WHO estimates of the global, regional, and national burden of eight foodborne non-diarrhoeal enteric disease hazards, 2000–21: an updated data synthesis

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Summary

Background Foodborne diseases cause substantial illness and death globally. We updated WHO estimates of the burden caused by non-diarrhoeal enteric disease hazards: *Brucella* spp; *Clostridium botulinum*; hepatitis A virus; *Listeria monocytogenes*; *Mycobacterium bovis*, *Mycobacterium caprae*, and *Mycobacterium orygis*; invasive non-typhoidal *Salmonella enterica* (iNTS); *S enterica* serotypes Paratyphi A, B, and C; and *S enterica* serotype Typhi (*S* Typhi).

Methods We estimated illnesses, deaths, and disability-adjusted life-years (DALYs) for 194 countries for 2000–21 using data from systematic reviews, the 2021 Global Burden of Diseases, Injuries, and Risk Factors Study 2021, a structured expert judgement study, and WHO country consultations. We used disease-specific computational models and hierarchical metaregression modelling with geographical clustering, a global linear time trend, and uncertainty propagation.

Findings In 2021, transmission of these eight hazards by food collectively caused 24·0 million illnesses (95% uncertainty interval 16·9–31·7), 106 000 deaths (63 900–169 000), and 7·26 million DALYs (4·15–12·0). *S* Typhi, iNTS, and hepatitis A virus caused most DALYs. The greatest burden was in the WHO African region, followed by the South-East Asia region. Mortality was 5·2 times higher and DALY rates were 8·3 times higher in children younger than 5 years compared with people aged 5 years and older. The burden for all hazards, except *L monocytogenes*, decreased from 2000 to 2021, with *S* Typhi replacing iNTS as the leading cause of foodborne DALYs.

Interpretation Non-diarrhoeal enteric diseases still cause considerable foodborne disease burden, despite decreases over time. Vulnerable populations, particularly children in low-income countries, bear the greatest burden. Integrated efforts including vaccination, food safety, clean water, sanitation, hygiene, and improved health-care access are required.

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Introduction

Foodborne enteric diseases are an important cause of illness and death globally.[1,2] Although many predominantly manifest as diarrhoea, agents such as hepatitis A virus (HAV), *Listeria monocytogenes*, and *Salmonella enterica* serotype Typhi (*S* Typhi) are primarily invasive, causing manifestations including bacteraemia, hepatitis, and meningitis.[1,2] Although the incidence of invasive enteric diseases is lower than for diarrhoeal diseases, the associated mortality is high, resulting in a similar disease burden.[1] Other enteric hazards produce potent toxins in improperly preserved foods. Notably, *Clostridium botulinum* and related clostridial species produce toxins causing botulism, a severe illness affecting the nervous system that can be fatal.[3]

WHO, with support from the Foodborne Disease Burden Epidemiology Reference Group (FERG), estimated that invasive enteric pathogens transmitted via contaminated food resulted in 25·6 million illnesses, 147 000 deaths, and 9·11 million disability-adjusted life-years (DALYs) globally in 2010, with a disproportionately high burden in low-income and middle-income countries and among children younger than 5 years.[1,2] Estimates for four agents causing intoxication, including *C botulinum*, were generated for high-income countries only, due to insufficient data elsewhere.[1]

Global-level and national-level data on foodborne disease burden remain essential to justifying food safety and other disease prevention investments. In response to a World Health Assembly mandate to update estimates,[4] WHO reconvened the FERG technical advisory group in 2021 to estimate the global burden due to 42 hazards.[5–7] The Enteric Diseases Task Force provided technical leadership on estimating the burden of enteric diseases from viruses, protozoa, and bacteria, supported by the large network of

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Research in context

Evidence before this study

In 2015, WHO published the first global burden of foodborne diseases estimates; these showed that in 2010, invasive enteric agents transmitted via contaminated food resulted in 25·6 million illnesses, 147 000 deaths, and 9·11 million disability-adjusted life-years (DALYs) globally, with disproportionately high burden in low-income and middle-income countries and among children younger than 5 years. Estimates for four agents causing intoxication, including *Clostridium botulinum*, were generated for high-income countries only, due to insufficient data in much of the world. Although subsequent global estimates have shown that the burden of major invasive enteric pathogens—such as *Salmonella enterica* serotypes Typhi, Paratyphi A, Paratyphi B, and Paratyphi C, and hepatitis A virus (HAV)—are generally declining, updated estimates specific to foodborne transmission, and for other important foodborne pathogens such as *Listeria monocytogenes,* are absent. In 2020, the 73rd World Health Assembly called for updated global burden of foodborne disease estimates to support countries in improving food safety systems, and in 2021, WHO reconvened the Foodborne Disease Burden Epidemiology Reference Group to provide technical leadership on this task. From Sept 1, 2021 to Dec 15, 2022, we iteratively searched MEDLINE, PROSPERO, and healthdata.org to identify globally relevant estimates of the incidence, mortality, or DALYs caused by seven invasive enteric disease hazards and one intoxication hazard (hereafter non-diarrhoeal enteric disease hazards: *Brucella* spp; *C botulinum;* HAV; *L monocytogenes*; *Mycobacterium bovis, caprae,* and *orygis;* invasive non-typhoidal *S enterica* [iNTS]; *S* Paratyphi A, B, and C; and *S* Typhi). We searched by pathogen name, disease name (eg, brucellosis), and metric keywords (eg, incidence, burden, and DALYs), and considered studies in all languages. For hazards without estimates, WHO commissioned a series of systematic reviews on the incidence, aetiology, sequelae, and case fatality or mortality, to which we added further data meeting review inclusion criteria identified during WHO country consultation with member states.

Added value of this study

These findings provide updated global and regional estimates, and the first national estimates for 194 countries, of the foodborne burden of eight non-diarrhoeal enteric disease hazards for the period 2000–21. In 2021, these hazards resulted in 15·1 million DALYs, of which almost half (7·26 million DALYs) were due to contaminated food. Despite declines over time, these hazards have remained substantial causes of foodborne disease burden particularly in children younger than 5 years—in whom the burden was ten times that in older children and adults—and in low-income and middle-income countries, with the burden highest in the African region, followed by the South-East Asia region and the Eastern Mediterranean region. S Typhi, iNTS, and HAV have remained responsible for the greatest foodborne burden among hazards considered here, although this varied by region and country. By 2021, S Typhi had replaced iNTS as the leading cause of foodborne DALYs globally. These findings show, for the first time, internally consistent national patterns and changes in foodborne disease burden over time, with substantial improvements in the past decades for many hazards but not all, and with persisting inequalities revealed.

Implications of all the available evidence

Improved safety of the worldwide food supply and in water and sanitation, and the impact of human and animal vaccination programmes, have contributed to a general decline in the foodborne disease burden due to non-diarrhoeal enteric hazards. Nevertheless, the current burden of non-diarrhoeal enteric diseases remains high enough for countries and national and international health and food safety agencies to justify targeted and context-specific interventions to prevent foodborne diseases, and improved health-care access to mitigate serious consequences, focusing on young children for whom there is the greatest need. Interventions include: food supply chain improvements such as pasteurisation and prevention of food contamination during growing, harvest, processing, and preparation; further improvements in water and sanitation; consumer food safety programmes that improve safe handling and preparation of food by individuals; expanded human vaccination programmes; and elimination efforts and vaccination in animals. These estimates, together with new WHO estimates of the foodborne burden due to diarrhoeal, invasive parasitic, and chemical hazards, provide a comprehensive picture of the full global burden of foodborne diseases.

WHO collaborators.[7] In this study, we report updated WHO estimates of incidence, mortality, and DALYs for 194 countries for the period 2000–21 caused by seven invasive enteric disease hazards and one intoxication hazard (hereafter, non-diarrhoeal enteric disease hazards), defined as the following groups: *Brucella* spp; *C botulinum;* HAV; *L monocytogenes*; *Mycobacterium bovis, caprae,* and *orygis* (hereafter zoonotic *Mycobacterium* tuberculosis complex, MTBC); invasive non-typhoidal *S enterica* (iNTS); *S enterica* serotypes Paratyphi A, Paratyphi B, and Paratyphi C (*S* Paratyphi A, B, and C)*;* and *S* Typhi.

Methods

Overall approach

We estimated the global, regional, and national disease burden of foodborne hazards for all people over time for 2000–21 inclusive, following a standard FERG protocol by which the 42 FERG hazards were analysed using the same computational framework by a single analysis team.[7,8] For each hazard, we either used an envelope approach or used a natural history approach when a syndrome or disease envelope was absent (appendix 1 p 8). We followed global health (GATHER)[9] and burden of disease (STROBOD)[10]

study reporting guidelines (appendix 1 pp 47–56), and report regional results for the six WHO regions.[7,8]

The Enteric Diseases Task Force systematically assessed potential hazards using a risk prioritisation matrix (appendix 1 pp 2–4),[8] excluding those we considered infrequently foodborne or with sparse data. 21 enteric disease hazards were identified (appendix 1 pp 4–5), including the eight above.

WHO commissioned a series of systematic reviews on the incidence, aetiology, sequelae, and case fatality or mortality of these hazards, which formed the basis of our estimation. We also used draw-level estimates from the Global Burden of Diseases, Injuries, and Risk Factors Study (GBD) 2021, stratified by age, sex, country, and year from 2000 to 2021, obtained directly from the Institute for Health Metrics and Evaluation (appendix 1 pp 6, 9–21). We included additional data that met review inclusion criteria identified during internal FERG review and the WHO obligatory country consultation process (appendix 1 p 7). For HAV, zoonotic MTBC, and iNTS, we considered subregions, which were the six WHO regions subdivided by World Bank income classifications (appendix 1 pp 11, 14–17).[8]

All decisions, data sources, reviews, and assumptions are detailed and referenced in appendix 1; datapoints by hazard used in the analyses are detailed elsewhere.[8]

Estimating illnesses, sequelae, and deaths

For HAV, *S* Paratyphi A, B, and C, and *S* Typhi, we used draw-level incidence and mortality estimates from GBD 2021 to estimate the incidence of acute hepatitis A, paratyphoid fever (including the sequela paratyphoid intestinal perforation), typhoid fever (including the sequelae typhoid intestinal perforation and gastrointestinal bleed), and mortality. Following feedback during the WHO country consultation process, acute hepatitis incidence estimates in subregion A countries were reduced by a factor of 58 (appendix 1 p 11), to align estimated incidences with countries' current HAV case numbers from established national surveillance systems, corrected for underascertainment.

We used data from a review to estimate the incidence of acute and chronic brucellosis and associated mortality caused by *Brucella* spp (appendix 1 pp 9–10). 30 countries with *Brucella*-free status in both domestic and wild animals in 2021 per the World Organisation for Animal Health were assigned the lowest estimated incidence from the review (appendix 1 p 9). We used data from a review on perinatal and non-perinatal listeriosis to estimate the incidence of invasive *L monocytogenes* infections,[11] which included septicaemia (defined as bacteraemia), central nervous system infection, and neurological sequelae, and estimated mortality from a previous review (appendix 1 pp 12–14).[11] We used data from a review to estimate the incidence and mortality of classic foodborne botulism in people aged 5 years and older caused by *C botulinum* (appendix 1 pp 21–22). We used data from an update of a previous review (appendix 1 pp 16–18)[12,13] to estimate the incidence of iNTS disease, with an adjustment for the fraction of iNTS resulting from HIV using country-specific population-attributable fractions from GBD 2021, stratified by 5-year increment and age, obtained directly from the Institute for Health Metrics and Evaluation (appendix 1 p 17).

See Online for appendix 1

For zoonotic MTBC, we estimated the incidence and mortality using an envelope approach. We used incidence and mortality estimates for all tuberculosis for 2021 from GBD Compare,[14] and applied the proportion of tuberculosis that is zoonotic based on a review (appendix 1 pp 14–16). 70 countries with tuberculosis-free status in both domestic and wild animals, in 2020 according to the World Organisation for Animal Health or in 2022 according to the EU, were assigned the lowest proportion of tuberculosis that was zoonotic from the review. Mortality was reduced by 20% in all countries, to account for zoonotic tuberculosis causing more extrapulmonary infections that have a lower case-fatality ratio than pulmonary infections. WHO data for all tuberculosis were used to estimate the age and sex distribution of zoonotic MTBC (appendix 1 pp 14–16).

We aimed to collect sex-disaggregated data, and specified sex-specific distributions where data were available (appendix 1 pp 9–22).

Estimating DALYs

We calculated years lived with disability and years of life lost due to premature mortality following a standard approach detailed elsewhere (appendix 1 p 6).[8]

Estimating the proportion foodborne

To estimate the proportion of each hazard transmitted by contaminated food, we used results from a WHO-commissioned structured expert judgment study, where 83 distinct experts provided 245 specific hazard–subregion assessments across the 17 subregions.[15] For *L monocytogenes* and *C botulinum*, we considered 100% foodborne transmission.[1,2]

Statistical analysis

Analyses were done in R (version 4.5.0) to estimate illnesses, deaths, and DALYs by country-year using disease-specific computational models, as summarised in appendix 1 (pp 6–7) and detailed elsewhere (including data manipulations and modelling specifics).[8]

Role of the funding source

The study funder contributed to: reviews, review updates, and the structured expert judgment study (and helping to recruit experts and elicitors) that provided the data used; the computations (Sciensano); and expert consultation (University of Florida). The study funder managed the overall project and the country consultation process that identified additional data, although the Enteric Diseases Task Force determined whether data met inclusion criteria. The study funder cleared the paper in terms of methods and approach. WHO technical officers (YM and CR)

	Illnesses	Deaths	DALYs	Proportion of illnesses that are foodborne*	Foodborne illnesses	Foodborne deaths	Foodborne DALYs
Invasive enteric hazards	66 400 000 (59 800 000–73 100 000)	212 000 (137 000–316 000)	15 100 000 (9 590 000–23 000 000)	0·362 (0·261–0·463)	24 000 000 (16 900 000–31 700 000)	106 000 (63 900–169 000)	7 260 000 (4 150 000–12 000 000)
Brucella spp	225 000 (115 000–565 000)	21 (4–65)	10 800 (4570–27 000)	0·527 (0·337–0·710)	119 000 (51 800–312 000)	11 (2–37)	5730 (2180–16 600)
Hepatitis A virus	56 100 000 (49 500 000–62 000 000)	27 400 (18 700–43 200)	1 860 000 (1 270 000–2 950 000)	0·356 (0·238–0·466)	20 000 000 (13 100 000–26 600 000)	11 900 (4860–22 900)	821 000 (334 000–1 530 000)
Listeria monocytogenes	22 800 (8480–71 800)	5280 (1910–16 300)	192 000 (69 700–588 000)	1·000 (1·000–1·000)	22 800 (8480–71 800)	5280 (1910–16 300)	192 000 (69 700–588 000)
Mycobacterium bovis, caprae, and *orygis*	193 000 (102 000–346 000)	21 800 (12 000–38 400)	949 000 (536 000–1 620 000)	0·716 (0·514–0·846)	138 000 (69 900–256 000)	15 800 (8280–28 600)	689 000 (367 000–1 220 000)
Salmonella enterica, non-typhoidal invasive	437 000 (184 000–1 030 000)	48 200 (17 700–118 000)	3 540 000 (1 300 000–8 500 000)	0·655 (0·541–0·754)	286 000 (119 000–663 000)	31 500 (11 300–77 100)	2 310 000 (828 000–5 660 000)
Salmonella enterica Paratyphi A, B, and C	2 170 000 (1 570 000–2 970 000)	14 200 (6350–28 500)	1 060 000 (477 000–2 070 000)	0·348 (0·136–0·560)	757 000 (296 000–1 400 000)	5340 (1740–11 700)	400 000 (134 000–880 000)
Salmonella enterica Typhi	7 230 000 (5 630 000–9 300 000)	94 700 (46 900–161 000)	7 450 000 (3 800 000–12 900 000)	0·381 (0·155–0·634)	2 740 000 (1 060 000–4 940 000)	36 000 (11 900–74 600)	2 840 000 (960 000–5 910 000)
Intoxications	667 (375–1250)	35 (14–74)	1530 (611–3240)	1·000 (1·000–1·000)	667 (375–1250)	35 (14–74)	1530 (611–3240)
Clostridium botulinum	667 (375–1250)	35 (14–74)	1530 (611–3240)	1·000 (1·000–1·000)	667 (375–1250)	35 (14–74)	1530 (611–3240)
Total	66 400 000 (59 800 000–73 100 000)	212 000 (137 000–316 000)	15 100 000 (9 590 000–23 000 000)	0·362 (0·261–0·463)	24 000 000 (16 900 000–31 700 000)	106 000 (63 900–169 000)	7 260 000 (4 150 000–12 000 000)

Data are mean (95% uncertainty interval). DALY=disability-adjusted life-year. *Attribution estimates were derived subregionally; proportions shown here were calculated from the estimated total number of illnesses and the total number that were foodborne.

Table 1: **Global numbers of foodborne illnesses, deaths, and DALYs by non-diarrhoeal enteric disease hazard, 2021**

participated in drafting the manuscript and the decision to submit it for publication.

Results

In 2021, the eight non-diarrhoeal enteric disease hazards caused 66·4 million illnesses (95% uncertainty interval 59·8–73·1), of which 667 illnesses (375–1250) were due to *C botulinum* (table 1). The most frequent causes of illness were HAV, *S* Typhi, and *S* Paratyphi A, B, and C (table 1). *L monocytogenes* resulted in 22 800 illnesses (8480–71 800), of which 3600 (1200–12 000; 15·8%) were perinatal and 19 200 (7200–58 800; 84·2%) were non-perinatal.

Overall, 24·0 million (36·1% [uncertainty interval 26·1–46·3]) of the 66·4 million illnesses in 2021 were due to foodborne transmission (table 1), of which 2·47 million (uncertainty interval 1·61–3·48; 10·3%) were in children younger than 5 years. The most frequent foodborne causes were the same as the most frequent causes from all routes of transmission: HAV (20·0 million foodborne illnesses [13·1–26·6]), *S* Typhi (2·74 million foodborne illnesses [1·06–4·94]), and *S* Paratyphi A, B, and C (757 000 foodborne illnesses [296 000–1 400 000]); this rank order was the same in both age groups (table 2). Children younger than 5 years had a higher mean incidence of foodborne illnesses due to *L monocytogenes*, iNTS, *S* Paratyphi A, B, and C, and *S* Typhi, whereas those aged 5 years and older had a higher mean incidence of foodborne illnesses due to *Brucella* spp, HAV, and zoonotic MTBC compared with the other age group (table 2). Intoxication due to *C botulinum* was only estimated for individuals aged 5 years and older. Data were not robust enough to generate sex-disaggregated estimates.

The estimated incidence of foodborne illness due to the eight hazards became consistently smaller across the 2000–21 period in all regions (appendix 1 pp 32–34). iNTS (appendix 1 pp 32–34) and other hazards generally showed this same trend of either no change or a general decrease over time, with two exceptions noted below. We observed a pattern of convergence: regions that had higher incidences in 2000 generally had faster decline than regions with lower incidences, most notably for HAV and *S* Typhi in the South-East Asia region, and for iNTS in the African region. Exceptions to overall declining trends were *L monocytogenes* (increase; appendix 1 pp 32–34) and *Brucella* spp (stable).[16]

In 2021, the highest incidence of foodborne non-diarrhoeal enteric illnesses was in the South-East Asia region (appendix 1 pp 27–31, figure 1A), followed by the Eastern Mediterranean and African regions. The highest incidence of foodborne botulism was in the European region, followed by the Eastern Mediterranean and South-East Asia regions. HAV was the most frequent cause of foodborne illnesses in all WHO regions, and *S* Typhi was the second (African, Eastern Mediterranean, South-East Asia, and Western Pacific regions) or third (region of the Americas) most frequent cause in all regions except the European region, where iNTS was the second leading

	Age younger than 5 years			Age 5 years and older		
	Illnesses	Deaths	DALYs	Illnesses	Deaths	DALYs
Invasive enteric hazards	365·4 (237·3–513·6)	5·17 (2·56–9·15)	470·4 (233·0–830·6)	299·7 (206·2–391·3)	0·985 (0·620–1·53)	56·7 (34·7–91·1)
Brucella spp	0·352 (0·153–0·922)	<0·001 (<0·001–<0·001)	0·018 (0·007–0·053)	1·62 (0·705–4·25)	<0·001 (<0·001–<0·001)	0·078 (0·030–0·225)
Hepatitis A virus	177·9 (105·4–260·2)	0·530 (0·168–1·12)	48·8 (15·8–102·8)	260·8 (168·8–351·0)	0·116 (0·051–0·225)	6·81 (3·08–12·5)
Listeria monocytogenes	0·315 (0·086–1·05)	0·063 (0·020–0·194)	5·94 (1·86–18·3)	0·287 (0·110–0·898)	0·067 (0·024–0·208)	2·11 (0·755–6·48)
Mycobacterium bovis, caprae, and *orygis*	0·981 (0·585–1·49)	0·133 (0·077–0·210)	12·5 (7·24–19·7)	1·82 (0·914–3·41)	0·207 (0·107–0·381)	8·40 (4·36–15·2)
Salmonella enterica, non-typhoidal invasive	17·3 (6·88–39·2)	1·93 (0·658–4·61)	174·1 (59·5–416·1)	2·35 (0·929–5·62)	0·256 (0·090–0·657)	15·8 (5·56–40·1)
Salmonella enterica Paratyphi A, B, and C	28·3 (10·7–53·7)	0·262 (0·081–0·597)	23·7 (7·35–54·0)	7·85 (2·89–14·7)	0·050 (0·016–0·112)	3·32 (1·10–7·39)
Salmonella enterica Typhi	140·4 (50·1–264·2)	2·26 (0·724–4·75)	205·3 (65·8–431·5)	24·9 (9·67–43·8)	0·288 (0·096–0·599)	20·2 (6·79–41·9)
Intoxications	0 (0–0)	0 (0–0)	0 (0–0)	0·009 (0·005–0·017)	<0·001 (<0·001–0·001)	0·021 (0·008–0·045)
Clostridium botulinum	0 (0–0)	0 (0–0)	0 (0–0)	0·009 (0·005–0·017)	<0·001 (<0·001–0·001)	0·021 (0·008–0·045)
Total	365·4 (237·3–513·6)	5·17 (2·56–9·15)	470·4 (233·0–830·6)	299·7 (206·2–391·3)	0·985 (0·621–1·53)	56·7 (34·7–91·2)

Data are mean (95% uncertainty interval). DALY=disability-adjusted life-year.

Table 2: **Global rates of foodborne illnesses, deaths, and DALYs per 100 000 people by non-diarrhoeal enteric disease hazard and age group, 2021**

cause of foodborne illness and *Brucella* spp was the third. iNTS was also a leading cause of foodborne illness in the African region and the region of the Americas, and *Brucella* spp was a leading cause in the Western Pacific region. *S* Paratyphi A, B, and C was a leading cause of foodborne illness in the Eastern Mediterranean and South-East Asia regions and, in contrast to other invasive enteric diseases, was particularly low in the African region (appendix 1 pp 27–31).

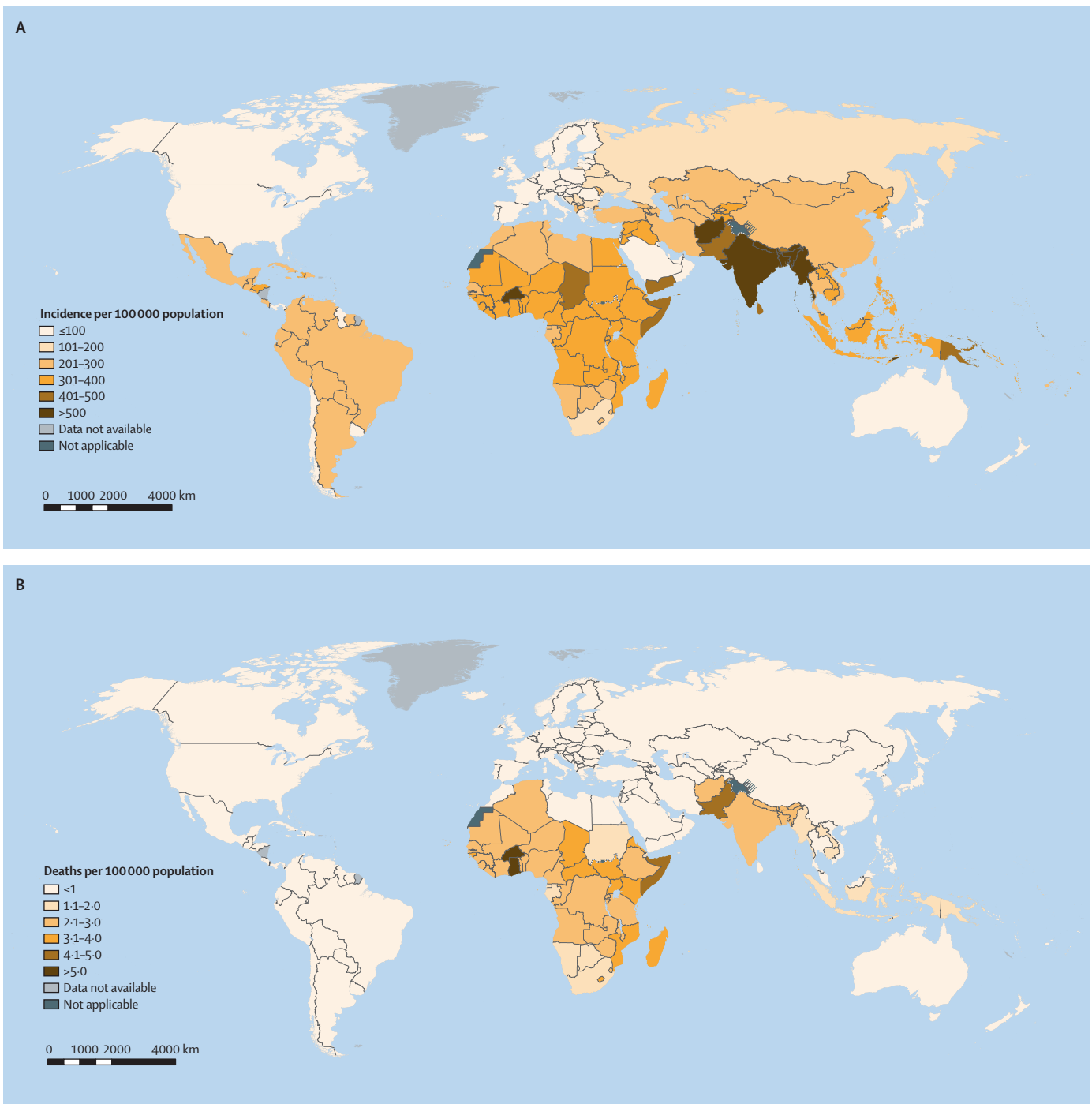
Overall, country-level differences in incidence followed the global socioeconomic gradient (figure 1A). Detailed national-level estimates are available in the WHO Global Health Observatory,[16] with time trends for all hazards available via the WHO interactive dashboard.[17]

In 2021, the eight non-diarrhoeal enteric disease hazards caused an estimated 212 000 deaths (uncertainty interval 137 000–316 000), of which 35 (14–74) were due to *C botulinum* (table 1). Of all deaths, 106 000 (63 900–169 000) were due to foodborne transmission, of which 35 000 (17 300–61 900; 33·0%) were in children younger than 5 years.

The two most frequent foodborne causes of death were *S* Typhi and iNTS, both overall (table 1) and in both age groups (table 2). Among children younger than 5 years, HAV was the third most frequent foodborne cause of death, and among those aged 5 years and older, the third most frequent cause was zoonotic MTBC (table 2). Children younger than 5 years had higher mean rates of foodborne deaths due to HAV, iNTS, *S* Paratyphi A, B, and C, and *S* Typhi, whereas those aged 5 years and older had higher mean rates of foodborne deaths due to *L monocytogenes* and zoonotic MTBC, compared with the other age group (table 2).

In 2021, the highest mortality from foodborne non-diarrhoeal enteric illnesses was in the African region (appendix 1 pp 27–31, figure 1B), followed by the South-East Asia and Eastern Mediterranean regions. The highest mortality from foodborne botulism was in the European and South-East Asia regions. The most frequent foodborne causes of death varied by WHO region, although zoonotic MTBC ranked second or third in all regions. iNTS resulted in the most foodborne deaths in the African, Americas, European, and Western Pacific regions, and *S* Typhi resulted in the most foodborne deaths in the Eastern Mediterranean and South-East Asia regions (appendix 1 pp 27–31). Foodborne disease deaths generally followed the time trends of incidence (appendix 1 pp 32–34).

In 2021, the eight non-diarrhoeal enteric disease hazards resulted in 15·1 million DALYs (uncertainty interval 9·59–23·0), of which 1530 DALYs (611–3240) were due to *C botulinum* (table 1). Of these, 7·26 million DALYs (4·15–12·0) were the result of foodborne transmission, of which 3·18 million DALYs (1·58–5·62; 43·8%) occurred in children younger than 5 years. The hazards causing the most DALYs were *S* Typhi, iNTS, and HAV, both from all routes of transmission and from foodborne transmission (table 1, figure 2), following the same rank order of hazards



(Figure 1 continues on next page)

causing foodborne deaths in children younger than 5 years (table 2). Children younger than 5 years had 205·3 DALYs per 100 000 people (uncertainty interval 65·8–431·5) from *S* Typhi, 174·1 DALYs per 100 000 people (59·5–416·1) from iNTS, and 48·8 DALYs per 100 000 people (15·8–102·8) from HAV. In comparison, people aged 5 years and older had 20·2 DALYs per 100 000 people (6·8–41·9) from *S* Typhi, 15·8 DALYs per 100 000 people (5·56–40·1) from iNTS, and 8·4 DALYs per 100 000 people (4·4–15·2) from zoonotic MTBC (table 2).

See Online for appendix 2

In 2000, iNTS resulted in the most DALYs from all routes of transmission, followed by *S* Typhi, HAV, *S* Paratyphi A,

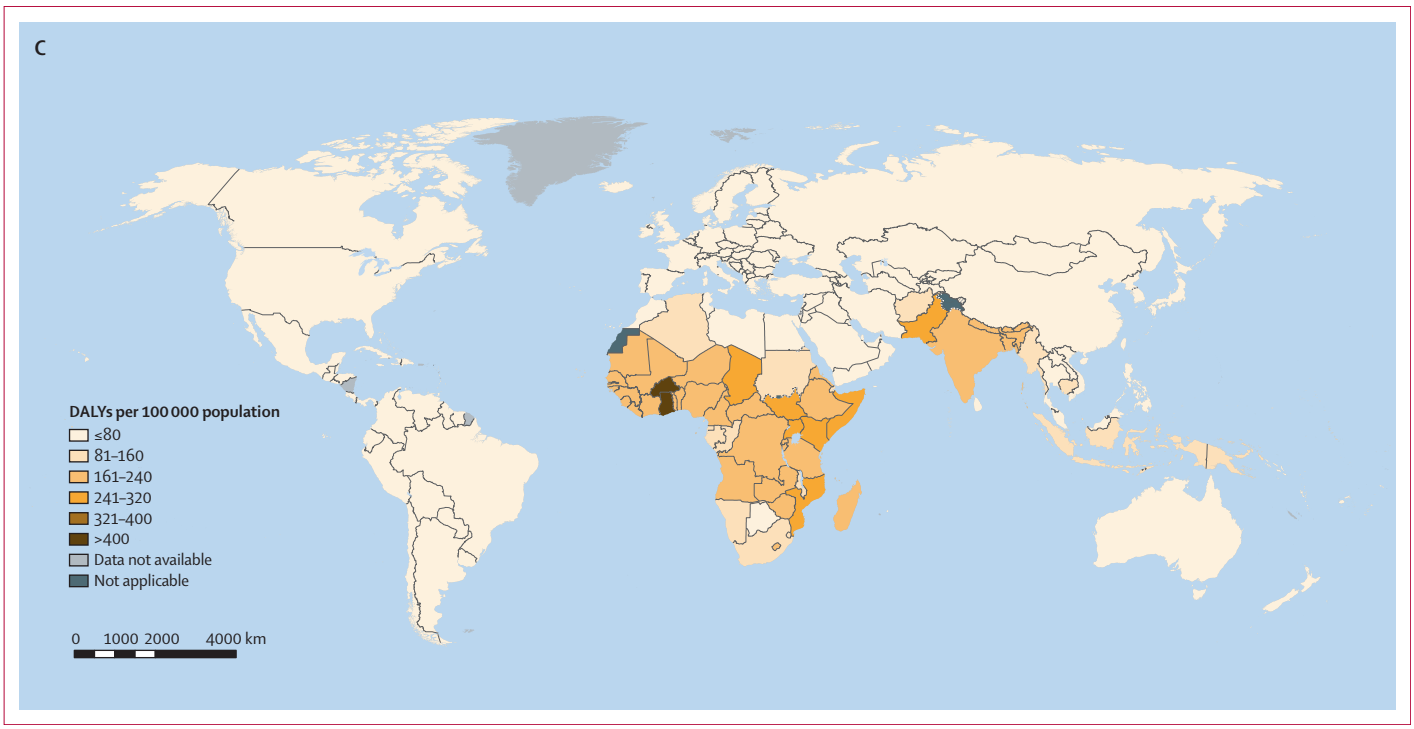


Figure 1: **Mean national rates of foodborne illness incidence (A), deaths (B), and DALYs (C) per 100 000 people due to eight non-diarrhoeal enteric disease hazards, 2021**
Non-diarrhoeal enteric disease hazards: *Brucella* spp; *Clostridium botulinum*; hepatitis A virus; *Listeria monocytogenes;* zoonotic *Mycobacterium* tuberculosis complex (*M bovis, M caprae,* and *M orygis*); invasive non-typhoidal *Salmonella enterica; S enterica* serotypes Paratyphi A, Paratyphi B, and Paratyphi C; and *S enterica* serotype Typhi (appendix 2). The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement. DALY=disability-adjusted life-year. Data Source: World Health Organization. Map Creation Date: April 23, 2026. Map Production: WHO GIS Centre for Health, DDA.

B, and C, zoonotic MTBC, *L monocytogenes*, *Brucella* spp, and *C botulinum*; this rank order was the same for foodborne transmission, except that zoonotic MTBC ranked above *S* Paratyphi A, B, and C (appendix 1 pp 35–36). DALYs for all hazards decreased over time, although this was more pronounced for hazards such as iNTS, such that by 2021, *S* Typhi replaced iNTS as the leading cause of foodborne DALYs globally (appendix 1 pp 35–36). Foodborne disease DALYs generally followed the time trends of incidence (appendix 1 pp 32–34).

In 2021, the greatest foodborne DALYs from the eight non-diarrhoeal enteric hazards occurred in the African region, with 220·3 DALYs per 100 000 people (uncertainty interval 102·3–436·4), followed by the South-East Asia region (147·3 DALYs per 100 000 people [56·8–276·2]; appendix 1 pp 27–31, figure 1C). The highest DALYs from foodborne botulism were in the European and Eastern Mediterranean regions (appendix 1 pp 27–31). The leading causes of foodborne DALYs varied by region (appendix 1 pp 27–31, 37–38) and country (figure 3, appendix 1 pp 39–46). iNTS resulted in the most foodborne DALYs in the African, Americas, and European regions, for all but a few countries. *S* Typhi resulted in the most foodborne DALYs in the Eastern Mediterranean, South-East Asia, and Western Pacific regions, although iNTS and zoonotic MTBC were leading causes in some countries.

Country-level differences in foodborne DALYs also followed the global socioeconomic gradient (figure 1C). Major heterogeneity was estimated, with over 100-fold difference between the country with the lowest DALYs (Japan: 6·59 DALYs per 100 000 people [uncertainty interval 1·41–25·4]) and the country with the highest (Ghana: 731·6 DALYs per 100 000 people [116·6–2840]).

Discussion

In this study, we present updated WHO estimates of the global burden of eight non-diarrhoeal enteric disease hazards, showing that in 2021 they resulted in 15·1 million DALYs, of which almost half (7·26 million DALYs) were due to contaminated food. Despite declines during the period 2000–21, these hazards remained substantial causes of foodborne disease burden particularly in children younger than 5 years—for whom the burden was ten times that in older children and adults—and in low-income and middle-income countries, with the burden highest in the African region followed by the South-East Asia and Eastern Mediterranean regions. *S* Typhi, iNTS, and HAV remained responsible for the greatest global foodborne burden among the hazards considered in this study,[1,2] although this varied by region and country as expected given differences in agriculture, food supply chains, food consumption, and cultural practices.

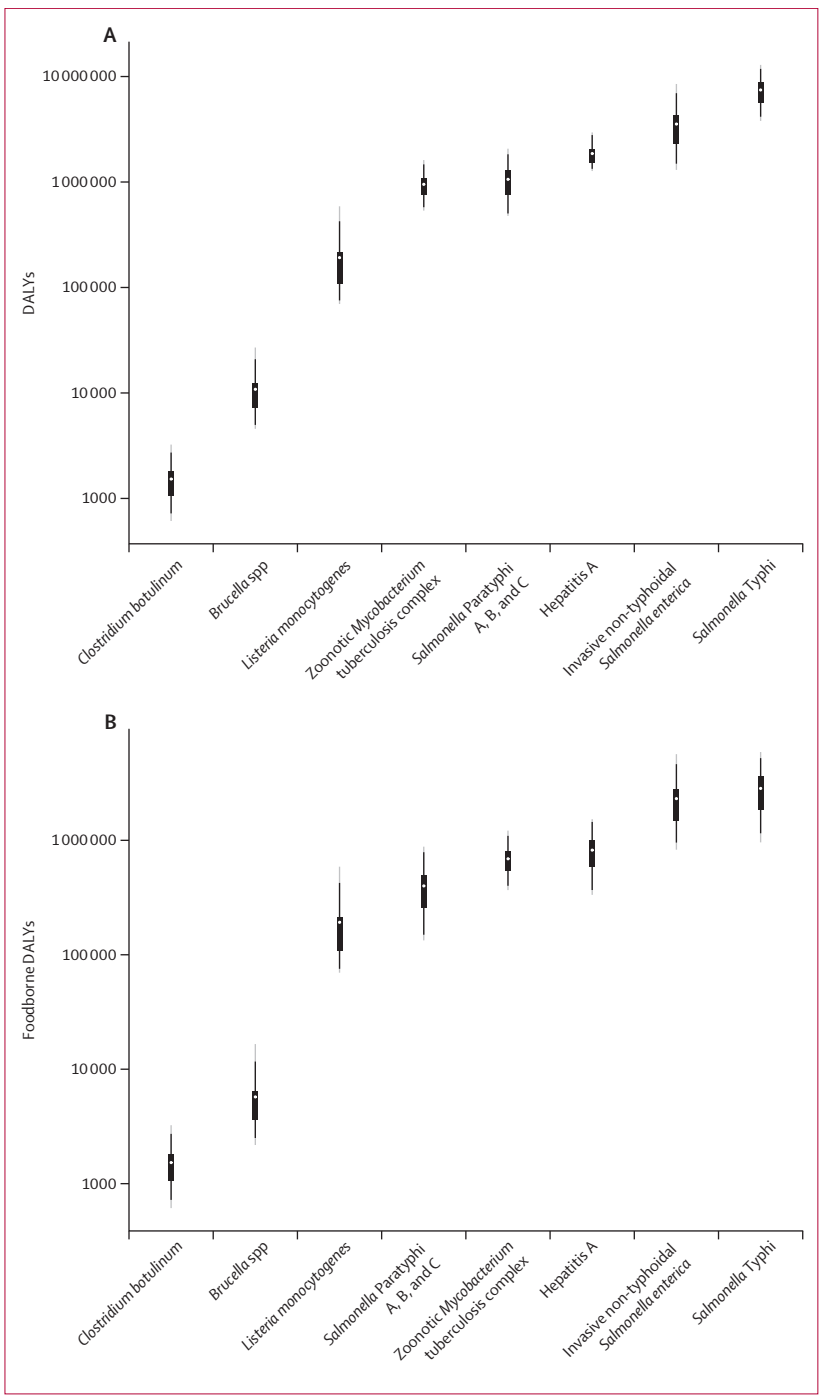


Figure 2: **Total DALYs globally for eight non-diarrhoeal enteric disease hazards, 2021**
All routes of transmission (A) and foodborne transmission (B), ranked from lowest to highest with 95% uncertainty intervals (appendix 2). Logarithmic scale, showing the mean (white dot), IQR (ie, 50% uncertainty interval and 25th and 75th percentiles; thick black line), 90% uncertainty interval (ie, 5th and 95th percentiles; thin black line), and 95% uncertainty interval (ie, 2·5th and 97·5th percentiles; thin grey line). DALY=disability-adjusted life-year.

Collectively, invasive infections with *Salmonella* serotypes contributed the greatest combined burden,[18] largely due to the high associated mortality, particularly in children younger than 5 years in the African and South-East Asia regions.

The temporal declines in incidence and mortality observed in this study could reflect the improving safety of the worldwide food supply and in water and sanitation, and the impact of human and animal vaccination programmes.[19–21] Other disease burden estimates also show reductions over time, although for some, such as iNTS, incidence has reportedly increased.[22,23] Our observed reductions in iNTS burden might be due to changes in host risk factors such as those mediated by malaria control and HIV care and treatment, and reduced exposure to iNTS organisms through improved food supplies and food and water safety. In contrast, the burden of *L monocytogenes*, an opportunistic pathogen common in food production environments in industrialised countries, increased over time; this might reflect greater recognition of *L monocytogenes* as a cause of serious and highly publicised outbreaks, and an increase in the size of at-risk populations including older people and those undergoing immunosuppressive therapy. Despite observed declines, many of our hazards are climate sensitive, and increased global temperatures, floods, and droughts could result in increased incidence and burden. These potential effects emphasise the need to improve and maintain national and global food safety efforts.

These updated estimates have many strengths compared with the 2010 estimates,[1,2] including specific inclusion of zoonotic MTBC species beyond *M bovis*, updated data with increased geographical coverage, updated source attribution estimates from more geographically diverse experts, an improved modelling approach, and burden estimates over time and down to country level. Another strength was the country consultation process, through which additional data were identified and national estimates were reviewed by countries. Although the changes in methods and data from the 2015 WHO estimates make it difficult to directly compare results, our burden rankings by hazard were generally similar.[1] Collectively, these improvements also allow countries to better design specific interventions and optimise resource allocation.

These estimates also have several limitations. Typical of global burden of disease studies, there were insufficient data to estimate incidence and mortality in many countries. Although we addressed this limitation by imputing from other countries in the region,[8] there is a need for countries and international agencies to establish and improve disease surveillance systems to capture locally valid data on foodborne illnesses and hazards potentially transmitted by food.[24] This improvement, with capacity building to investigate outbreaks, would also enhance countries' abilities to improve the safety of their food supply and monitor changes over time.[25] Another limitation was the reliance on incidence and mortality estimates generated by others for some hazards, making it difficult to validate some data inputs. For example, for typhoid, we might have overestimated the incidence in children younger than 5 years.

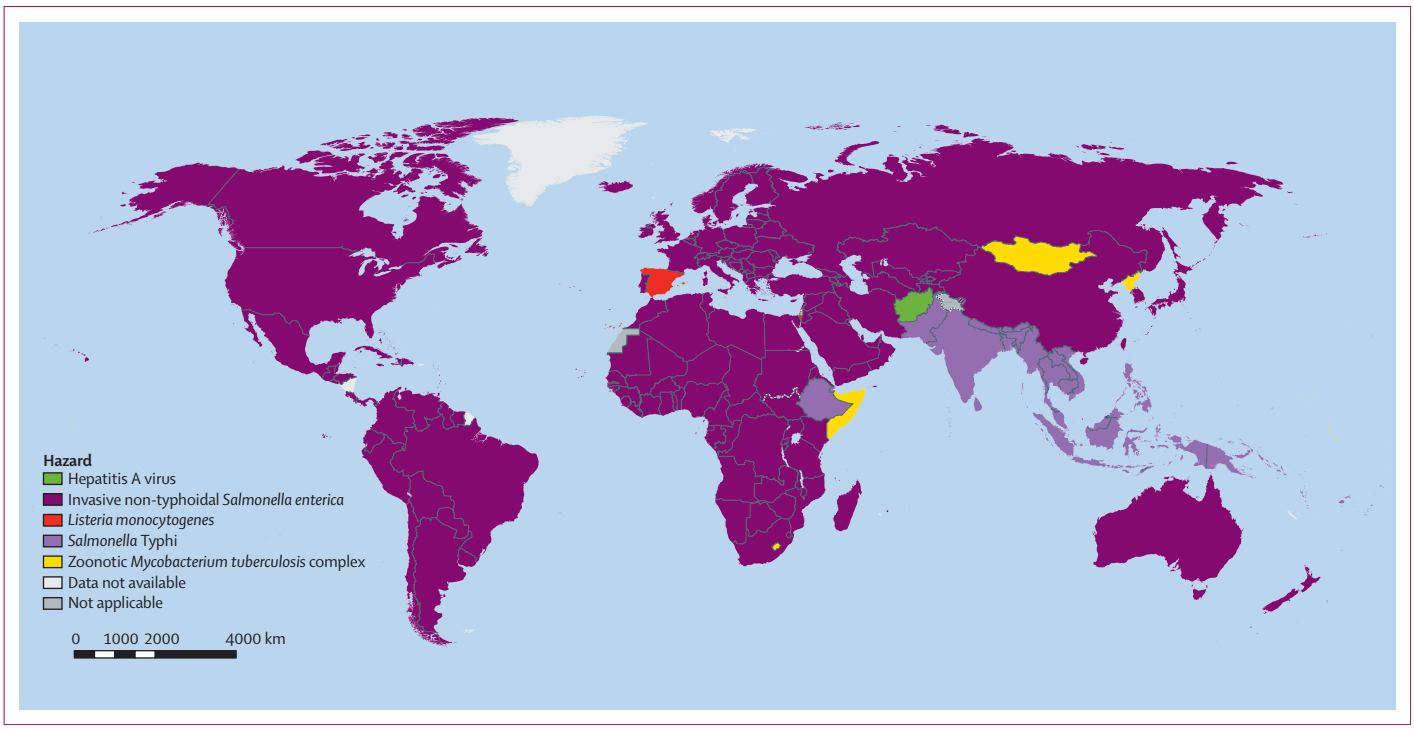


Figure 3: **Non-diarrhoeal enteric disease hazards causing the most foodborne disability-adjusted life-years by country, 2021**
For data see appendix 2. The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement. Data Source: World Health Organization. Map Creation Date: April 23, 2026. Map Production: WHO GIS Centre for Health, DDA.

Other limitations include the absence of sex-specific inputs for many hazards and the challenge of foodborne attribution. We relied on a global structured expert judgment study that attributed sources of infection to different transmission modes at a subregional level.[15] Despite efforts to engage subregional expertise, the number of experts for some hazards and subregions was low, necessitating imputation from other subregions. For *L monocytogenes* and *C botulinum*, we attributed all disease to contaminated food but recognise that other modes of transmission, although very rare, might emerge, such as botulism due to improperly handled cosmetic injections of botulinum toxin.[26]

In this study, we prioritised major non-diarrhoeal enteric foodborne hazards and health states with available data, meaning that those that are important but under-recognised as a foodborne disease hazard, or that have insufficient robust data, were excluded. For example, we did not include infant botulism, due to insufficient data availability and clarity around transmission. Another potentially foodborne pathogen we did not include was extra-intestinal pathogenic *Escherichia coli*, which potentially results in a substantial burden of disease despite unclear links to food.[27] Finally, we did not attribute any burden to stillbirths due to *L monocytogenes* and *Brucella* spp, and we were unable to consider the impact of antimicrobial resistance on burden. Thus, the values reported here are likely to underestimate the true burden of foodborne non-diarrhoeal enteric diseases.[11] Future efforts to estimate such burden should include additional invasive hazards and intoxications, and more data from additional countries.

Despite these limitations, our findings have important policy implications for health and food safety agencies to direct targeted and context-specific interventions to prevent foodborne diseases, including focusing efforts on young children for whom there is the greatest need. Many hazards estimated in this study are preventable through food supply chain interventions, improved water and sanitation, or vaccination programmes. For *Brucella* spp and zoonotic MTBC, milk pasteurisation is an essential food safety intervention, along with elimination efforts in animals. For *L monocytogenes* and *C botulinum*, improvements in a safe and secure food supply are required, from food chain interventions through to an emphasis on safe handling and preparation of food by consumers. For HAV, for which we observed a high incidence, food contamination can occur during growing, harvest, processing, and preparation, highlighting the need for improvements across the food supply chain. Finally, invasive *Salmonella* infections are preventable through vaccination programmes, including existing typhoid conjugate vaccines,[21] and potentially via vaccines in development for *S* Paratyphi A and NTS serotypes associated with invasive disease in sub-Saharan Africa.[18,28,29] Additionally, vaccines for animals, including

poultry and cattle, often result in dramatic improvements in food safety.[20,30]

In conclusion, these updated WHO estimates provide improved global estimates for serious foodborne hazards, including country-specific estimates that can guide action and interventions. Although the burden of these foodborne diseases has declined over time, the current burden remains substantial enough for countries to justify One Health public health surveillance for these important diseases, as well as targeted and context-specific interventions including vaccination, food safety and water and sanitation interventions, and improved health-care access.

Foodborne Disease Burden Epidemiology Reference Group for 2021–25
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*Also members of the Enteric Diseases Task Force.

Contributors
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Declaration of interests
SEM reports grants and contracts from the Canadian Institutes for Health Research, National Science and Engineering Research Council, and Bill & Melinda Gates Foundation and the UK's Department for International Development; and consulting fees from Western University. ESW reports grants and contracts from the US Centers for Disease Control and Prevention, the US Department of Agriculture, the Colorado Department of Public Health and Environment, Human Resources and Services Administration, the National Network of Public Health Institutes, and the Council for State and Territorial Epidemiologists. BD, CdB, LV, and KF report grants and contracts from the European Food Safety Agency. AHH reports consulting fees from WHO. RJL reports grants and contracts from the New Zealand Institute of Public Health and Forensic Science; and participation on data safety monitoring boards or advisory boards for New Zealand Food Safety. JAC reports grants and contracts from the Gates Foundation; and participation on data safety monitoring boards or advisory boards for the Wellcome Trust (funder) and Oxford University Clinical Trials Unit Nepal (sponsor). MDK reports grants and contracts from the Medical Research Future Fund, the National Health and Medical Research Council, Food Standards Australia New Zealand, and the Australian Centre for International Agriculture Research; and participation on data safety monitoring boards or advisory boards for the Communicable Disease Network Australia. All other authors declare no competing interests.

Data sharing
Data collected by WHO for this study and data sources are publicly available at 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 protocol and statistical analysis plan are available in the study by Devleesschauwer and colleagues.[8] The analysis code is available via GitHub (https://github.com/fbdburden).

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References
1 Kirk MD, Pires SM, Black RE, et al. World Health Organization estimates of the global and regional disease burden of 22 foodborne bacterial, protozoal, and viral diseases, 2010: a data synthesis. *PLoS Med* 2015; **12:** e1001921.
2 WHO. WHO estimates of the global burden of foodborne diseases: Foodborne Disease Burden Epidemiology Reference Group 2007–2015. 2015. https://www3.paho.org/hq/dmdocuments/2015/2015-cha-who-estimates-global-foodborne-diseases.pdf (accessed Dec 28, 2025).
3 Courtot-Melciolle L, Jauvain M, Siefridt M, et al. Food-borne botulism outbreak during the Rugby World Cup linked to marinated sardines in Bordeaux, France, September 2023. *Euro Surveill* 2023; **28:** 2300513.

4 World Health Assembly. Seventy-third World Health Assembly WHA73.5. Agenda item 15.3: Strengthening efforts on food safety. 2020. https://apps.who.int/gb/ebwha/pdf_files/WHA73/A73_R5-en.pdf (accessed Dec 28, 2025).

5 WHO. WHO global strategy for food safety 2022–2030: towards stronger food safety systems and global cooperation. 2022. https://iris.who.int/server/api/core/bitstreams/d7d3a517-f794-4d25-9ebf-02a7e6a01f42/content (accessed Dec 28, 2025).

6 WHO. Terms of reference for the Foodborne Disease Burden Epidemiology Reference Group (FER). https://cdn.who.int/media/docs/default-source/food-safety/call-for-experts/tor-for-reference-ferg-31aug2020.pdf?sfvrsn=b0a3d1f_8 (accessed Dec 28, 2025).

7 Lake RJ, Devleesschauwer B, Majowicz SE, et al. WHO estimates of the global, regional, and national burden of 42 foodborne infectious and chemical hazards, 2000–21: an updated data synthesis. *Lancet Glob Health* 2026; **14:** 103994.

8 Devleesschauwer B, Vaes L, Fernandez K, et al. Computational framework for the World Health Organization estimates of the global, regional and national burden of foodborne diseases 2026 edition. *medRxiv* 2026; https://doi.org/10.64898/2026.05.13.26353030.

9 Stevens GA, Alkema L, Black RE, et al. Guidelines for Accurate and Transparent Health Estimates Reporting: the GATHER statement. *Lancet* 2016; **388:** e19–23.

10 Devleesschauwer B, Charalampous P, Gorasso V, et al. Standardised reporting of burden of disease studies: the STROBOD statement. *Popul Health Metr* 2024; **22:** 28.

11 de Noordhout CM, Devleesschauwer B, Angulo FJ, et al. The global burden of listeriosis: a systematic review and meta-analysis. *Lancet Infect Dis* 2014; **14:** 1073–82.

12 Marchello CS, Fiorino F, Pettini E, Crump JA, Vacc-iNTS Consortium Collaborators. Incidence of non-typhoidal *Salmonella* invasive disease: a systematic review and meta-analysis. *J Infect* 2021; **83:** 523–32.

13 Marchello CS, Birkhold M, Crump JA, Vacc-iNTS Consortium Collaborators. Complications and mortality of non-typhoidal *Salmonella* invasive disease: a global systematic review and meta-analysis. *Lancet Infect Dis* 2022; **22:** 692–705.

14 Institute for Health Metrics and Evaluation. GBD Compare. https://vizhub.healthdata.org/gbd-compare/ (accessed Dec 28, 2025).

15 Pires SM, Mughini-Gras L, Hoffmann S, et al. World Health Organization attribution of burden of foodborne diseases to transmission pathways and foods. *Research Square* 2026; published online April 2. https://doi.org/10.21203/rs.3.rs-9449162/v1 (preprint).

16 WHO Global Health Observatory, Foodborne disease estimates https://www.who.int/data/gho/data/themes/topics/foodborne-diseases-estimates (Accessed Dec 19, 2025).

17 WHO. WHO Foodborne Disease Estimates 2026 edition. 2026. https://www.who.int/teams/nutrition-and-food-safety/monitoring-nutritional-status-and-food-safety-and-events/foodborne-disease-estimates/2026-edition (accessed May 26, 2026).

18 Martin LB, Tack B, Marchello CS, et al. Vaccine value profile for invasive non-typhoidal *Salmonella* disease. *Vaccine* 2024; **42** (suppl 1)**:** S101–24.

19 WHO/UNICEF Joint Monitoring Programme for Water Supply, Sanitation and Hygiene. Progress on household drinking water, sanitation and hygiene 2000–2024: special focus on inequalities. 2025. https://data.unicef.org/resources/jmp-report-2025/ (accessed Dec 29, 2025).

20 Lane CR, LeBaigue S, Esan OB, et al. *Salmonella enterica* serovar Enteritidis, England and Wales, 1945–2011. *Emerg Infect Dis* 2014; **20:** 1097–104.

21 Haposan JH, Icanervilia AV, Watts E, et al. Real-world vaccine effectiveness of typhoid conjugate vaccine in children and adolescents: a systematic review and meta-analysis. *Vaccine* 2025; **67:** 127872.

22 GBD 2023 Causes of Death Collaborators. Global burden of 292 causes of death in 204 countries and territories and 660 subnational locations, 1990–2023: a systematic analysis for the Global Burden of Disease Study 2023. *Lancet* 2025; **406:** 1811–72.

23 Liu G, Zhang X, Cao Q, Chen T, Hu B, Shi H. The global burden of typhoid and paratyphoid fever from 1990 to 2021 and the impact on prevention and control. *BMC Infect Dis* 2025; **25:** 919.

24 Kanzi AM, Smith SI, Msefula C, et al. Expediting pathogen genomics adoption for enhanced foodborne disease surveillance in Africa. *EBioMedicine* 2025; **111:** 105500.

25 Vachon MS, Edmundson AR, White AE, et al. CDC directed funding improves foodborne outbreak reporting in US states, 2009–2022. *J Food Prot* 2025; **88:** 100581.

26 Jasperse J, Wilson K, Akbar S, et al. A local outbreak of iatrogenic botulism associated with cosmetic injections of botulinum neurotoxin-containing products, England, 2025. *Euro Surveill* 2025; **30:** 2500746.

27 Manges AR, Johnson JR. Food-borne origins of *Escherichia coli* causing extraintestinal infections. *Clin Infect Dis* 2012; **55:** 712–19.

28 McCann N, Paganotti Vicentine M, Ebrahimi N, et al. Safety, efficacy, and immunogenicity of a *Salmonella* Paratyphi A vaccine. *N Engl J Med* 2025; **393:** 1704–14.

29 WHO. Research and development technology roadmap for invasive non-typhoidal *Salmonella* vaccines against invasive disease. 2025. https://www.who.int/publications/i/item/9789240110212 (accessed Dec 29, 2025).

30 Hugas M, Beloeil P. Controlling *Salmonella* along the food chain in the European Union—progress over the last ten years. *Euro Surveill* 2014; **19:** 20804.