

World Health Organization Attribution of Burden of Foodborne Diseases to Transmission Pathways and Foods

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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 diets. We present global estimates of the proportions of burden of disease attributable to foodborne transmission, other major pathways, and food categories for 29 viral, bacterial, parasitic, and chemical hazards, based on a structured expert judgment (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 1,463 assessments across 17 subregions within six WHO regions. Expert judgments were weighted using Cooke's Classical Model and reviewed by FERG. We found that 13 of 29 hazards were >50% foodborne. Vegetables and "fruits and nuts" were important sources for multiple enteric and invasive pathogens, and animal-source foods, including poultry, beef, eggs, seafood, and dairy remained critical targets for intervention. Regional differences highlight the influence of local epidemiology, 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 the most feasible approach to generate evidence supporting efforts to reduce foodborne disease.

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^{1,2}. 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^{3,4}. 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 hazards are not exclusively transmitted through food. Transmission depends on disease epidemiology, the type of hazard, and contextual factors, e.g., geography, seasonality, and local food consumption patterns and preparation practices⁵⁻⁷. Source attribution, where the proportion of disease attributable to contaminated food, and to specific food groups, is determined is therefore critical for estimating the burden of foodborne disease⁸⁻¹⁰. Source attribution also informs targeted disease prevention and food safety interventions, including resource allocation to maximize public health benefits and enables monitoring of intervention impacts⁴.

Source attribution methods include those based on public health surveillance, food consumption and food monitoring data, epidemiological studies, intervention studies, and structured expert judgements (SEJ)⁷. While data-driven methods are preferred, persistent data gaps have limited the use of such studies to a few hazards and countries^{11,12}. SEJ offers a framework to address these gaps and produce global source attribution estimates^{13,14}. SEJ has been applied in national studies and by the WHO to estimate foodborne illness source attribution^{6,14,15}.

Here, 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.

Methods

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^{16,17} based on the World Bank's four gross national income per-capita categories (Supplementary Table 1). Source attribution was derived using a SEJ approach 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.

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^{18,19}. 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* (classical 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.

Structured expert judgment

Full details of the process and steps taken within the SEJ study are detailed elsewhere²⁰. Briefly, on 10 July 2023 WHO opened a call for experts in food safety and related fields (e.g., microbiology, water, environment and hygiene)²¹. 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 SEJ team applied the Classical Model^{22,23}, which aggregates expert estimates based on performance on “calibration” variables from the experts’ field whose values were retrievable but not known by the experts themselves during the elicitation. Experts were scored on statistical accuracy and informativeness.

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 studies¹¹, and a summary of national food consumption patterns derived from Food and Agriculture Organization Food Availability Data for 2010 and 2020²⁰. 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 tool²¹. Expert data were aggregated by hazard and subregion and analyzed. All analyses were performed in R statistical software²⁴.

Each hazard-subregion panel required at least four experts²². 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).

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 process¹⁷.

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 whom 146 completed assessments, providing 1,463 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) (Figure 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^{6,14}. For *E. multilocularis*, elicited estimates were deemed inconsistent with empirical data, and estimates of attribution to food were obtained from a systematic review²⁵.

Source attribution results

Figures 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 Figures S1-6 and Data Supplement 1.

Transmission pathway-level attributions

Thirteen of the 29 hazards were >50% foodborne. Among enteric pathogens, *Campylobacter* (45-71%) and non-typhoidal *Salmonella* (59-74%) were predominantly foodborne in nearly all subregions, whereas the proportion of diarrheagenic *E. coli* (enterotoxigenic (29-79%), enteroaggregative (23-80%), and enteropathogenic (37-75%)), Shiga toxin-producing *E. coli* (STEC) (32-73%), and *Mycobacterium bovis*, *M. caprae*, and *M. orygis* (19-82%) that was foodborne varied by region (Table 3-5, Figures 2-7). *Cyclospora* was the only enteric protozoan 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 in the European Region and the Region of the Americas (30-50%). Foodborne transmission accounted for a smaller proportion of rotavirus (1-17%), norovirus (19-45%), and hepatitis A virus (28-53%) compared with human-to-human contact (Figures 2–7 and Data Supplement 1). *Fasciola* and *Fasciolopsis* were almost entirely foodborne (98–100%). *Ascaris* was attributed to both food and soil transmission, with foodborne

transmission highest in the European and South-East Asia Regions (56-85%), and soil transmission highest in the Western Pacific Region. *Entamoeba histolytica* was largely transmitted via water (29-56%) and human-to-human contact (~30-50%). *Trypanosoma cruzi* is only present in the Region of the Americas^{26,27} and was 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%)¹⁴. Foodborne attribution of *E. multilocularis* ranged from 4% to 58% in endemic sub-regions²⁵. Lead exposure was mainly foodborne in the South-East Asia Region (46-59%), whereas attribution to food within remaining 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 (Figures 2-7).

Food-level attributions

Food-level attribution estimates also varied across hazards and regions but showed consistent rankings for several pathogens. Poultry meat was the primary source of *Campylobacter* spp. in all subregions (36-74 %), followed by beef (9-12%) or dairy (5-28%). The top sources of *Salmonella* spp. included poultry meat (22-43%), pig meat (8-37%), and eggs (15-29%). Beef was the main source of Shiga toxin-producing *E. coli* (15-55%). Dairy contributed substantially to *L. monocytogenes* (22-57%) and *Brucella* spp. (35-94%, excluding Western Pacific C; Figures 2-7).

Vegetables, fruits and nuts, and fresh produce, were deemed to be the only source of *Cyclospora*, *Giardia*, *Cryptosporidium*, *Ascaris*, *E. granulosus*, and *Fasciola* and *Fasciolopsis*, and important sources of norovirus (~30-40%), rotavirus (25-85%), hepatitis A virus (~70 %), *Shigella* (20-85%), diarrheagenic *E. coli* (Enterotoxigenic/Enteropathogenic/Enterotoxigenic) (8-60%), *Entamoeba* (90-95%), and lead (7-50%). Shellfish was the leading food source for norovirus (22-60%), and finfish and shellfish for *Vibrio cholerae* (66-86%). Grains and beans (1-33%), and to a lower extent shellfish (3-

20%), were relevant sources of lead exposure (Figures 2-7). It was not possible to obtain food attributions for *E. multilocularis*.

Discussion

This study provides new subregional source-attribution estimates for 29 foodborne hazards across all WHO regions. Transmission pathways and food categories vary widely by hazard and subregion, reflecting diverse epidemiological dynamics shaped by biological characteristics, local socio-economic conditions, and food consumption patterns, and demonstrate the importance of locally relevant estimates. When combined with disease burden information, the study findings can be used to design and evaluate targeted, context-specific interventions across heterogeneous food systems, allowing policymakers and other stakeholders to prioritize resources, strengthen prevention strategies, and address food safety inequities.

Variation in attribution patterns across hazards and regions was expected, given global differences in pathogen epidemiology, agricultural systems, food supply chains, consumption behaviors, and cultural practices²⁸. Subregional heterogeneity was particularly evident in the European Region and the Region of the Americas. Some differences likely reflect real underlying variation, while others may arise from uneven data availability and 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 limitations highlight the need for stronger surveillance, more empirical research, and locally tailored control strategies. Although regional estimates support high-level planning, effective public health action ultimately depends on interventions adapted to local contexts.

Enteric pathogens, e.g., *Campylobacter* and non-typhoidal *Salmonella*, were predominantly foodborne across all regions and subregions, consistent with available national-level, empirical attribution studies^{11,29–36}. 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.

As expected, 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 enterica*), pork (Non-typhoidal *Salmonella enterica*), meat from small ruminants (Shiga toxin-producing *E.coli*, other diarrheagenic *E. coli*, *Brucella* spp.), and dairy products (*Listeria monocytogenes*, *Brucella* spp.). Our findings 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*^{19,37–39}. As dietary guidelines and food system interventions worldwide increasingly promote plant-rich diets⁴⁰, simultaneously reducing foodborne hazard contamination on plant foods will be particularly important. Hazard- and subregion-specific attribution estimates can assist in this effort, identifying specific foods where interventions are needed to ensure diets are 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^{6,14}. 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 Figure S2) ¹⁴. 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.

Our food attribution estimates are generally aligned with previously published estimates¹¹. When comparing our regional estimates with country-specific estimates within those regions, available for 25 pathogens, we observed similar rankings for most (Supplementary Figures S2). Notably, for well-studied pathogens, like *Salmonella*, variation in attribution estimates across certain sources highlights both the value of comprehensive assessments like ours and the importance of country-level studies, which may capture genuine differences in the relative contribution of different sources within 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 ²². 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 LMICs, 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 detailed insights into the relative contributions of major transmission pathways to disease burden, and specific foods to foodborne transmission. These findings are particularly valuable for low and middle-income countries, where surveillance for foodborne diseases is limited and reliable data for prioritization remain scarce. Our results complement data-driven approaches, strengthen the evidence base for targeting food safety interventions, identify areas for empirical source attribution data collection, and support public health policy, surveillance, and control strategies. By offering globally consistent baseline estimates, our results fill a critical evidence gap and point to priority areas for intervention and research. Beyond direct public health applications, these estimates also inform wider global health debates, including dietary guidance and food system transformation, ensuring that both nutritional benefits and food safety risks are fully considered in policy and research agendas.

Data Sharing Statement

Data collected for this study and the analysis code are publicly available at Nane et al.²⁰, the GitHub repository [WorldHealthOrganization/FERG_2025](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/2nd-edition-\(2026\)](https://www.who.int/teams/nutrition-and-food-safety/monitoring-nutritional-status-and-food-safety-and-events/foodborne-disease-estimates/2nd-edition-(2026)). The overall study and modelling steps are available at Nane et al.²⁰.

Role of the funding source

WHO funded the structured expert judgement study that provided data for this analysis. WHO recruited experts who participated in the study and the elicitors who conducted the expert elicitations, coordinated the overall project and the country consultation process. WHO cleared the paper in terms of methods

and approach and results. WHO technical officers (YM, CR) participated in drafting the manuscript and the decision to submit it for publication.

Competing interests

Co-author Willy Aspinall is the owner of Aspinall Consulting Ltd. He was supported partly by TUDelft through a sub-contract. While the specific roles of this author are articulated in the 'author contributions' section, Aspinall Consulting Ltd. did not have any additional role in the study design, data collection and analysis, decision to publish, or preparation of the manuscript.

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Supplementary Information

Supplementary Table 1. Classification of World Health Organization Members States according to WHO Regions and subregional clusters adopted for the WHO foodborne disease estimates 2026 edition

Supplementary Table 2. List of 42 hazards included in the WHO foodborne disease estimates 2026 edition

Supplementary Table 3. Overview of blocked pathways and foods for 21 diarrhoeal disease and invasive enteric disease and intoxication hazards included in the structure expert judgement for the WHO attribution of foodborne hazards to transmission pathways and foods

Supplementary Table 4. Overview of blocked pathways and foods for seven parasitic hazards included in the structure expert judgement for the WHO attribution of foodborne hazards to transmission pathways and foods

Supplementary Table 5. Criteria for selection of experts for the structured expert judgement for the World Health Organization attribution of foodborne hazards to transmission pathways and foods

Supplementary Table 6. Number of expert assessments per hazard and sub-region for the World Health Organization attribution of foodborne hazards to transmission pathways and foods

Supplementary Figures 1-6. Detailed source attributions (median, 2.5% and 97.5% percentiles) for all hazards in each region and subregion.

Supplementary Figure S1. Attributions (median, 2.5% and 97.5% percentiles) to transmission pathways to foods for 29 hazards for the African Region.

Supplementary Figure S2. Attributions (median, 2.5% and 97.5% percentiles) to transmission pathways to foods for 29 hazards for the Region of the Americas.

Supplementary Figure S3. Attributions (median, 2.5% and 97.5% percentiles) to transmission pathways to foods for 29 hazards for the Eastern Mediterranean Region.

Supplementary Figure 4. Detailed attributions (median, 2.5% and 97.5% percentiles) to transmission pathways to foods for 29 hazards for the European Region.

Supplementary Figure S5. Attributions (median, 2.5% and 97.5% percentiles) to transmission pathways to foods for 29 hazards for the South-East Asia Region.

Supplementary Figure S6. Attributions (median, 2.5% and 97.5% percentiles) to transmission pathways to foods for 29 hazards for the Western Pacific Region.

Supplementary Figure S7. Estimated attribution proportion to main pathways in FERG 2015 (median and 95% Confidence Interval) (Hald et al., 2016) and FERG 2026 (mean and 95% Confidence Interval) for nine enteric hazards.

Supplementary Figure 9. Estimated attribution proportion to main pathways (mean and 95% Confidence Interval) in FERG 2015 (Hald et al., 2016) and FERG 2026 for invasive parasites.

Supplementary Figure 9. Estimated attribution proportion to main pathways in FERG 2015 (median and 95% Confidence Interval) (Hald et al., 2016) and FERG 2026 (mean and 95% Confidence Interval) for lead.

Supplementary Data, Tables S1-S28. Estimated attribution to transmission pathways and specific foods of 28 hazards for 17 sub-regions (mean, median, and 95% confidence interval)

Supplementary Figures 10. Estimated attribution to food categories in FERG 2026 and estimated in previous source attribution studies (mean and 95% Confidence Intervals). Estimates extracted from Davydova et al. (2025).

Supplementary Data 1. Source data for Figures 2-7 and Supplementary Figures S1-S6.

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Table 1. Transmission pathway definitions and food groups considered in the WHO global expert judgment 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.

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)
<i>Campylobacter</i> spp.	<i>Brucella</i> spp.	<i>Ascaris</i> spp.	Lead
<i>Cryptosporidium</i> spp.	<i>Clostridium botulinum</i>	<i>Echinococcus multilocularis</i>	
<i>Cyclospora</i>	Hepatitis A virus	<i>Echinococcus granulosus</i>	
<i>Entamoeba histolytica</i>	<i>Listeria monocytogenes</i>	<i>Trypanosoma cruzi</i>	
Enteroaggregative <i>E. coli</i>	<i>Mycobacterium bovis/caprae/orygis</i>	<i>Fasciola</i> spp. & <i>Fasciolopsis buski</i>	
Enteropathogenic <i>E. coli</i>	<i>Salmonella</i> Paratyphi*	<i>Toxoplasma gondii</i>	
Enterotoxigenic <i>E. coli</i>	<i>Salmonella</i> Typhi	<i>Trichinella</i> spp.	
<i>Giardia</i> spp.			
Norovirus			
Rotavirus			
Non-typhoidal			
<i>Salmonella enterica</i>			
<i>Shigella</i> spp.			
Shiga toxin-producing <i>E. coli</i>			
<i>Vibrio cholerae</i>			

*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.

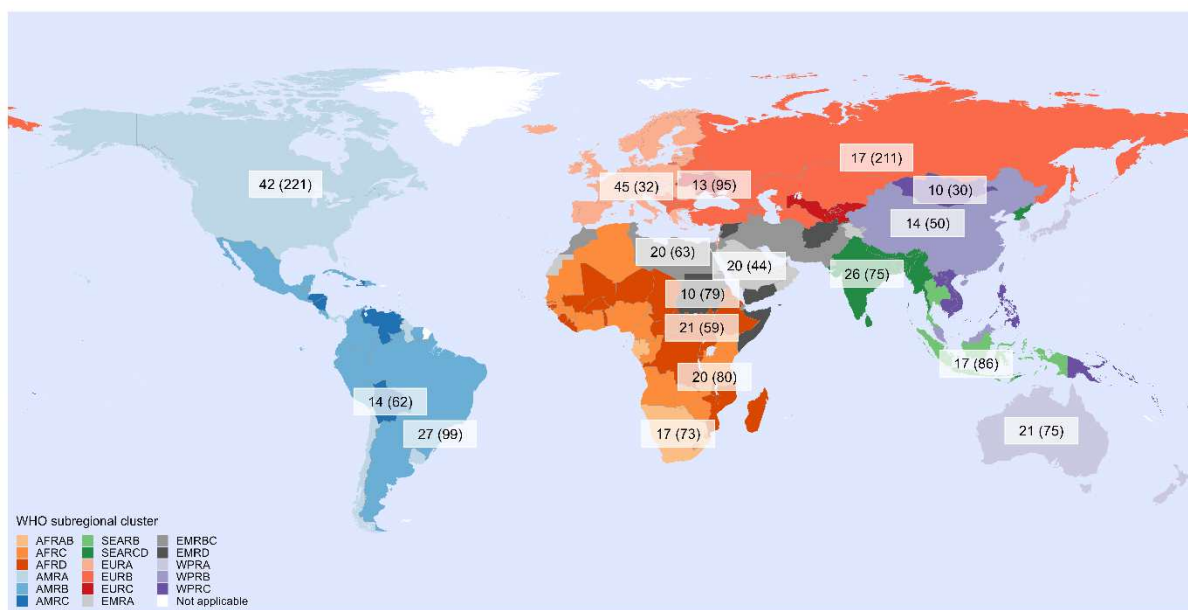


Figure 1. Number of expert assessments per WHO region. Assessments cover all hazards. See Supplementary Table 6 for detailed information on the number of expert assessments per hazard-subregion.

Region AFR

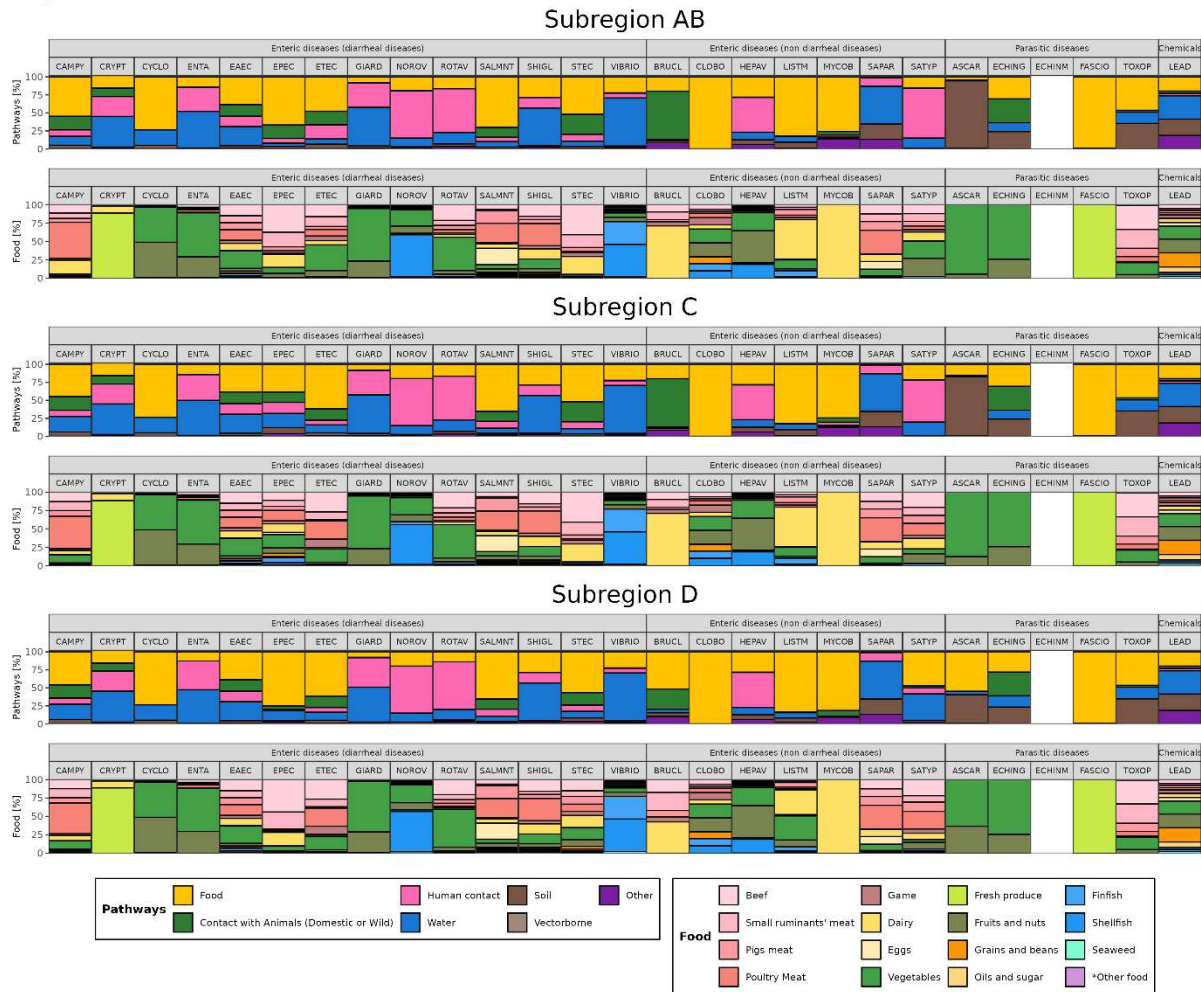


Figure 2. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in the subregions of the African Region, AFR. Transmission “vector-borne” is applicable only to *T. cruzi* in the Region of the Americas (AMR). The category “other food” in 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 = Enterotoxigenic *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD

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Region AMR

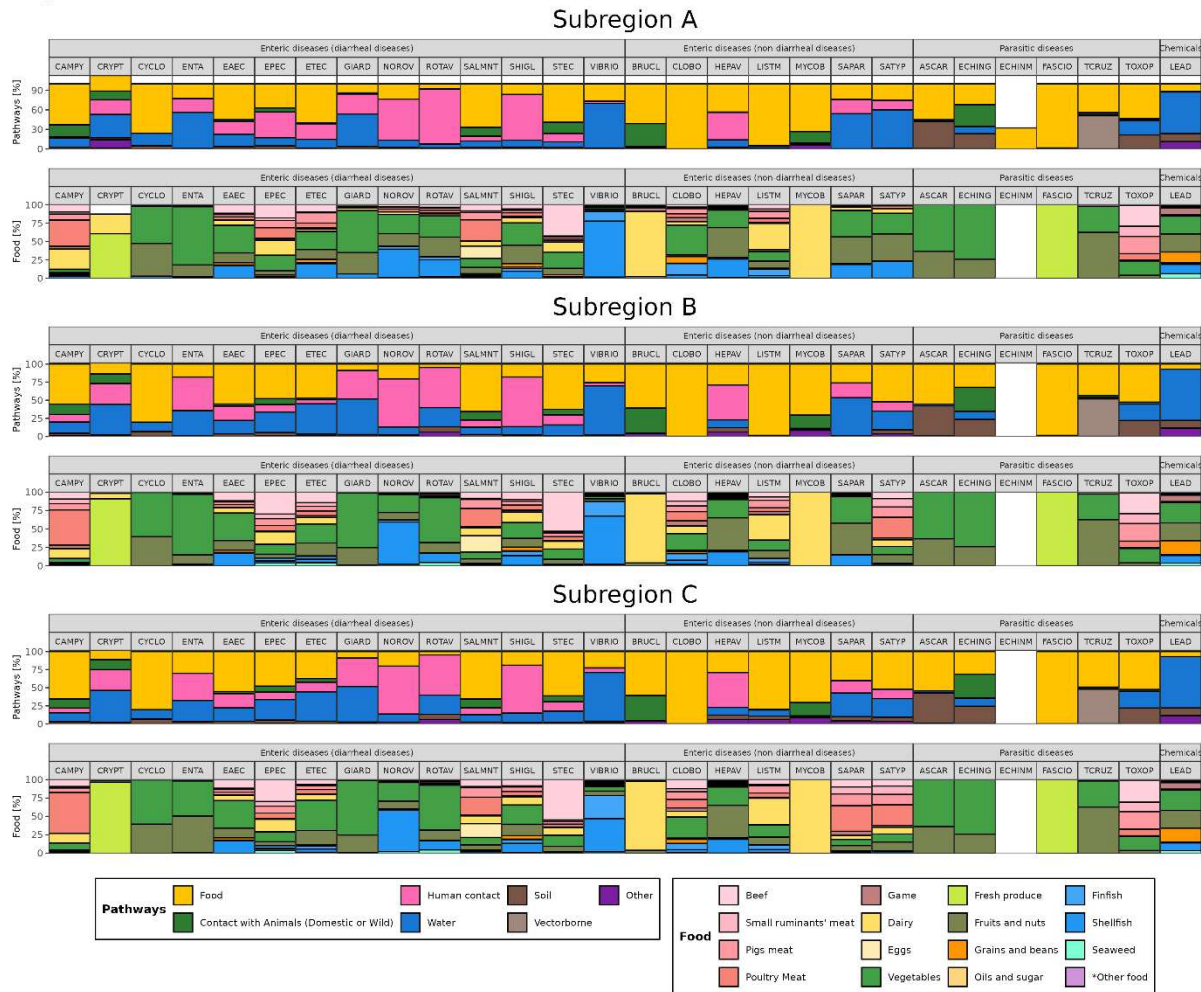


Figure 3. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the Region of Americas, AMR. The category “other food” in the food groups applies only to *Cryptosporidium* and includes all remaining food groups except “dairy” and “fresh produce”. Where estimated, “fresh produce” applies only to *Cryptosporidium* and *Fasciola/Fasciolosis*, 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 = Enterotoxigenic *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD

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Region SEAR

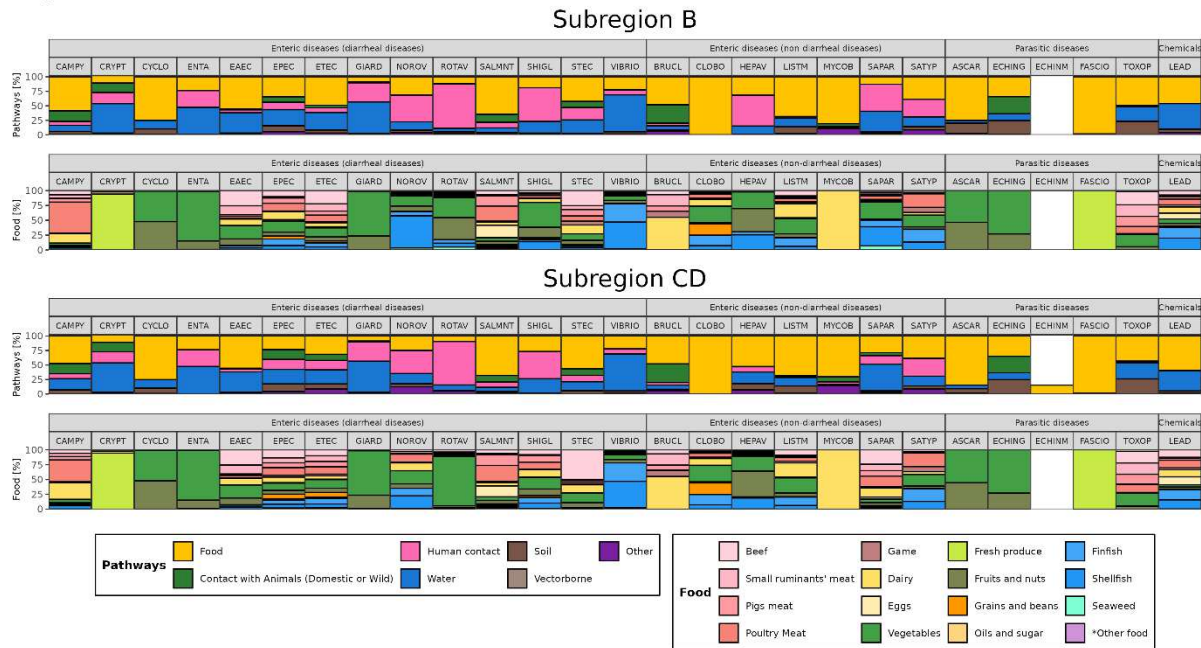


Figure 4. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the Southeast Asian Region, SEAR. Transmission “vector-borne” is applicable only to *T. cruzi* in the Region of Americas. The category “other food” in the 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*; HEPAN = 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.

Region EUR

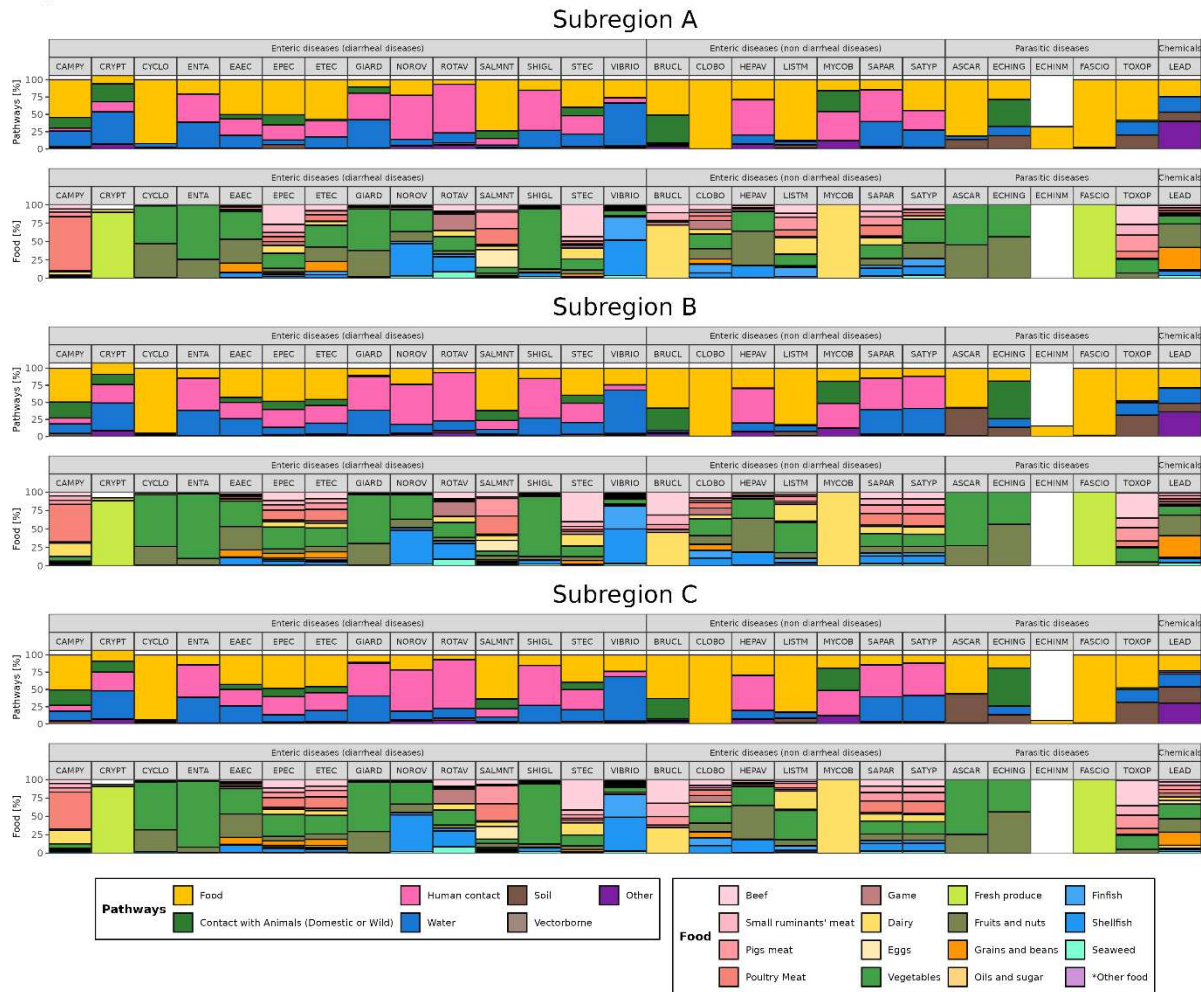


Figure 5. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the European Region, EUR. Transmission “vector-borne” is applicable only to *T. cruzi* in the Region of Americas. The category “other food” in the food groups 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 = Enteropathogenic *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD

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Region EMR

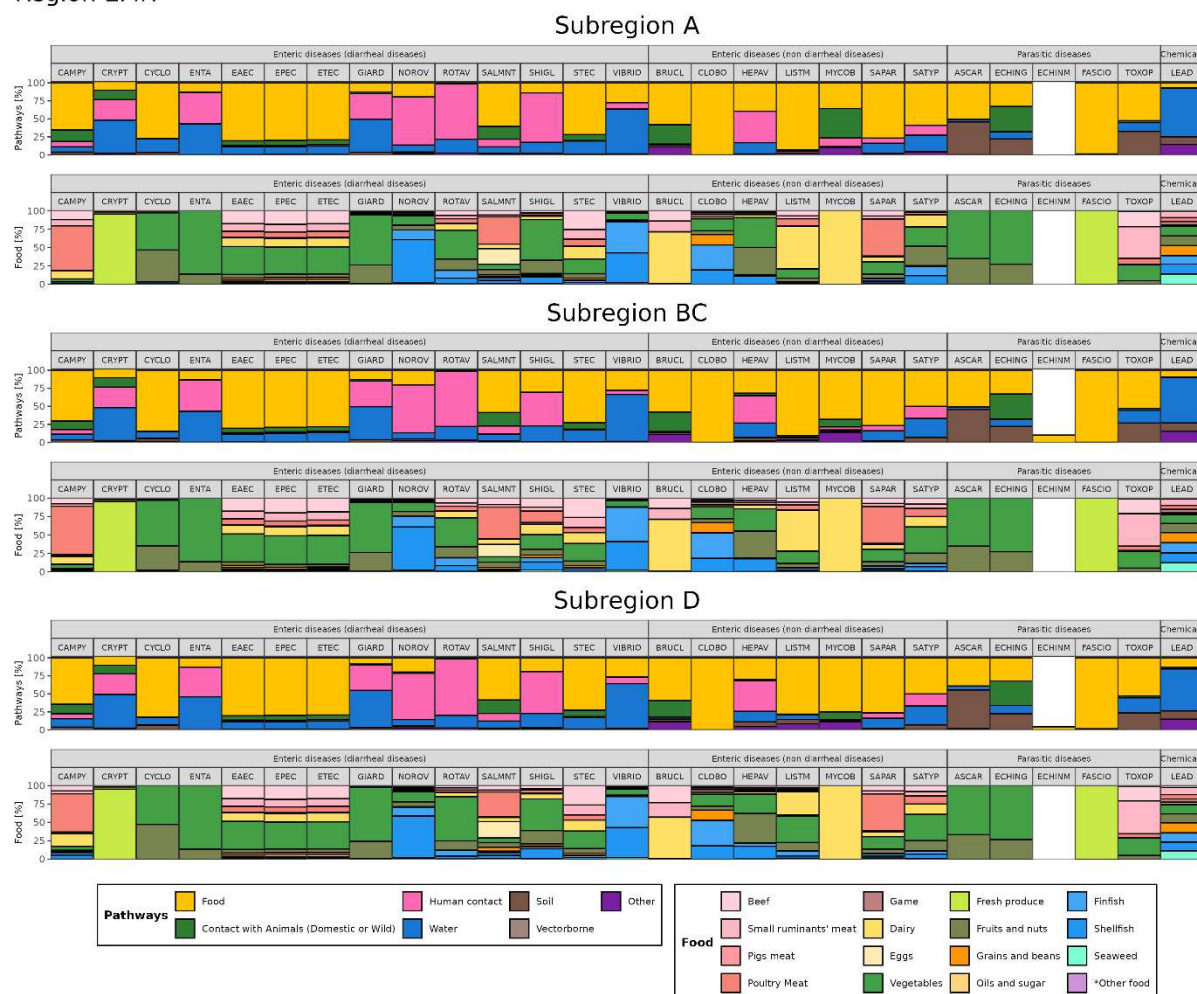


Figure 6. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the Eastern Mediterranean Region, EMR. Transmission “vector-borne” is applicable only to *T. cruzi* in the Region of Americas. The category “other food” 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 = Enteropathogenic *E. Coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*;

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Region WPR

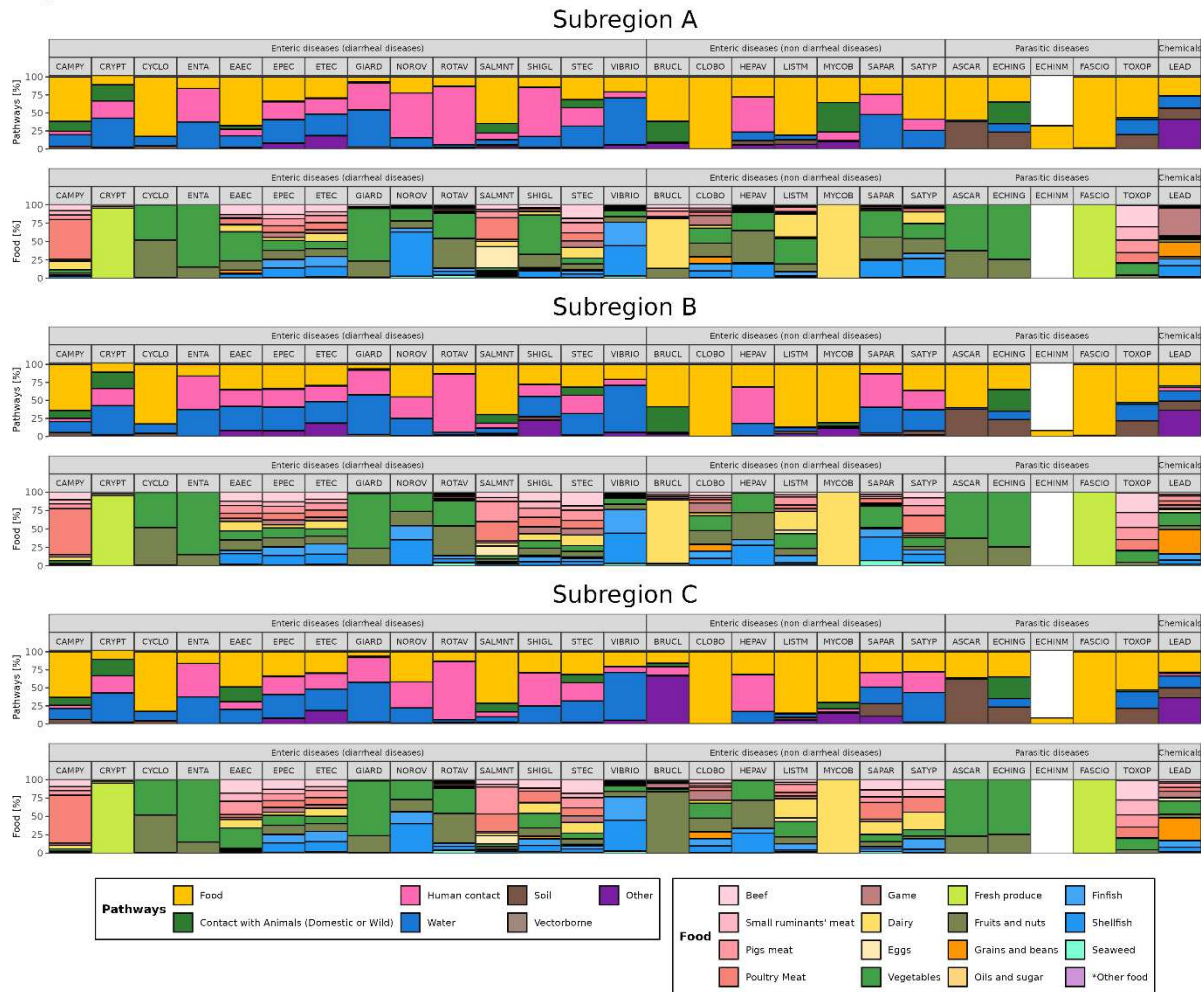


Figure 7. Attribution of illness (mean %) by enteric, parasitic, and chemical hazards to transmission pathways and specific foods in sub-regions of the Watern Pacific Asian Region, WPR. Transmission “vector-borne” is applicable only to *T. cruzi* in the Region of Americas. The category “other food” in 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 = Enteropathogenic *E. coli*; EPEC = Enteropathogenic *E. coli*; ETEC = Enterotoxigenic *E. coli*; GIARD

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