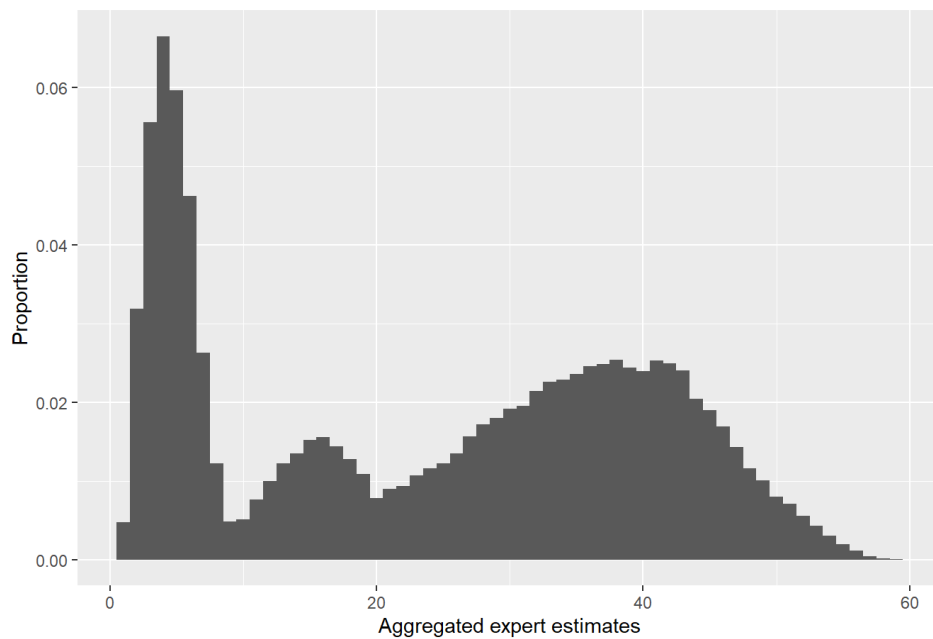


Figure 26 Combined distribution of expert estimates regarding the attribution of norovirus infection cases to the food pathway (n=100,000 iterations)

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