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World Health Organization attribution of burden of foodborne diseases to transmission pathways and foods

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ABSTRACT

Identifying the sources of foodborne diseases is crucial for guiding national food safety strategies and supporting policies that promote safe and sustainable food production. Here we present global estimates of the proportions of burden of disease attributable to foodborne transmission, other major transmission pathways, and specific food categories for 29 viral, bacterial, parasitic, and chemical hazards, based on a structured expert judgement (SEJ) study commissioned by the World Health Organization (WHO) and supervised by the WHO Foodborne Disease Burden Epidemiology Reference Group (FERG) for 2021–2025. One-hundred forty-six experts provided 1463 assessments across 17 subregions within six WHO regions. The assessments were analyzed using Cooke's Classical Model and reviewed by FERG. Results showed that 13 of the 29 hazards were mainly (>50%) attributable to foodborne transmission, with non-typhoidal *Salmonella* (59–74%) and *Campylobacter* (45–71%) estimated to be predominantly foodborne in nearly all subregions. While plant-based foods were important sources of several pathogens, such as hepatitis A virus (63–74%) and *Cryptosporidium* (60–95%), foods of animal origin,

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including poultry, beef, eggs, seafood, and dairy products, remain critical intervention targets for several others, e.g., *Campylobacter* (86–97%), *Salmonella* (77–92%), *Shiga* toxin-producing *E. coli* (67–96%), and *Listeria monocytogenes* (50–85%). Regional differences in attributions highlight the influence of local epidemiological patterns, food systems, sanitation, and cultural practices. These estimates provide a global, uncertainty-quantified knowledge base to guide context-specific food safety interventions and future empirical data collection. Given persistent data gaps, SEJ remains a feasible approach to generate evidence supporting efforts to reduce the burden of foodborne diseases.

1. Introduction

In 2015, the first estimates of the global burden of foodborne diseases were published, demonstrating the need to strengthen food safety systems and establishing prevention priorities across regions, hazards, and food production systems (Havelaar et al., 2015; WHO, 2015). The World Health Organization (WHO) reconvened its advisory Foodborne Disease Burden Epidemiology Reference Group (FERG) in 2021 to update these estimates, generate national-level estimates, and develop indicators to track food safety progress (WHO, 2022). Within FERG, the Source Attribution Task Force (SATF) was charged with estimating attribution of global disease burden to major transmission pathways and food categories for enteric, parasitic, and chemical hazards.

Estimating foodborne disease burden is complex because many foodborne hazards are not exclusively transmitted through food. Transmission depends on the specific epidemiology of the disease, the type of hazard, and contextual factors, such as geography, seasonality, and local food consumption patterns and food preparation practices (Hald et al., 2016; Hoffmann et al., 2017; Pires, 2013). Source attribution, in which the proportion of human illness cases attributable to contaminated food and to specific food groups is determined, is therefore critical for estimating the burden of foodborne disease (Batz et al., 2005; Mughini-Gras et al., 2019; Pires et al., 2009). Source attribution also informs targeted disease prevention and food safety interventions, including resource allocation to maximize public health benefits and enables monitoring of intervention impacts (WHO, 2022).

Source attribution methods include those based on public health surveillance, food consumption and food monitoring data, epidemiological studies, intervention studies, and structured expert judgments (SEJ) (Pires, 2013). These methods have been applied to estimate source attribution of several pathogens in multiple countries, both in ad hoc studies and routinely, to inform regulatory decision-making and to prioritize and evaluate food safety interventions (Batz et al., 2021; Davydova et al., 2025; Interagency Food Safety Analytics Collaboration, 2026). While data-driven source attribution methods are generally preferred because they rely on observed data, persistent gaps in surveillance, monitoring, and epidemiological data have limited the use of such studies to a few hazards and countries (Crotta et al., 2022; Davydova et al., 2025). Furthermore, different source attribution methods are suitable for different pathogens and data contexts. As a result, attribution estimates are often generated using different approaches across countries and hazards, limiting their global comparability. SEJ offers a framework to address these gaps and produce global source attribution estimates (Aspinall & Cooke, 2013). SEJ has been applied in national studies and by the WHO to estimate foodborne illness source attributions (Butler et al., 2015; Hald et al., 2016; Hoffmann et al., 2017; Wijnen et al., 2026).

In this study, we present the 2026 WHO source attribution estimates for foodborne diseases for 29 viral, bacterial, parasitic, and chemical hazards for 17 subregions within six WHO regions, derived from a SEJ study.

2. Methods

2.1. Overview of the study

We estimated attribution proportions for 6 major transmission pathways and 14 food categories (Table 1) across all 194 WHO Member States, grouped into six WHO regions subdivided in 17 subregions (Lake et al., 2026; WHO. Disease Estimates 2026) based on the World Bank's four gross national income per-capita categories (Supplementary Table 1). Transmission pathways and food categories were defined to ensure comprehensiveness and comparability with other studies. The 14 food categories reflect common contamination and consumption patterns and were defined at a high level of aggregation, with each category encompassing lower-level food groups (e.g., dairy includes milk, cheese, and other dairy products). Attributions were estimated using a SEJ study conducted by a WHO-commissioned team of expert uncertainty elicitation scientists, guided by the SATF and supported by the three FERG hazard-specific task forces (Enteric Diseases Task Force, Parasitic Diseases Task Force, Chemicals and Toxins Task Force), which identified relevant hazards, transmission pathways, and food categories, and critically reviewed the resulting estimates.

Table 1
Transmission pathway definitions and food groups considered in the WHO global expert judgement for source attribution, 2026.

Transmission pathway	Definition
Food*	Consumption of contaminated food, including non-water beverages such as juices. Experts were instructed to consider contamination of food until the point where the food entered the place where it was prepared for consumption (e.g. kitchen). This excluded cross-contamination during food preparation.
Contact with animals (domestic, farmed, or wild)	Direct contact with an animal or its bodily fluids (excluding raw milk or other fluids consumed as food), fur, hair, feathers, scales, or skin, or by contact with the local environment where an infected animal, its visible excreta, fur, hair, feathers, scales, or skin was simultaneously present with the exposed person (e.g., barns, petting zoos, and pet stores).
Human-to-human contact	Direct contact with infected persons or their bodily fluids, by contact with the local environment where an exposed person is simultaneously present with an infected person, or through vertical transmission (i.e. from mother to child).
Water	Consumption of water, direct contact with water, or inhalation of aerosols originating from water. Includes drinking water, bottled water, recreational water (treated and untreated), and other water sources.
Soil	Exposure to contaminated soil or mud.
Other	Any other transmission not attributable to foodborne, waterborne, person-to-person, or animal contact transmission as defined above (e.g., airborne).
*Specific foods	Beef, small ruminant meat, pig meat, poultry meat, game, dairy, eggs, vegetables, fruits and nuts, grains and beans, oils and sugar, finfish, shellfish, seaweed, consumed raw or cooked.

2.2. Hazards and transmission pathways

The WHO global burden of foodborne disease estimates included 42 hazards (Supplementary Table 2). From these, we excluded seven pathogens that the task forces considered 100% foodborne and attributable to a single food category: *Taenia solium* (pig meat), *Clonorchis sinensis* (finfish), minute intestinal flukes (finfish), *Opisthorchis* spp. (finfish), *Paragonimus* spp. (shellfish), cassava cyanide (vegetables), and peanut allergens (fruits and nuts). Eight of the 9 chemicals in the WHO 2026 estimates were excluded because they are attributable to one single food, or because their source attribution is achieved via disease burden estimation that relies on exposure assessment through food sources within each population (Devleesschauwer et al., 2015; Jakobsen et al., 2026). Thus, we report source attribution estimates for 29 hazards: 14 diarrhoeal hazards, 7 invasive enteric hazards or intoxications, 7 parasitic hazards, and 1 chemical hazard (Table 2).

For some hazards, transmission pathways were restricted a priori using biological characteristics that render the pathways or sources highly implausible or impossible (Supplementary Tables 3 and 4). Attribution to major transmission pathways was performed for 26 hazards; *Clostridium botulinum* (foodborne botulism), *Listeria monocytogenes,* and *Trichinella* spp. were assumed to be 100% foodborne. Attribution to foods was performed for 27 hazards; zoonotic *Mycobacterium* spp. was assumed to be 100% dairy-borne, and *Fasciola* and *Fasciolopsis* 100% vegetable-borne.

2.3. Structured expert judgement

Full details of the process and steps taken within the SEJ study are detailed elsewhere (Nane et al., 2026). Briefly, on 10 July 2023 WHO opened a call for experts in food safety and related fields (e.g., microbiology, water sanitation, hygiene) (WHO, 2023). Additional experts were identified through snowball sampling and outreach through WHO and FERG professional networks. The elicitation process, including pre-elicitation screening and training, elicitation, and post-elicitation steps, ran from December 2023 to October 2025.

Expert screening and selection were conducted in collaboration with the WHO Collaborating Centre for Risk Assessment in Food and Water (National Institute for Public Health and the Environment of the Netherlands [RIVM]), based on a review of submitted curriculum vitae, publications, and professional experience, using criteria developed by the SATF (Supplementary Table 5).

The Cooke's Classical Model for SEJ (Cooke, 1991; Hanea & Nane, 2021) was applied, which aggregates expert uncertainty estimates based on performance on "calibration" variables from the experts' field and region whose values were retrievable but not known by the experts themselves during the elicitation. In short, experts provided their assessments using target questions, in which they were asked to quantify a best estimate (median), lower (5th), and upper (95th) uncertainty bounds. Individual probability distributions were constructed and combined over a shared range. To evaluate expert performance, the answers to calibration questions were analyzed to derive a calibration score measuring statistical accuracy (how well uncertainty intervals resulting from the three uncertainty assessments capture realizations), and an information score measuring how precise (narrow) the uncertainty assessments were. These scores were combined to assign performance-based weights to each expert. Weighted expert distributions were aggregated into decision makers, and final models were compared to select the best-performing aggregation. Experts received training and background materials for review, including an overview of source attribution studies conducted between 2010 and 2023, hazard- and country-specific estimates extracted from these studies (Davydova et al., 2025), and a summary of national food consumption patterns derived from Food and Agriculture Organization Food Availability Data for 2010 and 2020 (Nane et al., 2026). Hazard and region-relevant calibration questions were based on data from public statistics and scientific literature, tailored to the varied backgrounds and experiences of the experts. Experts answered calibration questions, hazard-specific target questions, and received additional instructions in Qualtrics, an online General Data Protection Regulation (GDPR)-compliant tool. Expert data were aggregated by hazard and subregion and analyzed. All analyses were performed in R statistical software (R Core Team, 2021).

Each hazard-subregion panel required at least four experts (Cooke, 1991). When this minimum was not met, a hierarchy of proxy strategies was applied. First, assessments from a neighboring subregion or from all subregions were merged to generate regional proxies. If this did not ensure input from four experts, proxies were constructed by combining assessments from subregions with similar economic classifications (e.g., subregion A). If neither approach yielded sufficient expert input, global attribution estimates were derived using judgments from all experts who provided data for that hazard. Sub-regional source attribution estimates for each pathogen were considered representative of all countries within that subregion (Supplementary Table 1).

Table 2
Hazards included in the WHO source attribution study of foodborne hazards.

Diarrhoeal disease hazards ($N = 14$)	Invasive enteric disease and intoxication hazards (N = 7)	Invasive parasitic disease hazards ($N = 7$)	Chemical hazards (N = 1)
Campylobacter spp.	*Brucella* spp.	*Ascaris* spp.	Lead
Cryptosporidium spp.	*Clostridium botulinum*	*Echinococcus multilocularis*	
Cyclospora	Hepatitis A virus	*Echinococcus granulosus*	
Entamoeba histolytica	*Listeria monocytogenes*	*Trypanosoma cruzi*	
Enteroaggregative *E. coli*	*Mycobacterium bovis/caprae/orygis*	*Fasciola* spp. & *Fasciolopsis buski*	
Enteropathogenic *E. coli*	*Salmonella* Paratyphi*	*Toxoplasma gondii*	
Enterotoxigenic *E. coli*	*Salmonella* Typhi	*Trichinella* spp.	
Giardia spp.			
Norovirus			
Rotavirus			
Non-typhoidal *Salmonella enterica*			
Shigella spp.			
Shiga toxin-producing *E. coli*			
Vibrio cholerae			

* As described in the SEJ's target questions. During the elicitation process, experts were informed that they should consider *Salmonella* Paratyphi A, B, and C.

2.4. WHO FERG task forces' review

The three Task Forces reviewed preliminary estimates and identified results that appeared biologically implausible or inconsistent with known epidemiology. Experts with outlier judgments were asked to rationalize and, if needed, revise their estimates, and anonymized responses were shared with the Task Forces. Based on their advice, WHO determined whether any expert judgments should be excluded due to insufficient domain expertise. The elicitation data were then reanalyzed to produce final attribution estimates, which were shared with the Task Forces for endorsement. Together with the SATF, they agreed on hazard-specific approaches to derive final source attribution estimates, including: retaining elicited estimates; aggregating food categories when distinctions were unreliable; or replacing elicitation results with alternative data sources. Decisions were shared with WHO for final approval. The final foodborne attribution estimates were reviewed by Member States through the formal country consultation process (Lake et al., 2026).

3. Results

Eight-hundred fifty experts applied from July 2023 to May 2024. Of these, 290 were deemed eligible. Another 152 experts were identified through WHO/FERG networks. Following initial contact with 442 experts, 400 provided background information. 392 experts were invited for interviews, of whom146 completed assessments, providing 1463 assessments, each contributing to one or more hazard-subregion panels. The number of experts providing assessments was highest in the Region of the Americas ($n = 83$) and lowest in the South-East Asia Region ($n = 43$) (Fig. 1; Supplementary Table 6).

Task Forces endorsed estimates for 26 of the 29 hazards. For *Trichinella* spp., it was not possible to distinguish between relevant meat types, and exposure was set as 100% attributable to the broader category "meat". For *Cryptosporidium* spp., *Cyclospora*, and *Giardia* spp. the food categories "vegetables" and "fruits and nuts" were grouped into a broader category "fresh produce" because it was not possible to distinguish between exposure through fresh vegetables and fruit. For *T. gondii,* elicited estimates were inconsistent with the parasite's life cycle, and attribution values were obtained from previous studies (Hald et al., 2016; Hoffmann et al., 2017). For *E. multilocularis,* elicited estimates were inconsistent with empirical data and estimates of attribution to food were obtained from a systematic review (Torgerson et al., 2020).

3.1. Source attribution results

Figs. 2–7 show mean attribution estimates to major transmission pathways and to specific food categories within the foodborne pathway, by region and subregion, for all hazards. Attribution medians, 2.5 and 97.5 percentiles are presented in Supplementary Figs. S1–6 and Data Supplement 1.

3.1.1. Transmission pathway-level attributions

Thirteen of the 29 hazards were mainly (>50%) attributable to foodborne transmission. Among the enteric pathogens, *Campylobacter* (45–71%) and non-typhoidal *Salmonella* (59–74%) infections were estimated as being predominantly foodborne in nearly all subregions, whereas the estimated foodborne proportions for infections with diarrheagenic *E. coli* (i.e., enterotoxigenic 29–79%, enteroaggregative 23–80%, and enteropathogenic 37–75%), Shiga toxin-producing *E.coli* (STEC) (32–73%), *Mycobacterium bovis, M. caprae,* and *M. orygis* (19–82%) showed greater variation across regions, with attributions to food generally highest in the Eastern Mediterranean subregions and lowest in the Western Pacific and African subregions (Table 3–5, Figs. 2–7). A wide variation was also observed for *Brucella* spp. (16–63%), *Salmonella* Typhi (12–64%), and *Salmonella* Paratyphi (1–77%). For bacterial hazard–subregion combinations where attribution to food was lower, water was the most important pathway for *Campylobacter* and *Salmonella* Paratyphi in the Western Pacific and African subregions, whereas human-to-human contact was the most important pathway of *Salmonella* Typhi and *M. bovis* in the European subregions, and contact with animals for *Brucella* spp. in the African subregions. *Cyclospora* was the only enteric protozoan estimated to be primarily transmitted through food (74–95%), while most transmission of *Giardia* spp. and *Cryptosporidium* was attributed to water (37–55% and 36–51%, respectively) and human-to-human contact (31–41% and 15–29%, respectively). For these hazards, waterborne transmission dominated in the African, South-East Asia, and Western Pacific Regions (40–55%), whereas human-to-human contact contributed substantially to disease in the European Region and the Region of the Americas (30–50%). Foodborne transmission was estimated to account for a smaller proportion of rotavirus (1–17%), norovirus (19–45%), and hepatitis A virus (28–53%) infections compared with human-to-human contact (Figs. 2–7 and Data Supplement 1). *Fasciola* and *Fasciolopsis* were almost entirely foodborne (98–100%). *Ascaris* was attributed to both foodborne and soilborne transmission, with foodborne transmission being highest in the European and South-East Asia Regions (56–85%), and soilborne transmission being highest in the Western Pacific Region. *Entamoeba histolytica* was largely attributed to water (29–56%) and human-to-human contact (~30–50%). *Trypanosoma cruzi* is only present in the Region of the Americas (Agudelo Higuita et al., 2024; Robertson et al., 2024a) and was estimated as being mainly vectorborne (~50%) and foodborne (~44%). *T. gondii* was largely attributed to foodborne transmission in most subregions, and soilborne transmission was important in African and Eastern Mediterranean Regions (34–38%) (Hald et al., 2016). Foodborne attribution of *E. multilocularis* ranged from 4% to 58% in endemic sub-regions (Torgerson et al., 2020). Lead exposure was estimated as mainly foodborne in the South-East Asia Region (46–59%), whereas attribution to food in the other regions was lower (7–30%).

In general, across all hazards, subregional differences in the relative contribution of pathways were most pronounced within the European Region and Region of the Americas, whereas in the African, Eastern Mediterranean, South-East Asia, and Western Pacific Regions, attributions were more homogeneous (Figs. 2–7).

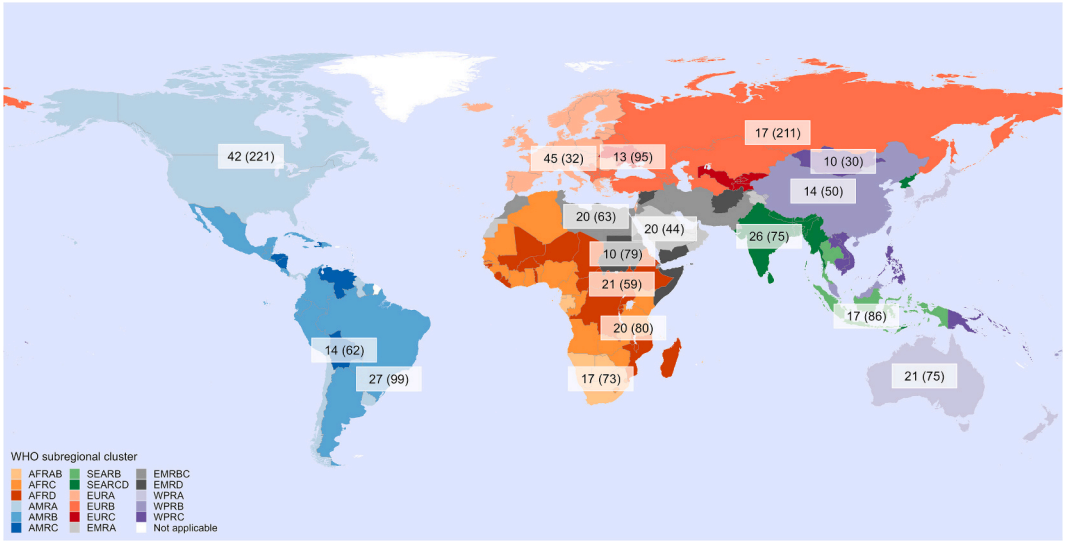

Fig. 1. Number of expert assessments per WHO region. Assessments cover all hazards. See Supplementary Table 6 for detailed information on the number of expert assessments per hazard-subregion.

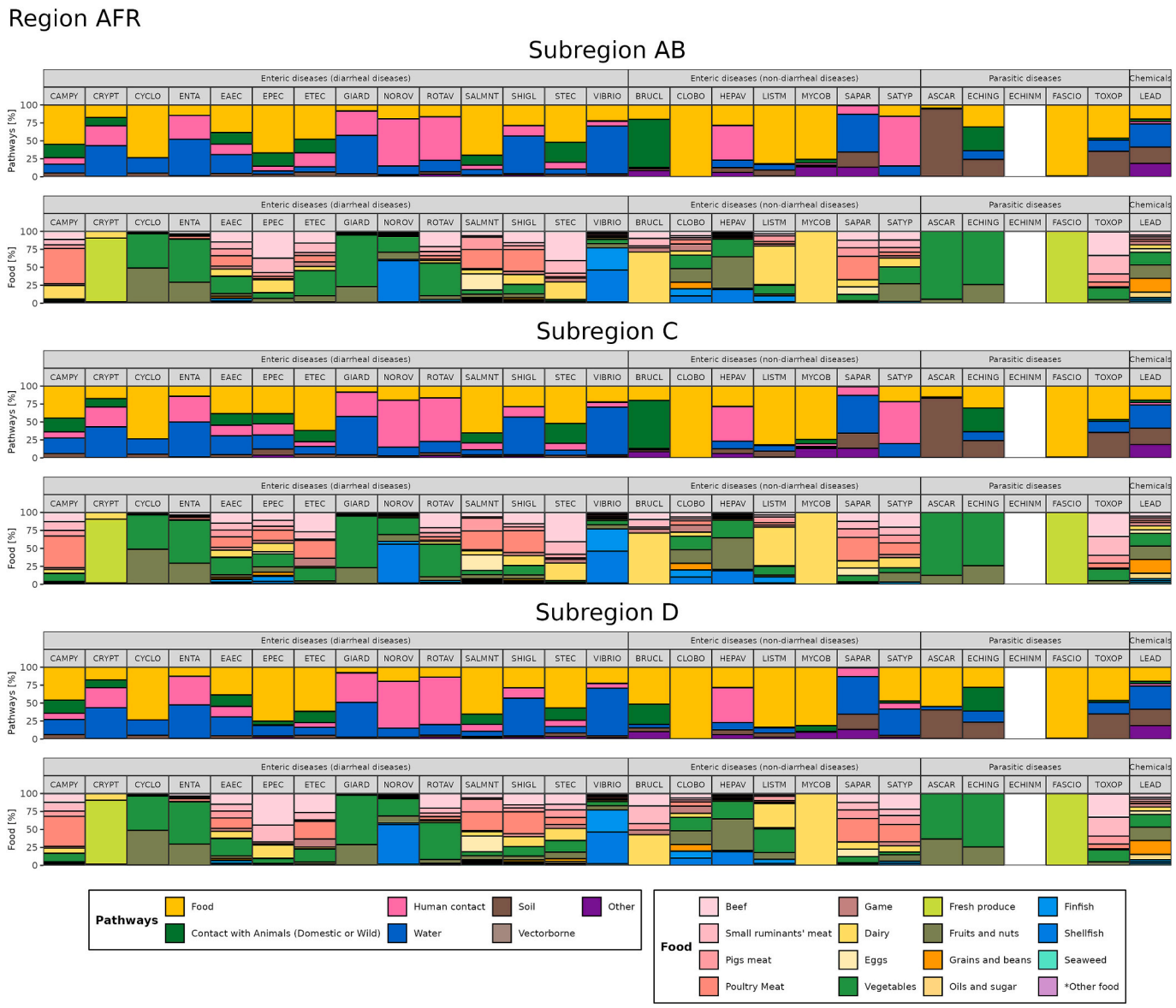

Fig. 2. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in the subregions of the African Region, AFR. Transmission "vector-borne" is applicable only to *T. cruzi* in the Region of the Americas (AMR). The category "other food" in the food groups applies only to *Cryptosporidium* and includes all remaining food groups except "dairy" and "fresh produce". Where estimated, "fresh produce" applies only to *Cryptosporidium* and *Fasciola/Fasciolopsis*, and includes both "vegetables" and "fruits and nuts". Pathway-level attribution estimates for *T. gondii* and *E. granulosus* were obtained from Hald et al. (2016b) and Torgerson et al. (2020), respectively. For food-level attribution estimates for these parasites (not shown in this picture), we refer to Hoffmann et al. (2017) and Torgerson et al. (2020), respectively. CAMPY = *Campylobacter*, CRYPT = *Cryptosporidium*; CYCLO = *Cyclospora;* ENTA = *Entamoeba histolytica*; EAEC = Enteroaggregative *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD = *Giardia*; NOROV = Norovirus; ROTAV = Rotavirus; SALMNT = Non-typhoidal *Salmonella enterica*; SHIGL = *Shigella*; STEC = Shiga toxin-producing *E. coli*; VIBRIO = *Vibrio cholerae*; BRUCL = *Brucella*; CLOBO = *Clostridium botulinum*; HEPAV = Hepatitis A virus; LISTM = *Listeria monocytogenes*; MYCOB = *Mycobacterium bovis/caprae/orygis*; SAPAR = *Salmonella* Paratyphi; SATYP = *Salmonella* Typhi; ASCAR = *Ascaris*; ECHING = *Echinococcus granulosus*; ECHINM = *Echinococcus multilocularis*; FASCIO = *Fasciola & Fasciolopsis*; TOXOP = *Toxoplasma gondii*; LEAD = Lead.

3.1.2. Food-level attributions

Food-level attribution estimates also varied across hazards and regions but showed consistent rankings for several pathogens. Poultry meat was the estimated primary source of *Campylobacter* spp. in all subregions (36–74%), followed by beef (9–12%) or dairy (5–28%). The estimated primary sources of *Salmonella* spp. included poultry meat (22–43%), pig meat (8–37%), and eggs (15–29%). Beef was estimated as the main source of *Shiga* toxin-producing *E. coli* (15–55%), while dairy products contributed substantially to *L. monocytogenes* (22–57%) and *Brucella* spp. (35–94%, excluding Western Pacific C; Figs. 2–7). Dairy (10–24%), small ruminants' meat (1–18%), pig meat (up to 14%), and, to a lesser extent, vegetables (2–24%), were relevant sources of *Shiga* toxin-producing *E. coli.* Vegetables were also an important source of L. *monocytogenes* (12–41%), followed by finfish (2–14%) and pig meat (up to 17%).

Vegetables, fruits and nuts, and fresh produce, were estimated to be the only foodborne source of *Cyclospora*, *Giardia, Ascaris, E. granulosus,* and *Fasciola* and *Fasciolopsis*, and important sources of *Cryptosporidium* (61–96%), norovirus (~30–40%), rotavirus (25–85%), hepatitis A virus (~70%), *Shigella* (20–85%), diarrheagenic *E. coli* (8–60%), *Entamoeba* (90–95%), and lead (7–50%). Shellfish was estimated as the leading food source for norovirus (22–60%), and finfish and shellfish for *Vibrio*

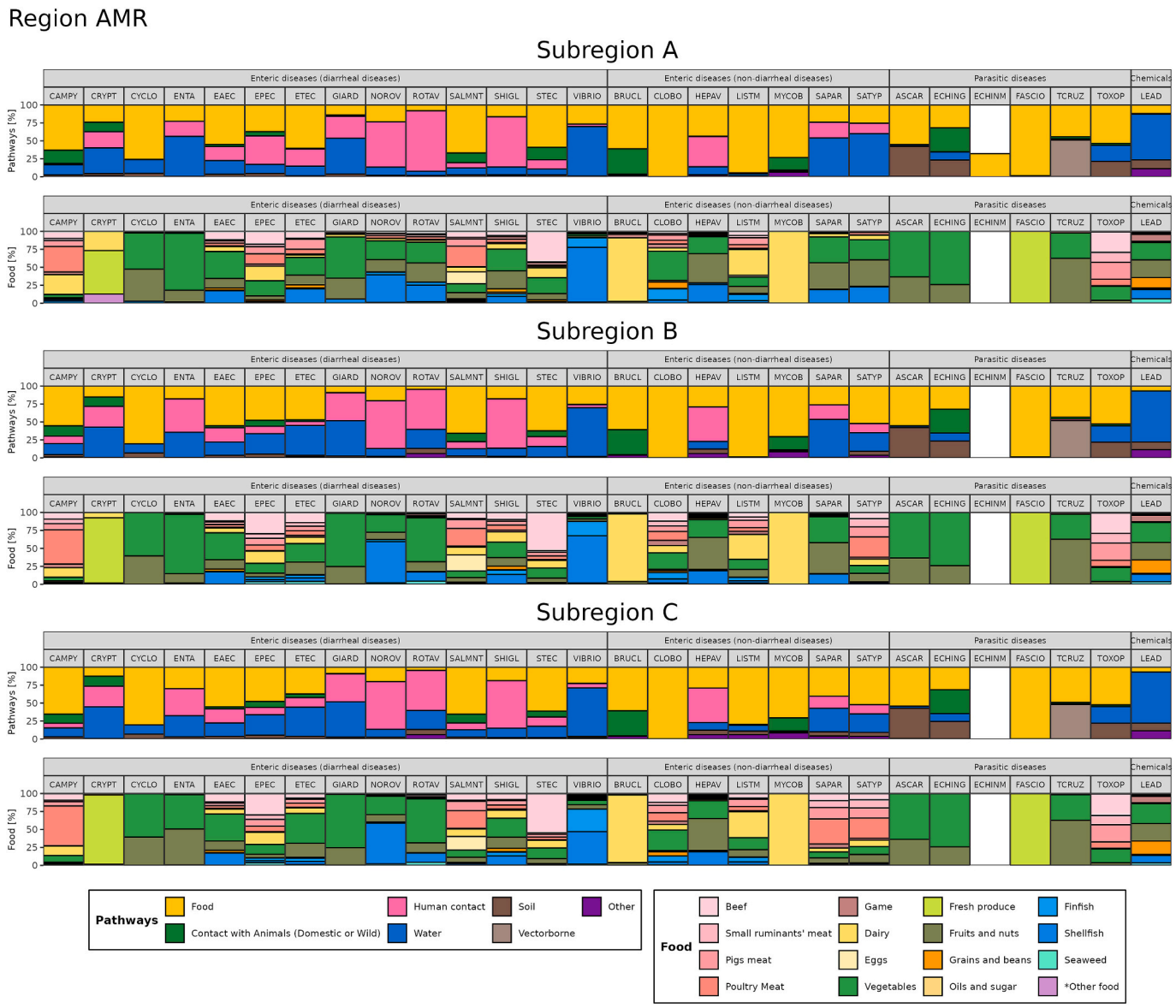

Fig. 3. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the Region of Americas, AMR. The category "other food" in the food groups applies only to *Cryptosporidium* and includes all remaining food groups except "dairy" and "fresh produce". Where estimated, "fresh produce" applies only to *Cryptosporidium* and *Fasciola/Fasciolopsis*, and includes both "vegetables" and "fruits and nuts". Pathway-level attribution estimates for *T. gondii* and *E. granulosus* were obtained from Hald et al. (2016b) and Torgerson et al. (2020), respectively. For food-level attribution estimates for these parasites (not shown in this picture), we refer to Hoffmann et al. (2017) and Torgerson et al. (2020), respectively. CAMPY = *Campylobacter*, CRYPT = *Cryptosporidium*; CYCLO = *Cyclospora;* ENTA = *Entamoeba histolytica*; EAEC = Enteroaggregative *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD = *Giardia*; NOROV = Norovirus; ROTAV = Rotavirus; SALMNT = Non-typhoidal *Salmonella enterica*; SHIGL = *Shigella*; STEC = Shiga toxin-producing *E. coli*; VIBRIO = *Vibrio cholerae*; BRUCL = *Brucella*; CLOBO = *Clostridium botulinum*; HEPAV = Hepatitis A virus; LISTM = *Listeria monocytogenes*; MYCOB = *Mycobacterium bovis/caprae/orygis*; SAPAR = *Salmonella* Paratyphi; SATYP = *Salmonella* Typhi; ASCAR = *Ascaris*; ECHING = *Echinococcus granulosus*; ECHINM = *Echinococcus multilocularis*; FASCIO = *Fasciola & Fasciolopsis*; TOXOP = *Toxoplasma gondii*; LEAD = Lead.

cholerae (66–86%). Grains and beans (1–33%), and to a lower extent shellfish (3–20%), were estimated as relevant sources of lead exposure (Figs. 2–7). Food attributions for *E. multilocularis* could not be obtained.

4. Discussion

This study provides new subregional source-attribution estimates for 29 foodborne hazards across all WHO regions. Attribution patterns varied markedly by hazard and subregion, reflecting hazard-specific characteristics as well as differences in food production systems, consumption practices, and local socio-economic conditions. The observed heterogeneity highlights the value of subregional analyses for capturing context-dependent epidemiological dynamics. When integrated with disease burden data, these findings offer an evidence base to support prioritization of food safety interventions, enabling more efficient allocation of resources.

Variation in attribution patterns across hazards and regions was anticipated given known differences in pathogen epidemiology, agricultural systems, food supply chains, consumption behaviors, and cultural practices (Waage et al., 2022). However, substantial subregional heterogeneity, particularly within the European Region and the Region of the Americas, suggests that important differences may exist at more granular geographic scales. While some differences likely reflect real underlying variation, others may arise from uneven data availability and

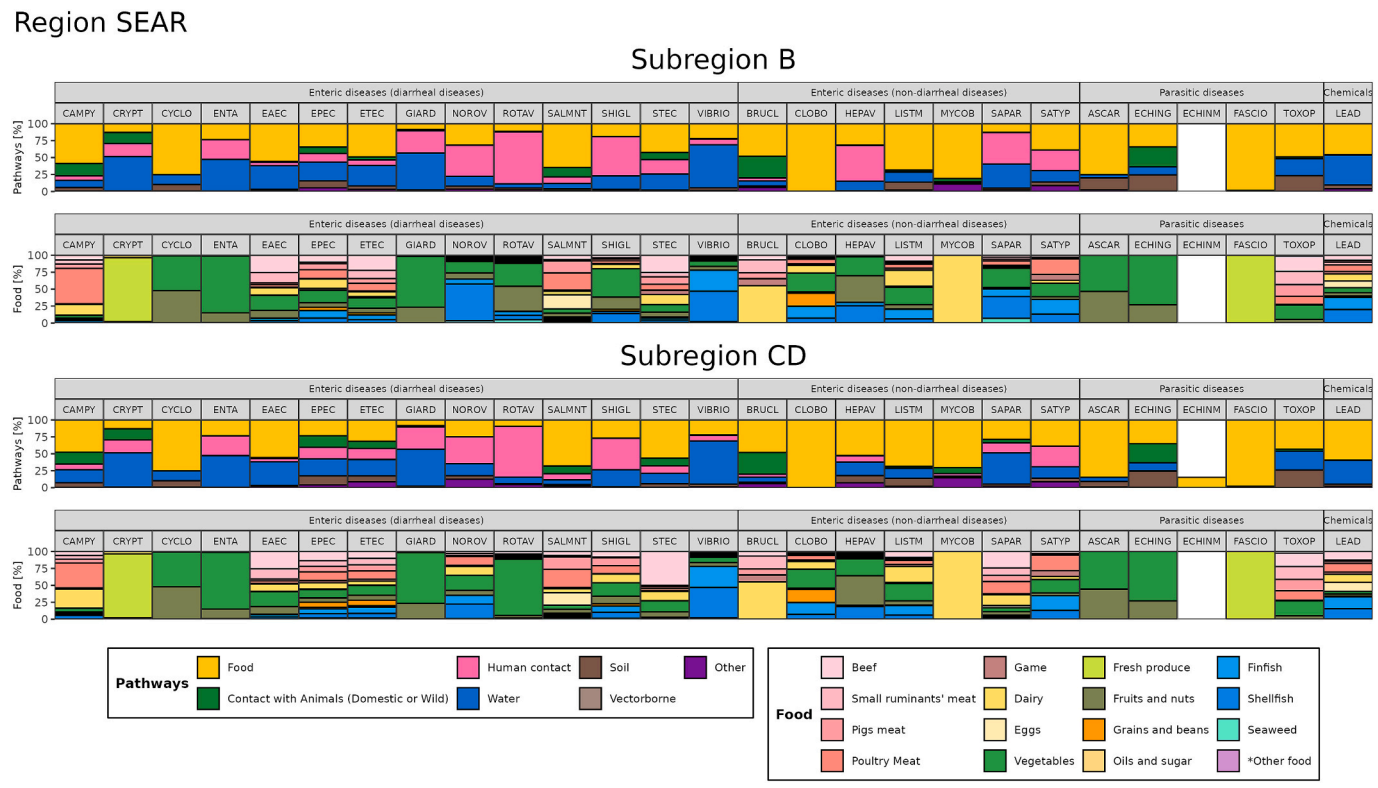

Fig. 4. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the Southeast Asian Region, SEAR. Transmission "vector-borne" is applicable only to *T. cruzi* in the Region of Americas. The category "other food" in the food groups applies only to *Cryptosporidium* and includes all remaining food groups except "dairy" and "fresh produce". Where estimated, "fresh produce" applies only to *Cryptosporidium* and *Fasciola/Fasciolopsis*, and includes both "vegetables" and "fruits and nuts". Pathway-level attribution estimates for *T. gondii* and *E. granulosus* were obtained from Hald et al. (2016b) and Torgerson et al. (2020), respectively. For food-level attribution estimates for these parasites (not shown in this picture), we refer to Hoffmann et al. (2017) and Torgerson et al. (2020), respectively. CAMPY = *Campylobacter*, CRYPT = *Cryptosporidium*; CYCLO = *Cyclospora;* ENTA = *Entamoeba histolytica*; EAEC = Enteroaggregative *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD = *Giardia*; NOROV = Norovirus; ROTAV = Rotavirus; SALMNT = Non-typhoidal *Salmonella enterica*; SHIGL = *Shigella*; STEC = Shiga toxin-producing *E. coli*; VIBRIO = *Vibrio cholerae*; BRUCL = *Brucella*; CLOBO = *Clostridium botulinum*; HEPAV = Hepatitis A virus; LISTM = *Listeria monocytogenes*; MYCOB = *Mycobacterium bovis/caprae/orygis*; SAPAR = *Salmonella* Paratyphi; SATYP = *Salmonella* Typhi; ASCAR = *Ascaris*; ECHING = *Echinococcus granulosus*; ECHINM = *Echinococcus multilocularis*; FASCIO = *Fasciola* & *Fasciolopsis*; TOXOP = *Toxoplasma gondii*; LEAD = Lead.

fewer expert assessments. In settings where transmission pathways are poorly characterized, or where proxy assessments were required, experts may tend to provide more uniform estimates, potentially masking true heterogeneity. These findings emphasize the need for stronger surveillance, improved empirical data collection and research, and continued refinement of source attribution methods to improve the resolution of the results. Although regional estimates support high-level planning, effective food safety action ultimately depends on interventions that are tailored to local conditions and supported by context-specific evidence.

Enteric pathogens such as *Campylobacter* and non-typhoidal *Salmonella* were predominantly foodborne across all regions and subregions, consistent with available national-level, empirical attribution studies (Davydova et al., 2025; De Knegt et al., 2015; Domingues et al., 2012; Interagency Food Safety Analytics Collaboration, 2026; Mughini Gras et al., 2012; Mughini-Gras et al., 2014; Munck et al., 2020; Pires et al., 2010; Wahlström et al., 2011). Other hazards had substantial attribution to water, human-to-human contact, and contact with animals. Some pathogens had relatively large attributions to human-to-human contact (rotavirus, norovirus, hepatitis A virus, and (para)typhoidal *Salmonella, Giardia* spp., and *Cryptosporidium* spp.), or water (*V. cholerae*, *Cryptosporidium* spp., (para)typhoidal *Salmonella*). This diversity of transmission routes underscores both the importance of considering multiple exposure routes when designing control strategies and the essential role of food safety measures in reducing the global burden of these diseases.

The substantial regional variation in the importance of sources of lead exposure reflects different mitigation strategies and underscores the need for context-specific interventions beyond food. Regional differences are expected for other chemicals entering the food chain through environmental pollution.

We presented the first source attribution estimates for *Trypanosoma cruzi*, present in the Region of the Americas. Our results show that foodborne transmission through consumption of vegetables and "fruits and nuts" is an important contributor to disease burden, suggesting that food safety interventions, in addition to measures against reduviid bug vectors, are important to prevent Chagas disease in populations at risk (Alarcón de Noya et al., 2024; Robertson et al., 2024b).

For 8 of the 29 pathogens our findings confirm that animal source foods remain critical targets for intervention, such as poultry (*Campylobacter* spp.), beef (*Campylobacter* spp., STEC, *T. gondii*), eggs (non-typhoidal *Salmonella*), pork (non-typhoidal *Salmonella*), meat from small ruminants (*Shiga* toxin-producing *E. coli*, other diarrheagenic *E. coli*, *Brucella* spp.), and dairy products (*Listeria monocytogenes*, *Brucella* spp.). Our results also demonstrate that vegetables, and "fruits and nuts" are critical targets for interventions for pathogens causing a high burden of disease globally, including *Ascaris lumbricoides*, *Cyclospora*, *Cryptosporidium* spp., norovirus, rotavirus, *Shigella* spp., *E. granulosus*, hepatitis A virus, and *Listeria monocytogenes* (Jakobsen et al., 2026; Majowicz, Colston, et al., 2026; Majowicz, Scallan Walter, et al., 2026; Robertson et al., 2026). As dietary guidelines and food system interventions worldwide increasingly promote diets rich in plant-based foods (FAO and WHO, 2019), simultaneously reducing foodborne hazard contamination on plant-based foods will be particularly important. Hazard- and

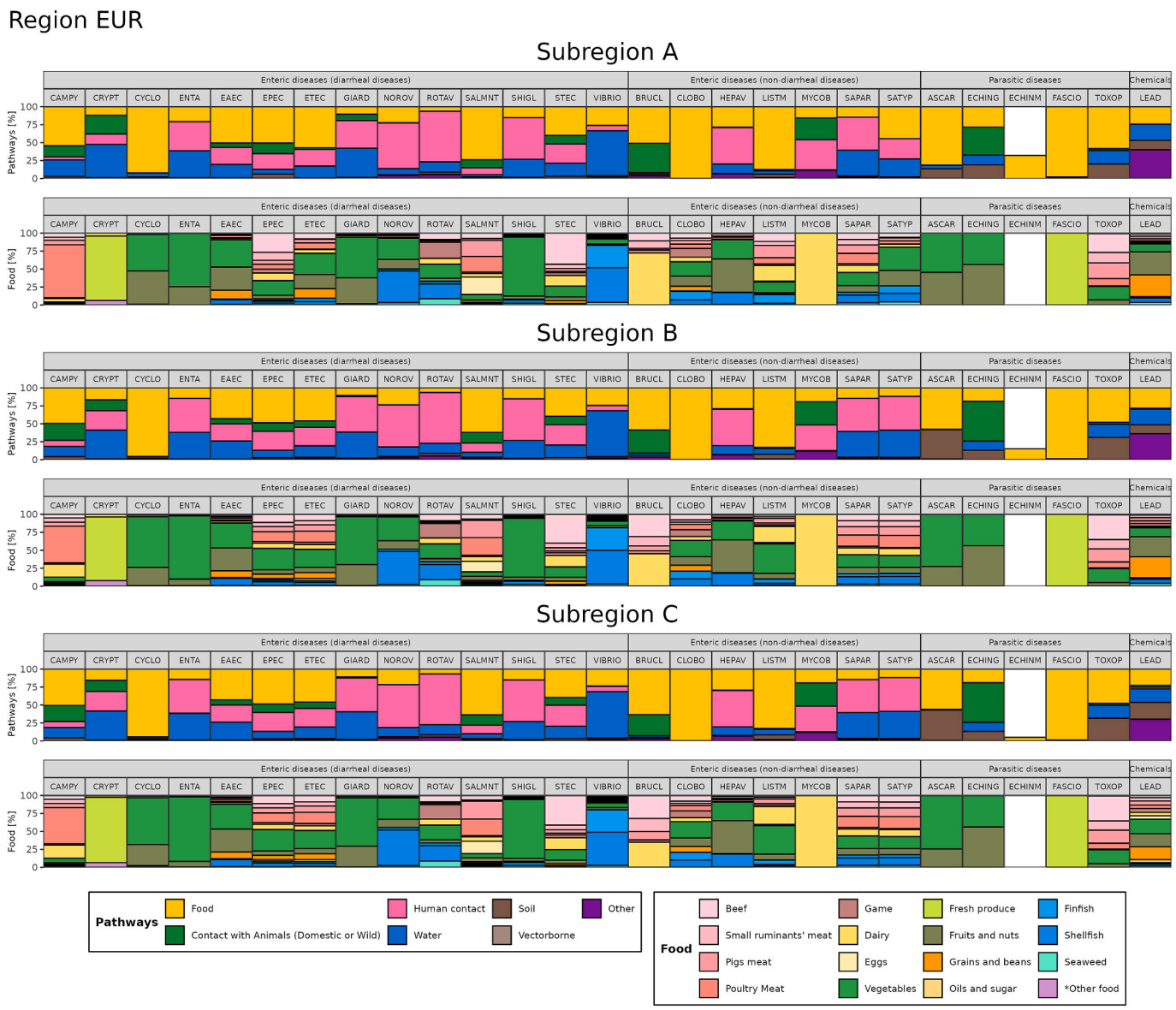

Fig. 5. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the European Region, EUR. Transmission "vector-borne" is applicable only to *T. cruzi* in the Region of Americas. The category "other food" in the food groups applies only to *Cryptosporidium* and includes all remaining food groups except "dairy" and "fresh produce". Where estimated, "fresh produce" applies only to *Cryptosporidium* and *Fasciola/Fasciolopsis*, and includes both "vegetables" and "fruits and nuts". Pathway-level attribution estimates for *T. gondii* and *E. granulosus* were obtained from Hald et al. (2016b) and Torgerson et al. (2020), respectively. For food-level attribution estimates for these parasites (not shown in this picture), we refer to Hoffmann et al. (2017) and Torgerson et al. (2020), respectively. CAMPY = *Campylobacter*, CRYPT = *Cryptosporidium*; CYCLO = *Cyclospora;* ENTA = *Entamoeba histolytica*; EAEC = Enteroaggregative *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD = *Giardia*; NOROV = Norovirus; ROTAV = Rotavirus; SALMNT = Non-typhoidal *Salmonella enterica*; SHIGL = *Shigella*; STEC = Shiga toxin-producing *E. coli*; VIBRIO = *Vibrio cholerae*; BRUCL = *Brucella*; CLOBO = *Clostridium botulinum*; HEPAV = Hepatitis A virus; LISTM = *Listeria monocytogenes*; MYCOB = *Mycobacterium bovis/caprae/orygis*; SAPAR = *Salmonella* Paratyphi; SATYP = *Salmonella* Typhi; ASCAR = *Ascaris*; ECHING = *Echinococcus granulosus*; ECHINM = *Echinococcus multilocularis*; FASCIO = *Fasciola & Fasciolopsis*; TOXOP = *Toxoplasma gondii*; LEAD = Lead.

subregion-specific attribution estimates can assist in this effort by identifying specific foods where interventions are needed to ensure that food consumption is not only sustainable and healthy, but also safe.

We sought to maintain methodological consistency with the expert elicitation source attribution study developed to support the 2015 WHO estimates of the global burden of foodborne disease (Hald et al., 2016; Hoffmann et al., 2017). Our study included all hazards in the 2015 attribution study plus 10 additional hazards, and elicited estimates from a larger, more geographically diverse expert panel. For hazards common to both studies, our estimates show greater regional variation, suggesting that experts participating in our elicitation may have incorporated more region-specific knowledge, including local food production systems, consumption patterns, environmental conditions, and public health infrastructure. We also observed that attribution to foodborne transmission was higher in 148 hazard-subregion pairs and decreased in 120 cases compared with the previous estimates (Supplementary Fig. S2) (Hald et al., 2016). These shifts likely reflect improved sanitation and water quality in some regions, changes in the relative importance of regulated food markets, variations in animal husbandry and food production practices, differences in human–animal contact patterns, and improved diagnostic practices for some hazards in some regions.

For some hazards, we assumed 100% attribution to foodborne

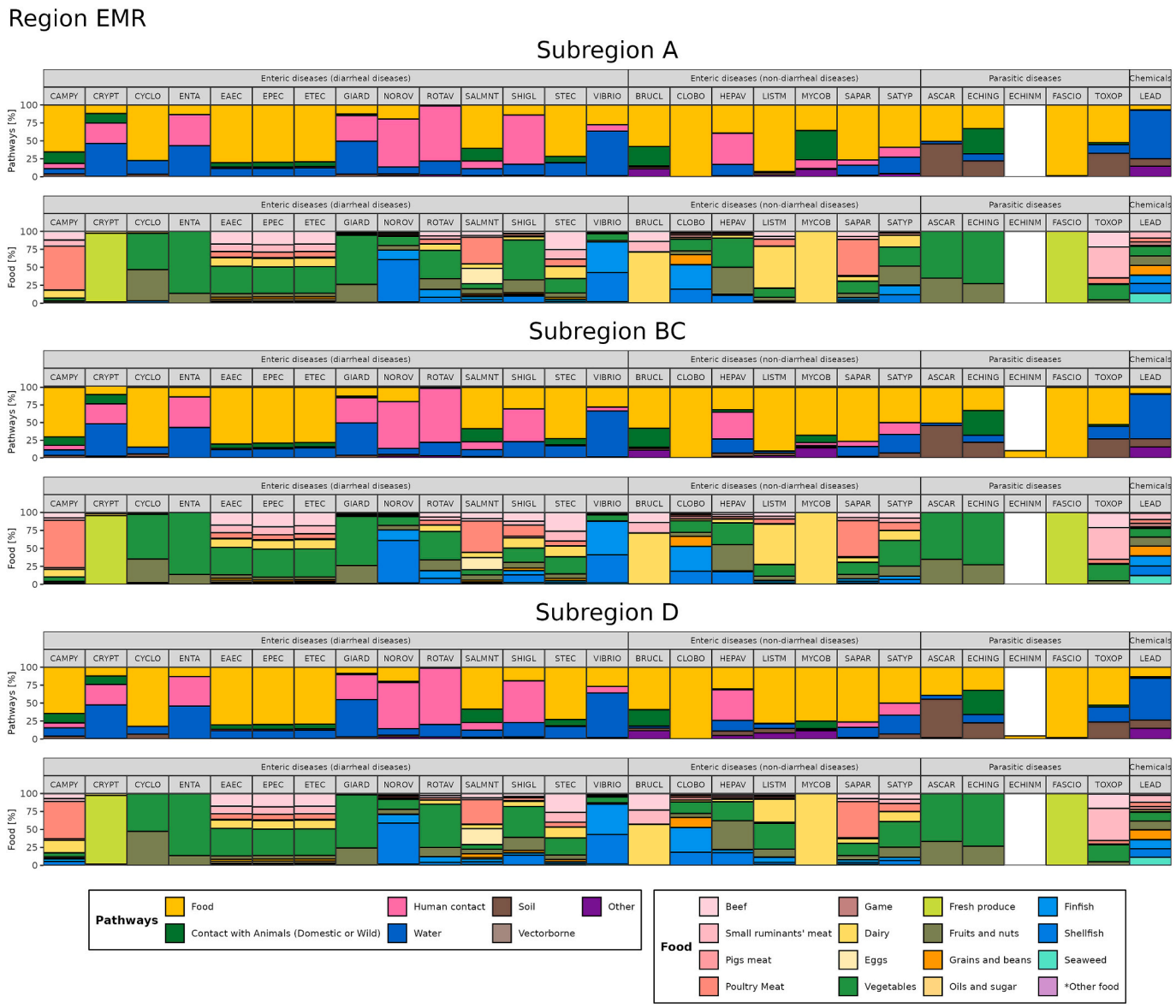

Fig. 6. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmissionpathways and specific foods in sub-regions of the Eastern Mediterranean Region, EMR. Transmission "vector-borne" is applicable only to *T. cruzi* in the Region of Americas. The category "other food" in the food groups applies only to *Cryptosporidium* and includes all remaining food groups except "dairy" and "fresh produce". Where estimated, "fresh produce" applies only to *Cryptosporidium* and *Fasciola/Fasciolopsis*, and includes both "vegetables" and "fruits and nuts". Pathway-level attribution estimates for *T. gondii* and *E. granulosus* were obtained from Hald et al. (2016b) and Torgerson et al. (2020), respectively. For food-level attribution estimates for these parasites (not shown in this picture), we refer to Hoffmann et al. (2017) and Torgerson et al. (2020), respectively. CAMPY = *Campylobacter*, CRYPT = *Cryptosporidium*; CYCLO = *Cyclospora;* ENTA = *Entamoeba histolytica*; EAEC = Enteroaggregative *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD = *Giardia*; NOROV = Norovirus; ROTAV = Rotavirus; SALMNT = Non-typhoidal *Salmonella enterica*; SHIGL = *Shigella*; STEC = Shiga toxin-producing *E. coli*; VIBRIO = *Vibrio cholerae*; BRUCL = *Brucella*; CLOBO = *Clostridium botulinum*; HEPAV = Hepatitis A virus; LISTM = *Listeria monocytogenes*; MYCOB = *Mycobacterium bovis/caprae/orygis*; SAPAR = *Salmonella* Paratyphi; SATYP = *Salmonella* Typhi; ASCAR = *Ascaris*; ECHING = *Echinococcus granulosus*; ECHINM = *Echinococcus multilocularis*; FASCIO = *Fasciola & Fasciolopsis*; TOXOP = *Toxoplasma gondii*; LEAD = Lead.

transmission or to specific foods. We recognize that other pathways or foods may be possible, although rare, resulting in a slight overestimation. As better empirical data becomes available, future assessments will be able to refine these estimates and better characterize associated uncertainties.

Our food attribution estimates are generally aligned with previously published estimates (Davydova et al., 2025). For 25 pathogens for which country-specific estimates were available, our regional estimates generally produced similar source rankings (Supplementary Fig. S2). However, for some pathogens, our estimates differed from source attribution estimates derived from outbreak data. For example, we estimated a relatively low contribution of vegetables to STEC infections in the American subregion A, whereas outbreak investigations have identified vegetable row crops as an important source (Interagency Food Safety Analytics Collaboration, 2026). Similar discrepancies between outbreak-based attribution estimates and estimates derived from methods incorporating sporadic case data have been previously reported and discussed (Pires et al., 2019). One possible explanation is that foods implicated in outbreaks are not necessarily representative of those responsible for sporadic infections. At the same time, for well-studied pathogens such as *Salmonella*, differences in attribution estimates across studies highlight both the value of comprehensive assessments

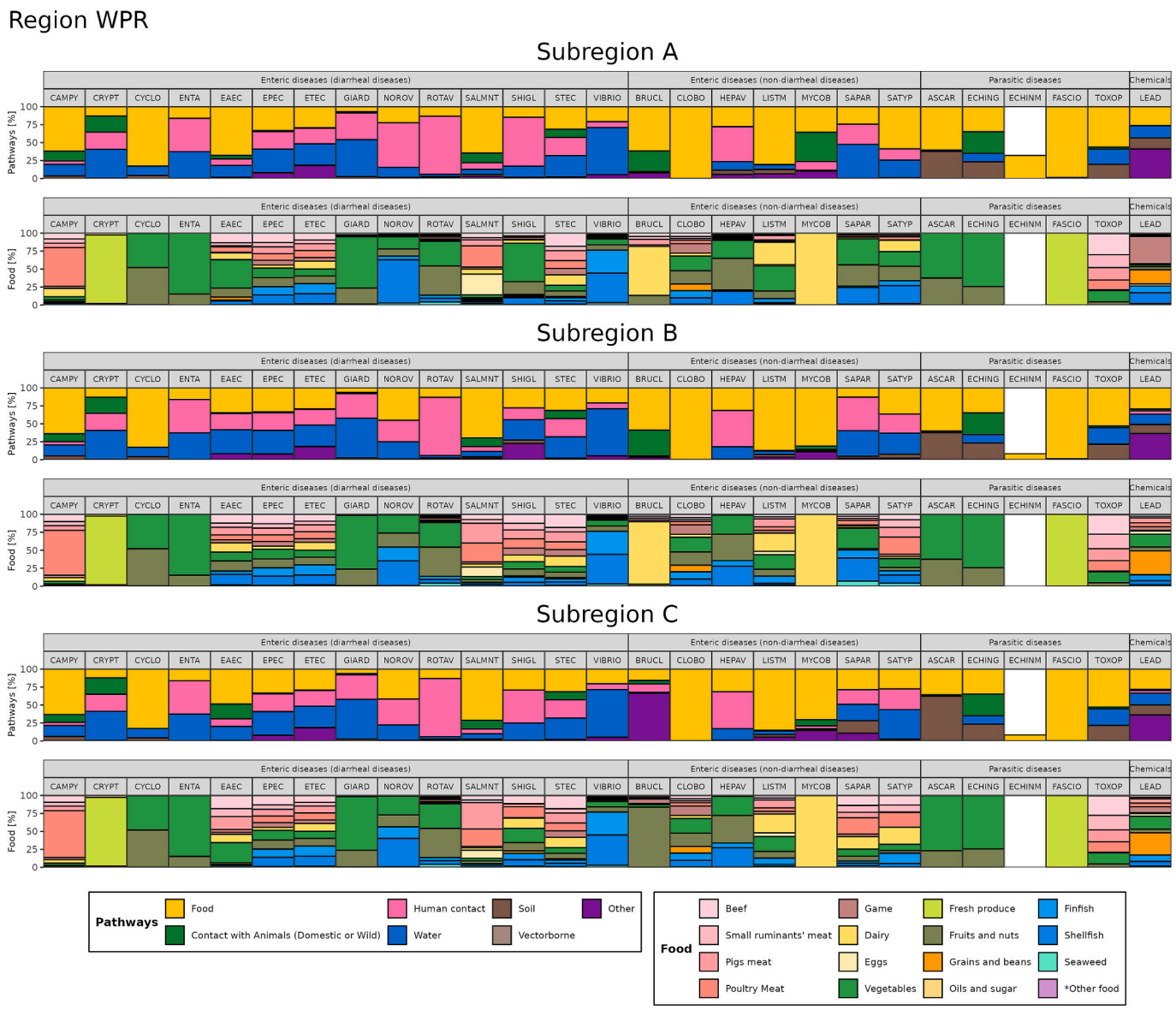

Fig. 7. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the Watern Pacific Asian Region, WPR. Transmission "vector-borne" is applicable only to *T. cruzi* in the Region of Americas. The category "other food" in the food groups applies only to *Cryptosporidium* and includes all remaining food groups except "dairy" and "fresh produce". Where estimated, "fresh produce" applies only to *Cryptosporidium* and *Fasciola/Fasciolopsis*, and includes both "vegetables" and "fruits and nuts". Pathway-level attribution estimates for *T. gondii* and *E. granulosus* were obtained from Hald et al. (2016b) and Torgerson et al. (2020), respectively. For food-level attribution estimates for these parasites (not shown in this picture), we refer to Hoffmann et al. (2017) and Torgerson et al. (2020), respectively. CAMPY = *Campylobacter*, CRYPT = *Cryptosporidium*; CYCLO = *Cyclospora;* ENTA = *Entamoeba histolytica*; EAEC = Enteroaggregative *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD = *Giardia*; NOROV = Norovirus; ROTAV = Rotavirus; SALMNT = Non-typhoidal *Salmonella enterica*; SHIGL = *Shigella*; STEC = Shiga toxin-producing *E. coli*; VIBRIO = *Vibrio cholerae*; BRUCL = *Brucella*; CLOBO = *Clostridium botulinum*; HEPAV = Hepatitis A virus; LISTM = *Listeria monocytogenes*; MYCOB = *Mycobacterium bovis/caprae/orygis*; SAPAR = *Salmonella Paratyphi*; SATYP = *Salmonella* Typhi; ASCAR = *Ascaris*; ECHING = *Echinococcus granulosus*; ECHINM = *Echinococcus multilocularis*; FASCIO = *Fasciola & Fasciolopsis*; TOXOP = *Toxoplasma gondii*; LEAD = Lead.

such as ours and the importance of country-level investigations, which may capture genuine variation in the relative contribution of sources within individual countries.

Our results are subject to several limitations. First, SEJ depends on the knowledge, experience, and uncertainty judgments of participating experts, informed by available evidence and relying on assumptions that can introduce bias. The Classical Model for SEJ minimizes these biases by identifying and mitigating overconfidence and consistent over- or under-estimation in expressing uncertainty assessments (Cooke, 1991). However, some elicited assessments were inconsistent with pathogen biology, epidemiology, or parasite life cycles. In such cases, the review and decision-making input of the task forces were essential to derive the final attribution estimates. Second, the wide uncertainty intervals might reflect the limited empirical data available for numerous hazards. Third, the number of experts per hazard-subregion panel varied considerably (Supplementary Table 6) and subregional representation was uneven, with fewer participants from certain low and middle-income countries, which may have led to widened uncertainty intervals. Fourth, the study assumes subregional attribution patterns apply uniformly within regions, potentially masking local variation in food production systems, consumption patterns, and environmental conditions. The use of WHO regions subdivided by World Bank income categories minimizes miss-

classification, although some ad hoc classifications were necessary (Supplementary Table 1). Together, these limitations highlight the need for continued empirical research, improved surveillance, and context-specific studies to refine attribution estimates.

Despite these limitations, this study provides a comprehensive and geographically resolved synthesis of the relative contributions of major transmission pathways to the global burden of foodborne disease, as well as the relative contributions of specific food groups to foodborne transmission. The findings are particularly relevant for low and middle-income countries, where foodborne disease surveillance remains limited and empirical evidence for risk-based prioritization remains scarce. By generating globally harmonized regional estimates across a broad range of hazards, this work strengthens the evidence base for the design and prioritization of food safety interventions, supports the identification of critical data gaps for future empirical source attribution studies, and informs public health policy, surveillance, and control strategies. Importantly, these estimates provide a globally consistent baseline that complements data-driven attribution approaches and enables more informed decision-making in settings with sparse epidemiological data, filling a critical evidence gap and pointing to priority areas for future intervention and research. The observed heterogeneity across hazards and regions further highlights the importance of context-specific food safety strategies and the need for continued refinement of source attribution methodologies. Beyond their direct relevance for public health practice, these findings also contribute to broader discussions on sustainable food systems and dietary transitions, enabling a more integrated consideration of both the nutritional benefits and food safety risks associated with different food sources within global policy and research agendas.

Declaration of generative AI and AI-assisted technologies in the manuscript preparation process

The authors used ChatGPT to produce the graphical abstract. After using this tool, the authors reviewed and edited the content as needed and take full responsibility for the content of the published article.

CRediT authorship contribution statement

Sara M. Pires: Writing – review & editing, Writing – original draft, Validation, Supervision, Methodology, Data curation, Conceptualization. **Lapo Mughini-Gras:** Writing – review & editing, Writing – original draft, Validation, Methodology, Conceptualization. **Sandra Hoffmann:** Writing – review & editing, Validation. **Kunihiro Kubota:** Writing – review & editing, Validation. **Shannon E. Majowicz:** Writing – original draft, Data curation. **Martyn D. Kirk:** Writing – review & editing, Validation. **Lucy J. Robertson:** Writing – review & editing, Validation. **Paul R. Torgerson:** Writing – review & editing, Validation. **Lea S. Jakobsen:** Writing – review & editing, Validation. **Antonio Agudo:** Writing – review & editing, Validation. **Li Bai:** Writing – review & editing, Validation. **Tety Rachmawati:** Writing – review & editing, Validation. **Yuki Minato:** Writing – review & editing, Project administration. **Charlee Roberts:** Writing – review & editing, Project administration. **Arie H. Havelaar:** Writing – review & editing, Validation. **Brecht Devleesschauwer:** Writing – review & editing, Validation. **Elisa Benincà:** Writing – review & editing, Visualization. **Robin J. Lake:** Writing – review & editing, Validation. **Tine Hald:** Writing – review & editing, Methodology. **Roger Cooke:** Writing – review & editing, Methodology. **Willy Aspinall:** Writing – review & editing, Methodology. **Gabriela F. Nane:** Writing – review & editing, Project administration, Methodology, Formal analysis, Data curation.

Ethics declaration

Informed consent and patient details

Written informed consent to take part in the study and to publish the article has been obtained from all participants or their legal representatives. The privacy rights of participants have been observed.

Studies in human

This study was performed in compliance with relevant laws, regulatory frameworks and guidelines where the research took place.

Ethics committee approval was not required under relevant laws and institutional guidelines. TU Delft's human Research Ethics Committee has evaluated that there are no personally identifiable research data (PIRD) used for the source attribution results and that a formal approval was therefore not needed.

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Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests: Willy Aspinall reports financial support was provided by TUDelft. Gabriela F. Nane, Tine Hald, Roger Cooke reports financial support was provided by World Health Organization. If there are other authors, they declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary Information

Supplementary data to this article can be found online at https://doi.org/10.1016/j.foodres.2026.120372.

Data availability

Data collected for this study and the analysis code are publicly available at Nane et al. (Nane et al., 2026), the GitHub repository https://github.com/WorldHealthOrganization/FERG_2025, and https://www.who.int/teams/nutrition-and-food-safety/monitoring-nutritional-status-and-food-safety-and-events/foodborne-disease-estimates/2026-edition. The overall study and modelling steps are available at Nane et al. (Nane et al., 2026).

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