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A comprehensive review of foodborne disease burden associated with protein foods: a 13-year evaluation of incidence and outbreaks in high-income countries

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Abstract

This investigation focused on the compilation and analysis of the incidence of foodborne diseases and foodborne outbreaks related to protein-based foods, published in official surveillance reports from the European Union (EU), United States of America (USA), Canada, and New Zealand (NZ), in the period of 2010-2023, for foodborne pathogens norovirus, *Campylobacter* spp., *Cryptosporidium* spp., *Listeria monocytogenes*, *Salmonella enterica* (non-typhoidal, typhoid, and paratyphoid) and Shiga-toxin-producing *Escherichia coli* (STEC).

Most outbreaks reported during this period were caused by non-typhoidal *Salmonella*, norovirus, and *Campylobacter* spp., predominantly in European Member States (MS), followed by the USA. This compilation analysis evidenced the heterogeneity between regions/countries in the contribution of protein foods to total strong evidence outbreaks that occurred in the studied period. For instance, whereas in the USA, "cheese" was the most frequent source of listeriosis (52.6%), in EU-MS, "meat" was the topmost contributor (43.1%). In EU-MS, norovirus outbreaks were mainly associated with "crustaceans and mollusks" (80.9%); "eggs" accounted for most salmonellosis (52.1%) outbreaks, followed by "meat" (27.1%), the latter of which was also the largest contributor to campylobacteriosis (66.9%) and STEC outbreaks (52.7%). Strong-evidence cryptosporidiosis outbreaks in EU-MS were attributed to "cheese," while in NZ and the USA, they were all linked to "milk." In the USA and NZ, salmonellosis was frequently associated with "meat" (44.3-46.9%); campylobacteriosis, with "milk" (44.9-45.2%); and norovirus outbreaks were attributed to "crustaceans and mollusks" (21.2-29%), "dough-based derivatives" (9.7-26.7%), and composite meals, *i.e.*, "meat-based meals" (16.3-32.3%) and "seafood-based meals" (12.9-14.1%). STEC was often linked to "milk" in NZ (62.5%) and to "meat" in the USA (54.1%).

Introduction

According to the World Health Organization (WHO), foodborne diseases (FBDs) are illnesses that result from the consumption of food contaminated with bacteria, viruses, parasites or even chemical substances, which may occur at any stage along the food supply chain (WHO, 2025). The WHO estimates indicate that every year, 600 million people - 1 in 10, worldwide - get sick after consuming unsafe foods, resulting in 420,000 deaths globally and 33 million healthy life years lost (WHO, 2015). Protein-based foods, particularly those derived from animal sources such as meat, eggs, dairy, or seafood, are frequently implicated in foodborne outbreaks (FBOs). This is primarily due to their high nutrient and moisture content, which creates ideal environments for bacterial growth. These foods are therefore more susceptible to pathogenic bacteria, and their improper processing and handling, as well as poor personal hygiene among food operators, are known key contributors to the emergence of new outbreaks (Ray and Bhunia, 2013; Augustin *et al*., 2020;).

Given the socioeconomic burden of FBDs and FBOs, gathering robust, precise data on their impact is vital to inform policymakers and allocate the necessary resources for food safety control and intervention strategies. This is even more crucial in high-income countries, where FBD surveillance reporting systems are well established (WHO, 2015). The WHO, alongside agencies such as the European Food Safety Authority (EFSA) and European Centre for Disease Prevention and Control (ECDC) in Europe, or the Centers for Disease Control and Prevention (CDC) in the USA, play critical roles in systematically gathering, analysing and reporting these data, so that legislators can effect real policy change (CDC, 2024a; EFSA and ECDC, 2012; WHO, 2015).

The aim of this work was to review the incidence of FBDs and FBOs associated with protein-based food products. The analysis covered data published in official surveillance reports from the European Union (EU), the United States of America (USA), Canada and New Zealand for the period of 2010-2023. The study focused on foodborne pathogens Norovirus (NoV), *Campylobacter* spp., *Cryptosporidium* spp., *Listeria monocytogenes*, *Salmonella enterica* (non-typhoidal, typhoid and paratyphoid), and Shiga-toxin-producing *Escherichia coli* (STEC).

Methods

Data sources and data collection

Data on annual incidences (or notification rates) of FBDs, FBOs (strong evidence, weak evidence and/or total) and sources of outbreaks were searched for the following bacteria/parasites/viruses: *Ascaris* spp., *Brucella* spp., *Campylobacter* spp., *Cryptosporidium* spp., *Echinococcus granulosus* and *Echinococcus multilocularis*, *Entamoeba histolytica*, *Giardia* spp., *Listeria monocytogenes*, NoV (or Calicivirus), *Salmonella enterica* (non-typhoidal, typhoid and paratyphoid), STEC, and *Toxoplasma gondii*.

The literature search was conducted between September and October 2024, and limited to publicly available, official surveillance data from Canada (Public Health Agency of Canada, 2024a), New Zealand (Armstrong *et al*., 2024; Horn *et al*., 2014, 2015, 2021, 2023; Lim *et al*., 2010, 2012; Lopez *et al*., 2013, 2016; Pattis *et al*., 2017, 2019a, 2019b, 2020, 2022), USA (Adams *et al*., 2012, 2013, 2014, 2015, 2016, 2017; CDC, 2024a, 2024b, 2024c) and the EU (ECDC, 2016a, 2016b, 2016c, 2017a, 2017b, 2017c, 2018a, 2018b, 2018c, 2018d, 2018e, 2018f, 2018g, 2018h, 2019a, 2019b, 2019c, 2019d, 2020a, 2020b, 2021a, 2021b, 2022a, 2022b, 2022c, 2022d, 2023a, 2023b, 2023c, 2024a, 2024b, 2024c, 2024d, 2024e, 2024f, 2024g, 2024h; EFSA and ECDC, 2012, 2013, 2014, 2015a, 2015b, 2016, 2017, 2018, 2019, 2021a, 2021b, 2022, 2023) (Table 1). EU data also included information from European countries which are non-Member States (non-MS), specifically Albania, Bosnia and Herzegovina, Iceland, Liechtenstein, Montenegro, Norway, North Macedonia, Serbia, Switzerland, and the United Kingdom. Whenever possible, FDB data were collected on a country basis, from the year 2010 onward.

During the search and compilation of the FBD data, several issues were detected:

1. Inconsistencies in *Salmonella* spp. FBD data reporting:

a. The EU and New Zealand report “non-typhoidal *Salmonella*” and “typhoid and paratyphoid *Salmonella*” data separately;

b. The USA reported “non-typhoidal *Salmonella* and paratyphoid” data until the year 2017, but started reporting “paratyphoid *Salmonella*” separate from “non-typhoidal *Salmonella*” from 2018 onwards;

c. Canada jointly reports “non-typhoidal *Salmonella* and paratyphoid” data for all years;

d. The USA and Canada report “typhoid *Salmonella*” throughout all relevant years.

2. No data was encountered for *Entamoeba histolytica* in the reports of the EU, the USA, Canada or New Zealand;

3. No data was encountered for *Toxoplasma gondii* in reports of the USA, Canada or New Zealand;

4. No total confirmed cases or notification rates for Calicivirus, including NoV, are provided in the reports of the EU, the USA, or New Zealand. These reports present only outbreak data.

5. The EU only started reporting the total number of outbreaks for Calicivirus, including NoV from 2015 onwards;

6. In the USA, campylobacteriosis became a Nationally Notifiable Disease only in 2015, hence there are no official published records of total number of cases or incidence rates before that year;

7. No national outbreak data (number of outbreaks or food vehicles associated) was found for any of the listed pathogens in the publicly available surveillance records of Canada;

8. In the publicly available surveillance reports of New Zealand, there are no data regarding *Brucella* spp., and data on typhoid and paratyphoid *Salmonella* are only available for numbers of outbreaks.

All these discrepancies in data reporting between countries/regions prevented a neat integration of the datasets.

Classification of food vehicles

Sixteen subcategories/classes of protein foods were considered - “milk”, “cheese”, “non-specific dairy”, “dairy desserts”, “cereal grains”, “legumes”, “dough-based derivatives”, “eggs”, “meat”, “preserved meats”, “offal”, “meat-based meals”, “fish”, “preserved fish”, “crustaceans and molluscs”, and “seafood-based meals” – in a classification based on the current EFSA’s FoodEx2 and the Pathogen-In-Food Database’s standardized food classification and description systems (EFSA, 2015; Gonzales-Barron *et al*., 2025). In cases where an ingredient from a composite dish was clearly identified as the source of the outbreak, then the outbreak was attributed to the category that ingredient belonged to. If a composite dish was associated to an outbreak and the causative ingredient not clearly identified, but a meat or seafood element was the main protein source (ex.: beef stew or pulled pork sandwich *vs*. sushi or tuna sandwich) the food vehicle was attributed to the category “meat-based meals” or “seafood-based meals”, respectively. When a food vehicle had multiple protein-based food ingredients and the element responsible for the outbreak could not be clearly identified, the outbreak was attributed to none of the categories considered.

Data compilation and statistical analysis

The datasets were extracted from all reports and supplementary files and built into a single Excel® file which included information on pathogen, country, year, total number of confirmed cases, incidence rate per 100,000, number of outbreaks (total, as well as strong and weak-evidence, when available), and distribution of outbreaks by food source according to the categories described before.

Based on the completeness of data regarding annual incidence, number of outbreaks and implicated food sources, six of the originally contemplated pathogens were selected for analysis: Calicivirus (including NoV), *Campylobacter* spp., *Cryptosporidium* spp., *L. monocytogenes*, non-typhoidal *Salmonella* and STEC.

Three types of compilation analysis were carried out on the FBD data:

(i) Incidence/notification rates and total outbreaks along the years by pathogen along the studied period. This information is displayed as graphs.

(ii) Contribution of protein foods to the total strong evidence outbreaks by pathogen. Considering the total number of known strong evidence outbreaks occurring in the 13-year period, the share (%) of each defined protein food category was calculated for every country/region. Results are presented as pie charts by FBD.

(iii) Percentual share of the six pathogens as causative agents of the total outbreaks occurred in the 13-year period by protein food category. Taking into account the total number of outbreaks in all the studied countries/regions having the given food category as likely source, the share (%) of each available pathogen was calculated. Results are presented as pie charts by food category.

All statistical analysis was carried out using the R software, version 4.4.2 (R Core Team, 2023), implemented with the packages sqldf, ggplot2 and dplyr. Compiled data and R scripts are available upon request.

Results

Annual incidence rates and total outbreaks

Figure 1 and *Supplementary Figures 1-5* illustrate the trends in annual incidence rates (A) and the total number of outbreaks (B), beginning in 2010, caused by Calicivirus including NoV, *Campylobacter* spp., non-typhoidal *Salmonella*, *Cryptosporidium* spp., *L. monocytogenes*, and STEC.

Calicivirus, including Norovirus

In Canada, NoV cases dropped sharply from nearly 30 cases in 100,000 population in 2010 to little over 10 cases per 100,000 population in 2011, remaining stable until a slight increase in 2018 (*Supplementary Figure 1A*). Notification rates fell again in 2019-2020, likely reflecting the effects of the global COVID-19 pandemic hygiene measures and restrictions, before rising in following years. None of the other regions documented incidence rates in their official public reports. As for outbreaks (*Supplementary Figure 1B*), both EU Member States (EU MS) and the USA reported very high numbers (250-350 annually), with an abrupt decline in 2020, and a post-pandemic rebound. Comparatively, New Zealand and EU non-MS reported far fewer outbreaks.

Campylobacter spp.

New Zealand consistently reported the highest rates of campylobacteriosis, ranging from 110 to over 170 cases per 100,000 annually (*Supplementary Figure 2A*). Although rates decreased from 2016 to 2020, they remained much higher than in other regions. EU MS and non-MS showed moderate incidence rates (about 40-70 cases per 100,000). The USA and Canada reported the lowest and most stable rates in the group. All regions experienced rate declines during the COVID-19 period. As for campylobacteriosis outbreaks (*Supplementary Figure 2B*), the EU reported the highest number of all regions, over 300 outbreaks in most years, compared with the 30 outbreaks on average reported by the USA each year. In New Zealand, campylobacteriosis outbreaks have slowly decreased over the last 12 years.

Non-typhoidal Salmonella

Salmonellosis cases were high and quite variable for all regions, although New Zealand exhibited the greatest rates (*Supplementary Figure 3A*). Notably, salmonellosis notification rates also registered a dramatic decline between 2019 and 2020 for all regions, followed by a slow recovery afterwards. Regarding outbreaks, EU-MS recorded the absolute highest number, exceeding 1000 outbreaks per year in most years, followed by the USA with over 100 outbreaks per year (*Supplementary Figure 3B*). Non-MS had generally low outbreaks (below 10 per year) but increased abruptly in 2016, and numbers have remained higher since. New Zealand presented the lowest frequency of salmonellosis outbreaks.

Cryptosporidium spp.

The highest and most volatile notification rates were again reported by New Zealand, spiking over thirty cases per 100,000 people in 2018 and dipping well below 15 per 100,000 in 2022 (*Supplementary Figure 4A*). After 2015, the increase in notification rates can be at least partly explained by changes in diagnostic practices. In June 2015, all fecal samples began being screened by multiplex PCR for a range of pathogens, including *Cryptosporidium* spp., whereas previously, this screening was performed only upon request (Pattis *et al.*, 2017; Pattis *et al.*, 2019a). All other regions reported low and steady rates, generally below five cases per 100,000 people (*Supplementary Figure 4A*). Outbreak-wise, despite some falls, EU-MS showed a growing trend in the number of outbreaks over the last few years. In New Zealand, outbreaks appear to have almost ceased (*Supplementary Figure 4B*).

L. monocytogenes

As illustrated in Figure 1A, listeriosis presented low incidence rates (<1 case per 100,000) across all regions. The USA registered the lowest and most stable rates, while other regions showed great fluctuation. The EU-MS experienced a slight increase in incidence (0.35 cases per 100,000 in 2010 *vs*. 0.6 in 2022), along with New Zealand (0.5 in 2010 *vs*. 0.7 in 2023). EU-MS countries reported the highest number of outbreaks, which rose significantly from 5 to 35 outbreaks between 2016 and 2022 (Figure 1B). The USA had variable outbreak numbers, generally lower than EU-MS. New Zealand and EU non-MS reported almost no outbreaks during this period.

Shiga toxin-producing E. coli

STEC infections in New Zealand showed a sharp increase, especially after 2014, peaking at 22.4 cases per 100,000 population in 2019 (*Supplementary Figure 5A*). This increase was not linked to a surge in the number of infections, but to changes in diagnostic practices, specifically the introduction in 2015 of routine culture-independent diagnostic testing for several enteric pathogens, including STEC, in all fecal samples (Pattis *et al.*, 2020; Wright *et al.*, 2025). Contrarily, the USA and EU-MS countries experienced low and stable incidence rates, but the highest frequency and volatility of STEC outbreaks. New Zealand and EU non-MS recorded very few to no outbreaks in some years (*Supplementary Figure 5B*).

Contribution of protein foods to total strong evidence outbreaks, expressed by region/country

By summing the types of protein foods linked to outbreaks between 2010 and 2022, their percentage contribution to each disease was calculated. Pie charts are represented in Figures 2 and 3 and *Supplementary Figures 6-10*. It should be noted that, as the contribution was calculated exclusively based on the number of total protein foods, it does not represent an absolute value and should instead be interpreted as an indicator of relative importance among the protein-based foods only.

Calicivirus, including norovirus

Protein food-related outbreaks caused by Calicivirus (including NoV) (*Supplementary Figure 6*) in EU-MS (n=509) were overwhelmingly dominated by “crustaceans & mollusks” (80.9%), with other categories contributing minimally, whereas in the USA (n=326), the attribution was split more evenly between “dough-based derivatives” (26.7%), “crustaceans & mollusks” (21.2%), “meat-based meals” (16.3%), and “seafood-based meals” (14.1%). In NZ (N=31), the topmost contributors were similar to those in the USA; “meat-based meals” (32.3%), “crustaceans & mollusks” (29%) and “seafood-based meals” (12.9%) and “dough-based derivatives” (9.7%).

Campylobacter spp.

Strong-evidence campylobacteriosis outbreaks in EU member states (n=281) were attributed primarily to “meat” (66.9%) and “milk” (28.5%). In New Zealand, “milk” alone accounted for 45.2% of the total strong-evidence outbreaks (n=73), followed by meat products, *i.e.*, “preserved meats” (24.7%), “meat” (15.1%), “meat-based meals” (8.2%) and “offal” (5.5%), the four of which together actually represented a higher share of 53.5%. As for the USA (N=216), “milk” represented 44.9% of strong-evidence outbreaks, slightly higher than the four meat-related categories together at 43% (Figure 2A).

Non-typhoidal Salmonella

In EU member states, strong-evidence outbreaks of salmonellosis (n=2473) were attributed predominantly to “eggs” (52.1%), followed by “preserved meats” (27.1%) and “dough-based derivatives” (11.2%) (Figure 2B). In New Zealand (n=32) and the USA (n=490) however, the main contribution to total strong-evidence outbreaks was given by the categories “meat” (44.3-46.9%) and “meat-based meals” (12.5-17.1%), while “eggs” (6.2-7.8%) were a lesser food vehicle along with “legumes” (5.3-6.2%). “Dairy desserts” also contributed to several salmonellosis outbreaks in New Zealand (9.4%).

Cryptosporidium spp.

EU-MS countries reported that their two strong-evidence cryptosporidiosis outbreaks were caused by “cheese”, while in New Zealand and the USA all outbreaks (n=7 and n=12, respectively) were linked to “milk” (*Supplementary Figure 7*).

Listeria monocytogenes

Figure 3 illustrates the protein-food sources for listeriosis outbreaks, which in case of EU-MS countries were quite varied. Almost 95% of all strong-evidence outbreaks (n=58) were caused either by “meat” (43.1%), “fish” (19%), “preserved fish” (10.3%) “cheese” (6.9%), “preserved meats”, “crustaceans and mollusks” or “dough-based derivatives” (5.2% each). In EU Non-MS countries, each one of the three listeriosis outbreaks was attributed to “meat”, “fish” and “preserved fish”. In New Zealand, the two strong-evidence listeriosis outbreaks registered were attributed one to “cheese” and the other to “preserved meat”. As for the USA (n=38), “cheese” was the main vehicle at 52.6%, with “preserved meats” (15.8%) and other dairy (“non-specific dairy” and “dairy desserts” combined, 18.5%) also representing important outbreak sources.

Shiga toxin-producing E. coli

Protein food-related strong-evidence outbreaks caused by STEC (*Supplementary Figure 8*) in EU-MS (n=55) were attributed mainly to "meat" (52.7%), and dairy categories i.e. "cheese" (18.2%), "milk" (16.4%) and "non-specific dairy" (9.1%). Similarly, in the USA (n=111), "meat" was also the largest food vehicle for STEC outbreaks at 54.1%, with "milk" (18%) as the second and "meat-based meals" (8.1%) the third largest contributors. Oppositely, strong-evidence STEC outbreaks in New Zealand (n=8) were caused primarily by "milk" (62.5%), while the remaining 37.5% were caused by "meat-based meals" and "meat".

Proportion of the selected pathogens responsible for strong-evidence outbreaks over the 13-year period

The share estimates illustrated in Figure 4 and *Supplementary Figures 9-20* are highly summarised, as they aggregate the number of strong-evidence outbreaks across 13 years and the contemplated regions/countries. While subject to significant uncertainty (due to the limited number of pathogens analyzed due to lack of reporting, and incomplete global coverage) they offer a useful visual representation of the relative importance of the six pathogens studied in the total outbreaks originated from the 16 distinct protein food sources considered. The share values in the pie charts should not be interpreted as absolute values, given that they were computed for only these six pathogens; furthermore, they always add up to 100%.

In the "milk" category, *Campylobacter* spp. was the main causative agent of strong-evidence FBOs (68% of 309 outbreaks) followed by *Salmonella* spp. and STEC (13.6% and 11%, respectively) (*Supplementary Figure 9*).

In 148 "cheese"-related strong-evidence outbreaks, most of the outbreaks (61.5%, n=91) were linked to *Salmonella* spp. (*Supplementary Figure 10*). Twenty-five outbreaks were caused by *L. monocytogenes*, 13 by STEC and ten and nine outbreaks were attributed to *Campylobacter* spp. and Calicivirus/NoV, respectively.

In both "non-specific dairy" and "dairy desserts" *Salmonella* spp. was the most frequent causal agent (58.1 and 66.7%, respectively) (*Supplementary Figures 11 and 12*). However, in "non-specific dairy", *Campylobacter* and STEC together represented over one quarter of all strong-evidence outbreaks, while in "dairy desserts" a similar share of outbreaks was caused by Calicivirus/NoV and *L. monocytogenes*.

Nineteen strong-evidence outbreaks were linked to "cereal grains", of which 15 were caused by Calicivirus/NoV. Only three outbreaks were attributed to STEC and one to *Salmonella* spp. (*Supplementary Figure 13*).

Fifty-five strong-evidence outbreaks were linked to "Legumes", the majority of which were caused by *Salmonella* spp. (80%, n=44 outbreaks) (*Supplementary Figure 14*). Calicivirus/NoV (12.7%, n=7) and STEC (5.5%, n=3) were the second and third most frequent foodborne pathogens linked to "legumes" FBOs.

As far as "dough-based derivatives" are concerned, 70.8% of 425 outbreaks were caused by *Salmonella* spp. and 27.3% by Calicivirus/NoV (*Supplementary Figure 15*), whereas in the "eggs" category - the protein food with highest outbreak association (n=1345 strong evidence-outbreaks) - a striking 98.7% of outbreaks (n=1328) were attributed to *Salmonella* spp., *vs*. only 15 outbreaks caused by Calicivirus and NoV (*Supplementary Figure 16*).

Of the 1304 "meat"-associated strong-evidence outbreaks (Figure 3A), *Salmonella* spp. was the pathogen responsible for the largest portion of these FBOs (69.1%, n=901), while *Campylobacter* spp. was the second most significant pathogen at 17.6% (n=230 strong-evidence outbreaks). STEC, Calicivirus/NoV, and *L. monocytogenes*, accounted for the remaining outbreaks, in descending order of frequency.

In "meat-based meals", *Salmonella* spp. was the pathogen implicated in the highest number of outbreaks (47.8%), succeeded by Calicivirus/NoV (34.8%), and less expressively by *Campylobacter* spp. and STEC (Figure 3B). Conversely, both in “offal” and “preserved meats”, *Campylobacter* spp. was the most frequent causative agent of FBOs (n=19 and n=51 and outbreaks, respectively) (Figure 3C and D) followed by *Salmonella* spp. (n=3 and n=20 outbreaks), except in “preserved Meats”, *L. monocytogenes*, STEC and Calicivirus and NoV also had a share as causative agents.

The “fish” food category was dominated by *Salmonella*-related outbreaks (51.9% of 81 total outbreaks), followed by Calicivirus/NoV (28.4%) and *L. monocytogenes* (14.8%) (*Supplementary Figure 17*).

Of the 12 strong-evidence outbreaks linked to “preserved fish”, two-thirds were caused by *L. monocytogenes* (n=8 outbreaks), a quarter was associated with *Salmonella* spp. (n=3), and the remaining outbreak was attributed to Calicivirus/NoV (*Supplementary Figure 18*).

“Crustaceans and mollusks”-linked outbreaks (*Supplementary Figure 19*) were overwhelmingly caused by Calicivirus (including NoV), totaling 490 outbreaks out of 545 registered for this study’s period. A smaller fraction of these strong-evidence FBOs s was also attributed to *Salmonella* spp. (n=36) and *Campylobacter* spp. (n=13).

Lastly, in 89 “seafood-based meals”-related strong-evidence outbreaks, NoV was the lead pathogen, implicated in 55 outbreaks (61.8%) (*Supplementary Figure 20*). *Salmonella* spp. was second, causing 31 outbreaks, followed by *Campylobacter* spp. (n=2) and *L. monocytogenes* (n=1).

Discussion

A recurrent trend revealed by this compilation analysis was the decline in the incidence of multiple foodborne illnesses and FBOs s across the globe observed in 2019-2020, one that with very little doubt can be attributed to the widespread public health interventions implemented to prevent SARS-CoV-2 transmission (Ray *et al*., 2021; Love *et al*., 2022). On one hand, travel restrictions, restaurant closures, improved hand hygiene, reduced social contact and increased cleaning of (food and non-food) contact surfaces are known to effectively reduce gastrointestinal infections, particularly those transmitted person-to-person and through environmental contamination. On the other hand, a higher-than-usual proportion of infections may have remained undetected due to changes in healthcare provision, health-seeking behavior or laboratory testing practices (Ray *et al*., 2021; Love *et al*., 2022).

The lack of NoV/Calicivirus incidence rate reporting by countries such as the EU, USA and New Zealand (*Supplementary Figure 1*) is multifactorial; the illness is short-lived and usually mild, and as a result, most infected people do not seek medical care, resulting in unreported cases (Inns *et al*., 2017). On the other hand, there are significant differences in the reporting requirements for NoV within each of these countries: routine reporting of individual cases is not mandatory in any of the three regions (although country-dependant in the EU), but outbreak reporting is required in all three. As for the unusually high incidence rate of NoV in Canada (*Supplementary Figure 1*) verified in 2010, studies have suggested it may be linked to the emergence of novel viral strains (GII.4 New Orleans and GII.12), which spread quickly through the immunologically naive population, leading to unusually high cases, altered seasonality and more outbreaks (Hughes *et al*., 2021). In high-income countries, NoV outbreaks are extremely hard to control, especially in large and densely populated areas, where they occur frequently in long-term care facilities, hospitals, restaurants and catered events, schools and childcare centers. As such, population size and density may be factors for the much greater number of outbreaks seen in the EU and USA (*Supplementary Figure 1*), compared to New Zealand (450 million people in the European Union and 343 million in the USA, *vs.* only 5.2 million in NZ) (Mathieu and Rodés-Guirao, 2022). High-risk foods for NoV infection include shellfish (*e.g*., oysters, mussels), leafy-green vegetables and fruits, but also any food, cooked or during processing, handled by individuals with a pre-existing NoV infection (Carlson *et al*., 2024). This is well reflected in the contribution of protein food to the total strong-evidence outbreaks of NoV, where “crustaceans and mollusks” was the dominant food vehicle in the EU, and a significant source in the USA and NZ alongside categories like “meat-based meals” and “seafood-based meals”, composite foods served in communal dining environments (long-term care facilities, restaurants, catering-settings, schools, *etc*.) by infected food handlers. At food category-level, NoV is also an important outbreak agent in “cereal grains” and “dough-based derivatives”, also likely due to handling by infected food operators in bakeries and other food-serving businesses. In source attribution studies (Greig and Ravel, 2009; Butler *et al*., 2015; Davydova *et al*., 2025), NoV was likewise linked to multi-ingredient-foods, seafood, bakery items, grains and beans, and produce, while a meta-analysis of NoV sporadic cases also verified that consumption of seafood and composite food were risk factors for the transmission of the virus (Thébault *et al*., 2021).

During the analyzed period, campylobacteriosis was the most frequently reported gastrointestinal illness in NZ, with incidence rates that largely surpass those of the USA. These numbers can be traced to a longstanding *Campylobacter* spp. epidemic, with fresh chicken meat as the single largest source of human infection (Baker *et al*., 2021). Incidence rates climbed between 1980 and 2005 with the increase in chicken meat consumption, peaked in 2006 (>380 per 100 000 population) and fell drastically after 2007, with the introduction of a risk management strategy to reduce the incidence of poultry-associated campylobacteriosis. NZ possesses highly integrated and closed poultry production systems, with all poultry meat at retail coming from national production and three processing companies supplying over 90% of the internal market, meaning that interventions at the local industry level had a contamination-reducing effect in all poultry consumed nationwide (Sears *et al*., 2011; Baker *et al*., 2021). Nonetheless, incidence rates and outbreaks are still much higher than in other high-income countries, but slowly descending every year thanks to surveillance and risk management efforts (Armstrong *et al*., 2024).In high-income countries, campylobacteriosis outbreaks can also be linked to other protein foods besides meat and meat products, such as raw milk - often the vehicle most commonly associated with FBOs by *Campylobacter jejuni* (CDC, 2013; Jaakkonen *et al*., 2020). In NZ and the USA, “milk” was the leading contributor to campylobacteriosis outbreaks (over 40% of occurrences), while in EU-MS the majority of campylobacteriosis outbreaks were attributed to “meat”, findings corroborated by source attribution studies (Batz *et al*., 2021; Mughini-Gras *et al*., 2025).

Salmonella enterica can be found in the intestinal tract of animals like poultry, cattle, and swine, which shed it into the environment through their feces. Infection occurs through the ingestion of contaminated drinking water or eating contaminated eggs, raw or undercooked meat, unpasteurized dairy and fresh produce (Mkangara, 2023). Fecal contamination of the shell during laying allows *Salmonella* spp. to adhere and penetrate the eggshell, particularly if eggs are washed or stored at warm temperatures, and undercooking the eggs does not inactivate the pathogen. Animal products, such as meat or seafood, are usually contaminated by *Salmonella* spp. present in the animal’s gut during evisceration and other processing stages (Mkangara, 2023).

Our results showed that “eggs” were the highest contributing category for salmonellosis in Europe, and “meat” was the category responsible for most of the salmonellosis FBOs in NZ and the USA. These results agree with earlier source attribution studies (Greig and Ravel, 2009), where outbreaks related to *Salmonella* Enteritidis and other *Salmonella enterica* in the EU were more frequently associated with “eggs” than in the USA, whereas in the USA, beef, pork and poultry products were the primary sources of other *S. enterica* (non-Enteritidis or Typhimurium).

Non-typhoidal *Salmonella* was also one of the pathogens with the highest share as causative agent of outbreaks in categories like “legumes” and dough-based derivatives”, food source attributions also reported by several studies (Greig and Ravel, 2009; Batz *et al*., 2021; Davydova *et al*., 2025). This highlights the ubiquity of *Salmonella* spp. across diverse food matrices, and the necessity for more rigorous hygiene practices in food preparation and handling in order to reduce contamination.

Contamination of recreational or drinking water drives a large part of cryptosporidiosis rates and outbreaks in high-income countries. However, FBOs linked to vegetables/fruits irrigated with contaminated water, and to cross-contaminated raw milk are increasingly more common (Ali *et al*., 2024). Additionally, according to source attribution studies based on expert elicitation, dairy foods are the protein-based foods with the greatest contribution to FBOs caused by *Cryptosporidium* spp. (Hoffmann *et al*., 2017). Cattle, particularly young calves, are a major reservoir of zoonotic *C. parvum*, shedding large quantities of the environmentally resistant oocysts through feces. Fecal contamination of bedding and pastures can lead to cross-contamination of teats, udders, milking equipment and even raw milk (Bulumulla *et al.*, 2025). Consumption of contaminated raw milk/dairy products (non-pasteurized, as pasteurization inactivates oocysts), can lead to illness and foodborne cryptosporidiosis outbreaks (Ursini *et al.*, 2020; Garcia-R and Hayman, 2023), as illustrated by the contribution of "milk" and "cheese" as protein food vehicles responsible for outbreaks in NZ, USA and EU-MS. New Zealand's economy relies heavily on dairy, cattle and sheep farming, resulting not only in a higher livestock density but also in an increased likelihood of direct contact with animal reservoirs of *Cryptosporidium* spp. than in other high-income countries, which might help explain such high notification rates in NZ compared to the other regions analysed (Lake *et al.*, 2008).

L. monocytogenes is ubiquitous in both plant and animal reservoirs and can persist in food production environments due to its ability to grow at refrigeration temperatures and its resistance to biocides (Fotopoulou *et al.*, 2024). Infection occurs primarily through the ingestion of contaminated food that is not subjected to a cooking step, such as unpasteurized milk and dairy products, soft cheeses, processed meat (*e.g.*, deli meats, fermented sausages), processed fish (*e.g.*, smoked salmon), and fresh vegetables and fruits (Fotopoulou *et al.*, 2024). In this study, fish products ("preserved fish" and "fish") have a significant share of outbreaks attributed to *L. monocytogenes*, followed by "preserved meat" and dairy products ("dairy desserts", "non-specific dairy" and "cheese"). In the US, dairy products ("cheese", "dairy desserts", "non-specific dairy") contributed the most to listeriosis outbreaks, an attribution also verified by Batz *et al.* (2021), while in EU-MS countries, meat products ("meat" and preserved meat") had the most expressive contribution to listeriosis FBOs, followed by "fish" and "preserved fish". This epidemiological attribution is not aligned with the outcomes of published source attribution studies (Filipello *et al.*, 2020; Mughini-Gras *et al.*, 2022), where dairy products generally appear as the primary protein-based source of foodborne exposure to *L. monocytogenes* in EU countries.

In Europe, except for the COVID-19-related drop, listeriosis outbreaks have been climbing steadily in a worrisome trend. According to the 2022 EFSA/ECDC report (EFSA and ECDC, 2023), the combination of European populations getting older and the unavoidable increase of chronic age-related diseases, is putting more people at risk of severe forms of listeriosis infections, while the increased consumption of ready-to eat foods, such as cold smoked salmon, meat and meat products, dairy products and frozen vegetables, is boosting the number of outbreaks.

STEC primary reservoirs are the intestinal tracts of large and small ruminants (cattle, sheep, goats), and bacterial shedding via faces can contaminate hides, carcasses, slaughtering environments, milking equipment, soil and water. Transmission to humans often occurs through consumption of contaminated raw or undercooked meat and produce, unpasteurized milk and dairy products, ready-to-eat foods or drinking water (Farrokh *et al.*, 2013). "Meat" appears as the main vehicles of STEC outbreaks across EU-MS and the USA, followed by "milk and other dairy products ("cheese" and "non-specific dairy") whereas in NZ, "milk" is the topmost contributor, trailed by "meat", contributions also verified by recent attribution studies (Pires *et al.*, 2019; Batz *et al.*, 2021; Mughini-Gras *et al.*, 2022).

The integration of disease incidence data and outbreak data across countries and years revealed substantial heterogeneity in data structure, reporting methods and public accessibility. National surveillance systems varied considerably in their criteria for defining outbreaks, categorization of foods, surveillance protocols and diagnostic tools, leading to inconsistencies in reporting, sometimes between reports from the same country over multiple years of the study period. These sources of data disharmonization limited direct comparability and demanded a very careful and time-consuming integration of the data.

One of the first major obstacles was the incompleteness or uneven availability of data – particularly for certain countries, pathogens or years: Example 1) The absence of any FBO data from Canada was due to unavailability of complete data, since the publicly available FoodNet Canada Annual Reports, only cover outbreak data from selected sentinel sites and not the entire population of Canada (Public

Health Agency of Canada, 2024b); Example 2) *Toxoplasma gondii* incidence rates were not reported or made publicly available by any other regions except the EU; Example 3) characterization of outbreak food vehicles was not consistently reported in the same manner throughout the years in the EU reports (in some years the reports provide pie charts with the distribution of vehicles for each pathogen, in other years reports provided detailed tables, in others provided no data at all or tables with non-matching/repeated data). Furthermore, across the region/countries studied, different surveillance agencies discarded or did not release specific yearly outbreak datasets after report consolidation, making it hard to track specific outbreak numbers and food vehicle data. Such variation reveals major systemic issues with data transparency and accessibility, underlining an urgent need for standardized surveillance and reporting standards across countries.

While these disparities limit the interpretability of the data, they also highlight a key point: observed differences in incidence rates or outbreak frequency very likely reflect real epidemiological variation and gaps in monitoring capabilities. Therefore, cross-country compilations should be interpreted with caution, considering the background context behind each dataset.

Efforts are being undertaken to improve national and international data sharing – such as EFSA/ECDC's One Health WGS system (EFSA *et al*., 2025) or FDA's GenomeTrakr (USFDA, 2025) – but these are mainly focused on the genomic characterization of foodborne pathogens related to outbreak investigation, which leave out important epidemiological surveillance data from individual case reporting. Developing standardized international protocols and databases, particularly for FBD surveillance, would significantly improve accuracy, reproducibility, reliability and transparency of such data and its relevance in food safety policy globally.

Conclusions

This compilation analysis showed that, among the studied agents, non-typhoidal *Salmonella*, followed by NoV and *Campylobacter* spp. remain the foodborne pathogens with the greatest disease burden in high-income countries, accounting for 93,8% of all 4726 strong-evidence outbreaks considered. More efforts must be carried out to mitigate their impact on the health of populations, particularly in food chains related to meat and meat products, dairy, egg production and ready-to-eat foods, in addition to more food safety education interventions for food processing and food service workers as well as consumers, to reduce the spread of foodborne pathogens through cross-contamination. Furthermore, this work evidenced the heterogeneity in protein foods contribution to the outbreaks among the different region/countries considered, and such country-specificity was observed in all the foodborne pathogens under investigation. In EU-MS countries, "eggs" were the main protein-food contributors to salmonellosis outbreaks, "crustaceans and mollusks" were strongly associated with NoV, and "meat" was frequently reported in association with multiple pathogens (*Campylobacter* spp., STEC, and *L. monocytogenes*). In the USA, "meat" was the main protein-food contributor to salmonellosis and to STEC FBOs; "milk" contributed the most to campylobacteriosis and solely to cryptosporidiosis outbreaks, while "cheese" was responsible for the majority of listeriosis FBOs, and multiple categories contributed to NoV. NZ presented outcomes similar to those in the USA, with the major difference that STEC outbreaks were attributed mostly to "milk".

Accurate foodborne illness estimates play a crucial role in guiding policymakers to set intervention priorities and allocate resources. To achieve that, a harmonized, global approach to data collection and reporting is essential for effective source attribution and estimation of the burden of FBDs.

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Online supplementary material

Supplementary Figure 1. Evolution of incidence rates of norovirus cases (A) and total calicivirus outbreaks including norovirus (B) by region/country. Non-MS includes Albania, Bosnia and Herzegovina, Iceland, Liechtenstein, Montenegro, Norway, Republic of Macedonia, Serbia, Switzerland and United Kingdom (since 2020).

Supplementary Figure 2. Evolution of incidence rates of campylobacteriosis (A) and total campylobacteriosis outbreaks (B) by region/country. Non-MS includes Albania, Bosnia and Herzegovina, Iceland, Liechtenstein, Montenegro, Norway, Republic of Macedonia, Serbia, Switzerland and United Kingdom (since 2020).

Supplementary Figure 3. Evolution of incidence rates of salmonellosis (A) and total salmonellosis outbreaks (B) by region/country. Non-MS includes Albania, Bosnia and Herzegovina, Iceland, Liechtenstein, Montenegro, Norway, Republic of Macedonia, Serbia, Switzerland and United Kingdom (since 2020).

Supplementary Figure 4. Evolution of incidence rates of cryptosporidiosis (A) and total cryptosporidiosis outbreaks (B) by region/country. Non-MS includes Albania, Bosnia and Herzegovina, Iceland, Liechtenstein, Montenegro, Norway, Republic of Macedonia, Serbia, Switzerland and United Kingdom (since 2020).

Supplementary Figure 5. Evolution of incidence rates of Shiga toxin-producing Escherichia coli (STEC) infection (A) and total outbreaks (B) by region/country. Non-MS includes Albania, Bosnia and Herzegovina, Iceland, Liechtenstein, Montenegro, Norway, Republic of Macedonia, Serbia, Switzerland and United Kingdom (since 2020).

Supplementary Figure 6. Contribution (%) of protein foods to the total strong-evidence outbreaks of calicivirus and norovirus disease occurred since 2010, by available country/region (in EU MS countries, N = 509; in New Zealand, N = 31; in the USA = 326).

Supplementary Figure 7. Contribution (%) of protein foods to the total strong-evidence outbreaks of cryptosporidiosis occurred since 2010, by available country/region (in EU MS countries, N = 2; in New Zealand, N = 7; in the USA = 12).

Supplementary Figure 8. Contribution (%) of protein foods to the total strong-evidence outbreaks of STEC infections occurred since 2010, by available country/region (in EU MS countries, N = 55; in New Zealand, N = 8; in the USA = 111).

Supplementary Figure 9. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to milk.

Supplementary Figure 10. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to cheese.

Supplementary Figure 11. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to dairy (non-specific).

Supplementary Figure 12. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to dairy-based desserts.

Supplementary Figure 13. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to cereal grains.

Supplementary Figure 14. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to legumes.

Supplementary Figure 15. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to dough-based derivatives.

Supplementary Figure 16. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to eggs.

Supplementary Figure 17. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to fish.

Supplementary Figure 18. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to preserved fish.

Supplementary Figure 19. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to crustaceans and molluscs.

Supplementary Figure 20. Share (%) of pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to seafood-based meals.

Figure 1. Evolution of incidence rates of listeriosis (A) and total listeriosis outbreaks (B) by region/country. Non-MS includes Albania, Bosnia and Herzegovina, Iceland, Liechtenstein, Montenegro, Norway, Republic of Macedonia, Serbia, Switzerland and United Kingdom (since 2020).

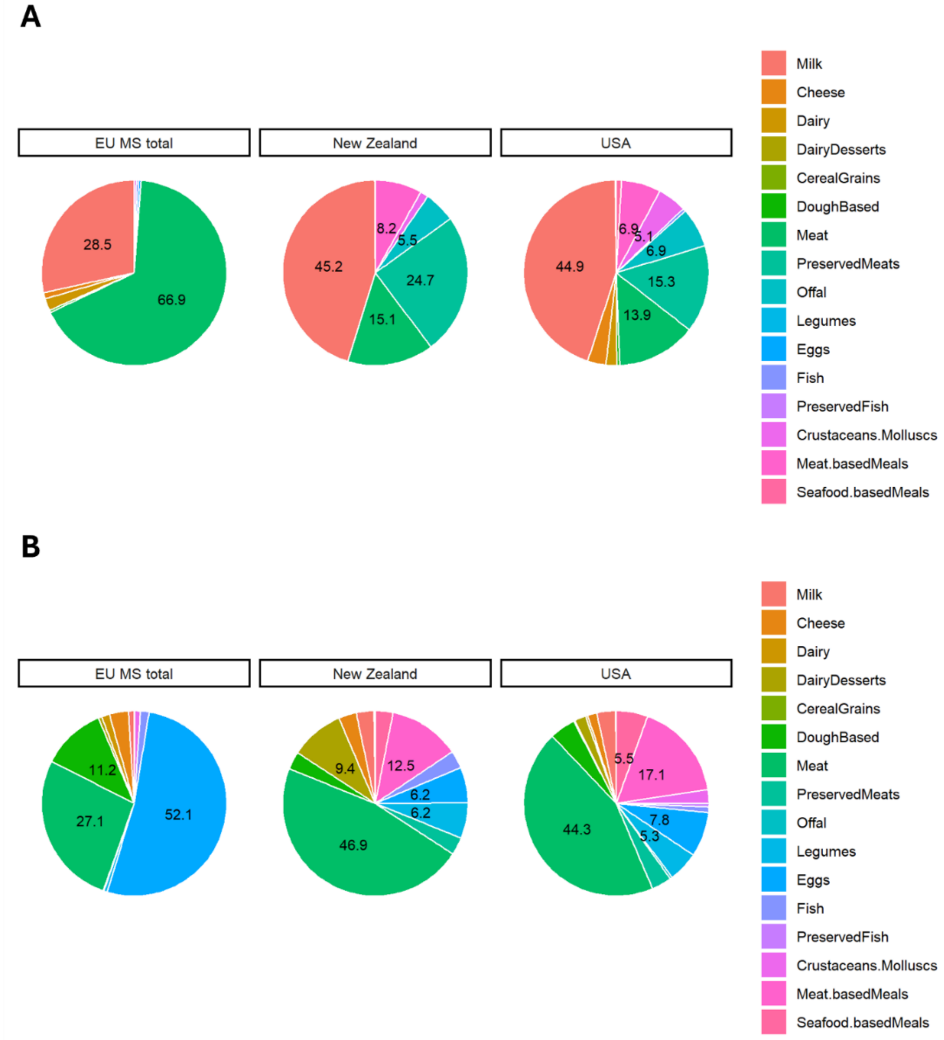

Figure 2. (A) Contribution (%) of protein foods to the total strong-evidence outbreaks of campylobacteriosis occurred since 2010, by available country/region (in EU MS countries, N = 281; in New Zealand, N = 73; in the USA = 216). (B) Contribution (%) of protein foods to the total strong-evidence outbreaks of salmonellosis occurred since 2010, by available country/region (in EU MS countries, N = 2473; in New Zealand, N = 32; in the USA = 490).

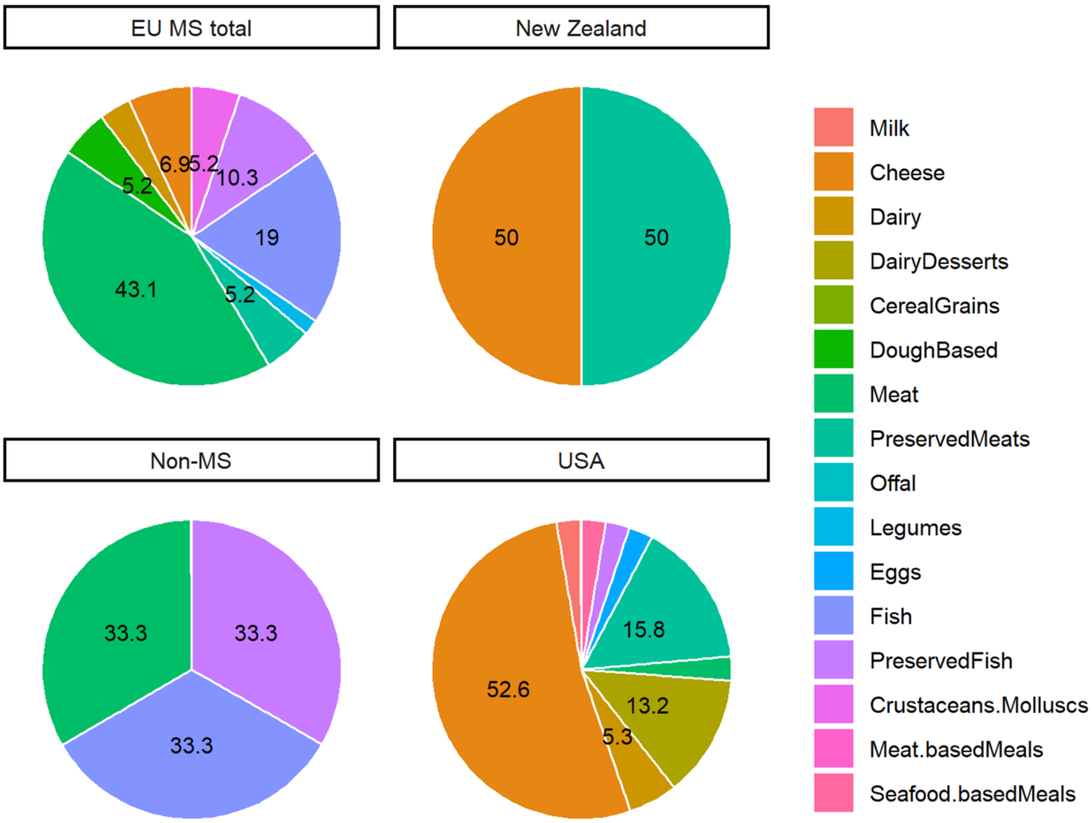

Figure 3. Contribution (%) of protein foods to the total strong-evidence outbreaks of listeriosis occurred since 2010, by available country/region (in EU MS countries, N = 58; in New Zealand, N = 2; in EU Non-MS countries, N = 3; in the USA = 38).

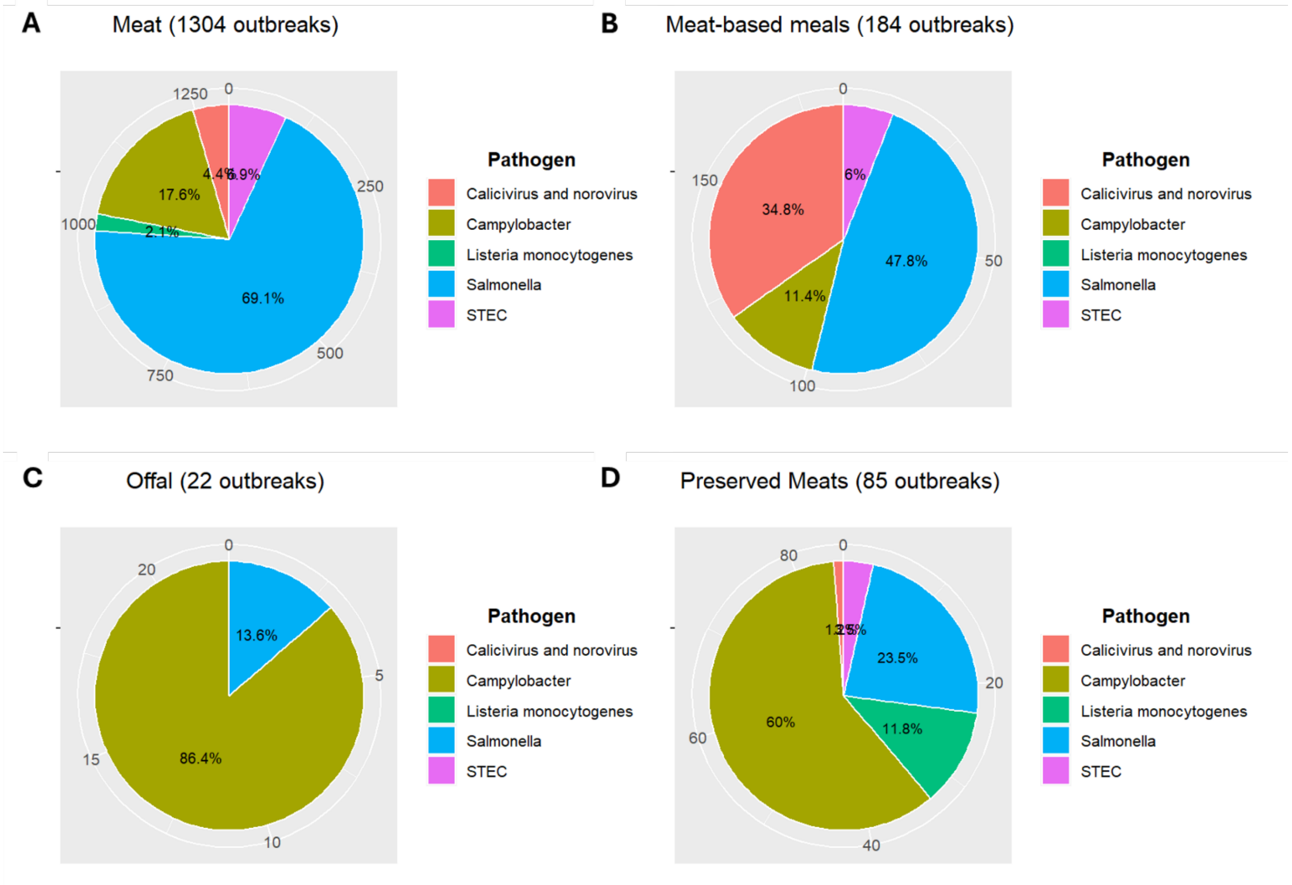

Figure 4. Share (%) of studied pathogens as causative agents of the 13-year strong-evidence outbreaks in Europe, North America and New Zealand attributed to (A) Meat, (B) Meat- based meals, (C) Offal and (D) Preserved Meats.

Table 1. Sources of foodborne disease surveillance consulted for data extraction.

Country/Region	Source	References
EU (MS and non-MS)	The European Union Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents and Food-borne Outbreaks (2010-2017) /The European Union One Health 2018 Zoonoses Report (2018-2022)	EFSA and ECDC, 2012, 2013, 2014, 2015a, 2015b, 2016, 2017, 2018, 2019, 2021a, 2021b, 2022, 2023
	ECDC Annual Epidemiological Reports - Typhoid and paratyphoid fevers (2014-2021)	ECDC, 2016a, 2018a, 2018b, 2020a, 2023a, 2023b, 2024a, 2024b
	ECDC Annual Epidemiological Reports - Cryptosporidiosis (2014-2021)	ECDC, 2017a, 2018c, 2018d, 2019a, 2021a, 2024c, 2024d
	ECDC Annual Epidemiological Reports - Giardiasis (2014-2019)	ECDC, 2017b, 2018e, 2018f, 2019b, 2022a, 2024e
	ECDC Annual Epidemiological Reports - Congenital toxoplasmosis (2014-2021)	ECDC, 2016b, 2018g, 2019c, 2019d, 2021b, 2022b, 2023c, 2024f
	ECDC Annual Epidemiological Reports - Echinococcosis (2014-2022)	ECDC, 2016c, 2017c, 2018h, 2020b, 2022c, 2022d, 2024g, 2024h
USA	Summary of Notifiable Diseases, United States (2010-2015)	Adams *et al*., 2012, 2013, 2014, 2015, 2016, 2017
	Notifiable Diseases Surveillance System (NNDSS) Annual Summary Data 2016-2021: Reported cases of notifiable diseases and rates, United States	CDC, 2024b
	BEAM dashboard - National Outbreak Reporting System (NORS) view	CDC, 2024a
	National Outbreak Reporting System (NORS) Dataset	CDC, 2024c
Canada	Canadian Notifiable Disease Surveillance System (CNDSS) - Large Data Extract - Notifiable diseases on-line	Public Health Agency of Canada, 2024a
New Zealand	Annual Report concerning Foodborne Disease in New Zealand (2010-2023)	Armstrong *et al*., 2024; Horn *et al*., 2014, 2015, 2021, 2023; Lim *et al*., 2010, 2012; Lopez *et al*., 2013, 2016; Pattis *et al*., 2017, 2019a, 2019b, 2020, 2022