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RESEARCH ARTICLE



Antimicrobial resistance in food-related sources: a One Health perspective through comparative meta-analysis

Md Shahidul Islam , Alemayehu Molla Wollie, Shaharior Razu, Daniel Teshome Gebeyehu ,
Nusrat Jahan and Gashaw Enbiyale Kasse

School of Health, Faculty of Medicine and Health, University of New England, Armidale, NSW, Australia

ABSTRACT

Antimicrobial resistance (AMR) is a global public health concern exacerbated by the transmission of resistant pathogens through food-related sources. This review examined the existing evidence on the prevalence of antimicrobial-resistant pathogens across various food sources. This review is grounded in the One Health framework, which views AMR as a systemic outcome of interconnected human, animal and environmental food systems. Following PRISMA guidelines, PubMed, Web of Science, and Scopus were searched. Pooled AMR prevalence rates were estimated using a random effects model. Forty cross-sectional studies reporting AMR in food sources were included. The pooled prevalence of resistance pathogens isolated from food sources was 45% (95% CI: 33, 57). High AMR was observed in *Salmonella* spp. from ready-to-eat foods (70%, 95% CI: 19, 90) and fish (43%, 95% CI: 13, 80). Overall, 38.2% of isolated bacterial pathogens were resistant to three or more antimicrobials. Multidrug resistance prevalence was 64% for *Salmonella* spp., 36% for *Staphylococcus* spp., and 59% for *Escherichia coli*. The review highlights a high prevalence of resistant bacterial pathogens in various food-related sources. Addressing AMR requires multisectoral collaboration, emphasising the control of foodborne transmission.

List of abbreviations: AMR: Antimicrobial resistance; MDR: Multidrug resistance; PROSPERO: Prospective register of systematic reviews; WHO: World Health Organization

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bacterial pathogens; food
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Introduction

Antimicrobial resistance (AMR) is a significant global public health concern, exacerbated by the transmission of resistant pathogens through various food sources (Prestinaci et al., 2015; Salamandane et al., 2022). As bacteria become more resistant, treating the associated illnesses becomes increasingly challenging. The World Health Organization (WHO) 2023 global report on AMR highlights the alarming levels of resistance even to third-generation antibiotics worldwide. AMR is estimated to have directly caused 1.27 million deaths and contributed to 4.95 million deaths globally in 2019 (CDC, 2022). If no actions are implemented, AMR could result in up to 10 million deaths per year by 2050 (Walsh et al., 2023). The World Health Organization (WHO) reported in 2019 that foodborne illnesses account for approximately 600 million cases and 420,000 deaths globally each year, with children under 5 years old making up one-third of the fatalities (WHO, 2024). The causes and impacts of AMR vary significantly between high-income and low-and middle-income countries due to differing social and healthcare management-related factors (Byrne et al., 2019; Minssen et al., 2020).

The spread of AMR is exacerbated by the transmission of resistant bacteria from animals and environments to humans (Tang et al., 2023), mainly due to the unregulated use of antimicrobials in food production, particularly in low- and middle-income countries (Almansour et al., 2023). In many low- and middle-income countries, antimicrobials are often used not only for treating sick animals but also for

CONTACT Dr Md Shahidul Islam  mislam27@une.edu.au

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disease prevention and growth promotion, sometimes without veterinary oversight (Musuka et al., 2025). The transmission of antimicrobial-resistant bacteria between animals and humans occurs through direct contact, food consumption and environmental pathways. The genomic studies highlight shared resistant strains and resistance genes circulating within livestock, humans and their environments, underscoring the complexity of AMR dissemination and the need for integrated One Health interventions (Almansour et al., 2023; Ludden et al., 2019; Muloi et al., 2018). For instance, animals treated with antibiotics can harbour AMR bacteria that possess resistance genes, which can potentially be transferred to humans (Vidic et al., 2023). Foodborne pathogens such as *Streptococcus* spp., *Campylobacter* spp., *E. coli*, *Staphylococcus* spp. and *Salmonella* spp. are commonly found in dairy, livestock and poultry products. In the United States, *Campylobacter* spp. and nontyphoidal *Salmonella* spp. cause common foodborne illnesses (Karp et al., 2017). The prevalence of multidrug-resistant *E. coli* and *Salmonella* spp. in the United States and Europe underscores the persistent challenges of managing AMR in foodborne pathogens (CDC, 2022; Van Boeckel et al., 2014). *Salmonella*, *E. coli* and *Campylobacter* in meat, poultry and dairy products are the primary causes of the disproportionately high prevalence of foodborne diseases in African countries (Thomas et al., 2020). In Asia, bacteria isolated in aquatic food sources used for human consumption exhibit alarming levels of resistance to therapeutically significant antibiotics (Schar et al., 2021). For example, 98% of *E. coli* isolates in Bangladesh and India are resistant to various antibiotics, including fluoroquinolones and cephalosporins (Jain et al., 2021; Singh et al., 2018).

In developed countries, robust healthcare infrastructure and regulatory frameworks allow more effective management of antimicrobial use in humans, animals, and the environment (Ajulo & Awosile, 2024; Pandey et al., 2022). However, AMR is challenging even in these countries due to over-prescription, inappropriate use of antimicrobials in agriculture, environmental contamination and limited resources (Endale et al., 2023; Salam et al., 2023). These issues, along with policy gaps, barriers to healthcare and poverty, contribute to the high rates of AMR-related deaths in such countries (Alvarez-Uria et al., 2016).

The transmission of resistant bacteria underscores the complexity of AMR, highlighting the need for a One Health approach. The One Health concept is a global approach to fostering interdisciplinary knowledge and collaboration in all areas of healthcare science and was introduced at the beginning of the 2000s (Gibbs, 2014). This approach interlinks the health of humans, animals and the environment, and it is essential to control diseases, ensure food security and safeguard environmental quality (Munkholm & Rubin, 2020). Although efforts to establish One Health initiatives have gained consideration among important policymakers, such as the World Health Organization (WHO), AMR pathogens are a global problem. Previous systematic reviews and meta-analyses on foodborne pathogens and AMR have mostly focused on single sample sources (e.g., only meat and meat products, Zelalem et al. (2019)), a single species in one country (e.g., Zenebe et al. (2020) in Ethiopia), or have compared AMR prevalence between specific countries (e.g., Vidic et al. (2023) comparing Italy and Thailand; and Egypt and the UK). However, to our knowledge, no comprehensive overview exists that compares AMR prevalence in food sources across the globe from a One Health perspective. Our study addresses this gap by comparing AMR in animal products, plant-based foods and slaughterhouse-related sources across multiple world regions, including Africa, Asia, Europe, North America, South America and Australia. Thus, this study aimed to explore the prevalence of AMR pathogens from different food sources across different regions. The findings can help policymakers and AMR in implementing effective policies and regulations and establishing comprehensive surveillance for monitoring AMR patterns.

Materials and methods

Protocol and registration

This systematic review was carried out following the PRISMA 2020 guidelines. The review protocol was registered with the International Prospective Register of Systematic Reviews (PROSPERO) under the registration number CRD42024580520.

Search strategy

A thorough systematic search was conducted using online databases such as PubMed, Web of Science, Scopus and Google Scholar to examine the prevalence of AMR across various food-related sources. In

this context, food-related sources refer to both the location from which food is obtained and the original sources of the food. The reference lists of the included studies were reviewed to identify additional articles that may have been overlooked during the database searches. The literature search was conducted from 24 August 2024 to 30 September 2024. The search strategies was based on MeSH terms such as 'Antimicrobial resistance' OR 'Antibiotic resistance' OR 'AMR' OR 'Drug Resistance, Microbial', 'Food sources' OR 'Foodborne diseases', 'Multi-drug resistance', 'Animals', 'Vegetables', 'Environment' and 'One Health'. The Boolean operators (AND, OR and *) were used to identify relevant and combined search terms. The full search plan is included as Supplementary Material ([Supplementary File 1](#)).

Inclusion

Based on the objectives of this review, the following inclusion criteria were applied: 1) studies assessed the prevalence of AMR among food pathogen bacteria; 2) their sample sources were from animal and foods of animal origin, vegetable food origin, environmental samples, food handlers and slaughterhouse; 3) clearly described their AMR assessment methods, which could include molecular techniques, disc diffusion or minimum inhibitory concentration (MIC) testing; 4) utilised an appropriate sample size; 5) original studies published in peer-reviewed journals, studies with recent information (published for the last 2019–2024) and written in the English language. The reason for restricting our meta-analysis to studies from 2019 to 2024 is that this period captures the most recent trends, interventions and challenges in combating antimicrobial resistance (AMR), including the emergence of new resistant pathogens and the impact of recent global events such as the COVID-19 pandemic, which have significantly influenced antibiotic use and resistance rates.

Exclusion criteria

Review articles, study protocols, conference abstracts, qualitative studies, those not published in peer-reviewed journals, case reports, letters, studies published before 2019 and editorials were excluded. Furthermore, studies that only considered the pathogen with no AMR report were excluded.

Study selection and data extraction

Studies identified through database searches were evaluated for eligibility. The search results were imported into EndNote 20. After removing duplicates, the two authors (GE and AW) independently screened the studies by abstract and conducted a full-text review. Articles that met the inclusion criteria were proceeded with for data extraction. Following the screening of studies, data were extracted using prepared data extraction forms. The extracted data included the first author, year of publication, study area, study period, study population, sample size, study design, sample source, sample type, number of positive samples, isolated bacteria, prevalence and resistance of isolated bacteria and prevalence of multidrug-resistant bacteria. All authors independently conducted data extraction. Any disagreements during the screening or data extraction process were resolved through discussion. The quality of the included studies was assessed using the modified critical appraisal tool developed by Munn et al. (2014).

Data analysis

The studies that met the inclusion criteria were included in the meta-analysis. R Studio version 4.1.2 (Meta/Metafor packages was used to analyse the extracted data. The prevalence of AMR was pooled using a random effect model with a 95% confidence interval (CI). The AMR rate results were presented based on a single sample to identify which contributed the most. Heterogeneity across the studies was assessed using Cochran Q statistics and I^2 (Naylor et al., 2016; Crowther et al., 2010). According to Higgins and Thompson (2002), if the values of I^2 levels of 0%–25%, 25%–50%, 50%–75% and above 75% were classified as low, moderate, substantial and high, respectively. The heterogeneity was explored graphically in a forest plot. Subgroup analysis investigates whether differences in the study

characteristics, such as sample sources, study area, pathogen type and antimicrobial types, explain the variability in effect sizes. The prevalence of AMR was compared between high-, low- and middle-income countries from different perspectives. A sensitivity analysis was performed to evaluate or identify outliers and influential studies on the final effect. Publication bias was assessed using a funnel plot. The Egger regression test was employed to assess the asymmetry of the funnel plot.

Results

Identification of studies

As shown in Figure 1, about 2,153 studies were identified through database searches, with 2,053 articles retrieved from PubMed, Scopus and Web of Science. The remaining 100 studies were identified through Google Scholar and the reference lists of previously identified articles. After 500 duplicate studies were removed, the titles and abstracts of 1,653 studies were screened. Screening indicated 200 studies for retrieval. Finally, 40 articles were included in the analysis according to the inclusion criteria.

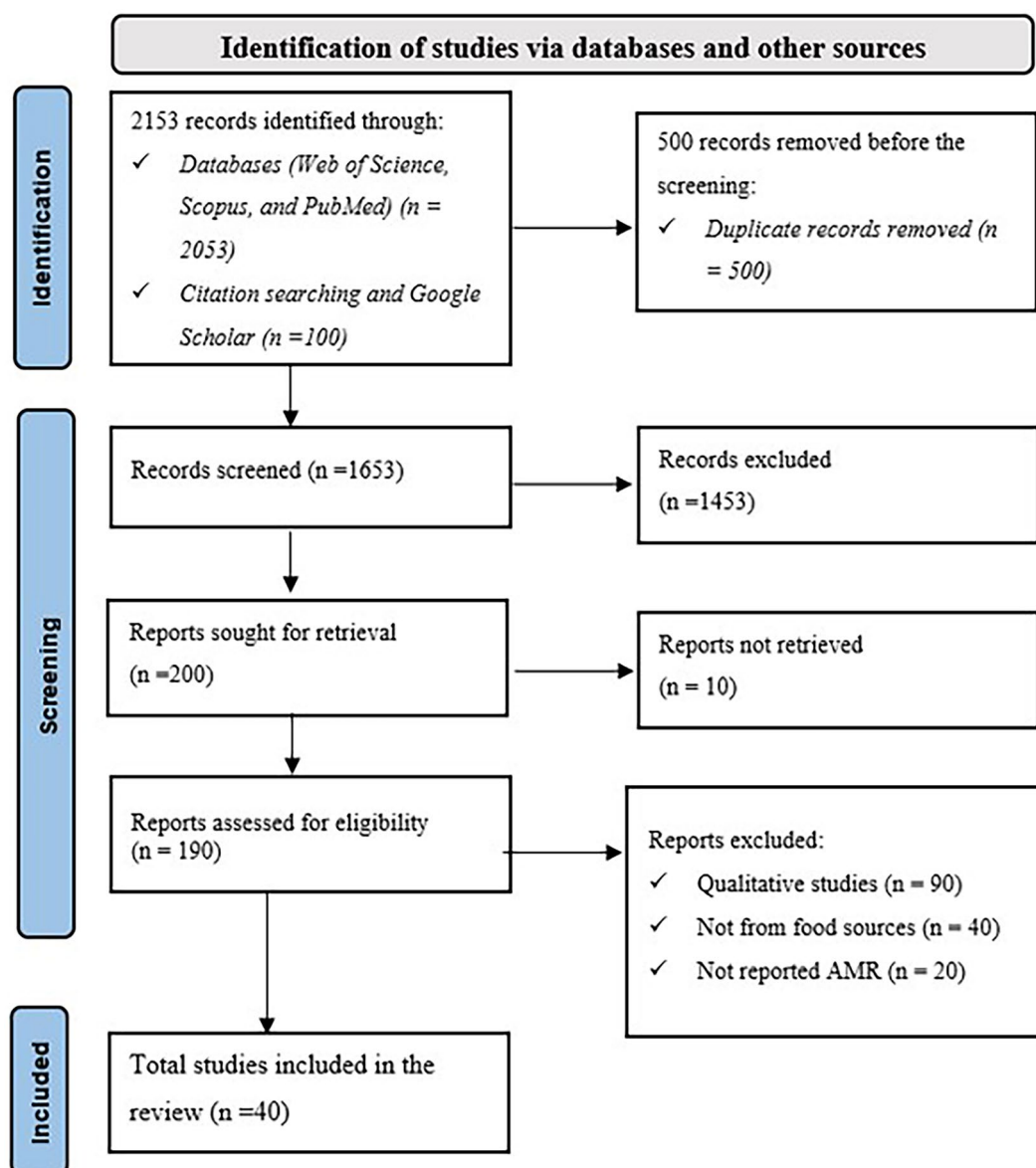


Figure 1. Flow diagram of study selection (PRISMA 2020).

Study characteristics

All studies were cross-sectional and focused on the prevalence and AMR status of bacterial pathogens. A total of 14,907 samples were combined from all studies, with 4,885 yielding bacterial positivity. The samples were sourced from cooked and ready-to-eat food ($n=1,712$), raw meat ($n=2,493$), dairy products (raw milk and the milk supply chain) ($n=820$), fish (raw and cooked fish and fish-based foods) ($n=2,233$), pigs ($n=1,153$) slaughterhouses (workers' hands, waters and equipment) ($n=720$), animal farms ($n=524$), vegetables and fruits ($n=293$) (Table 1, Supplementary File 2). In most studies, the isolates were identified and confirmed using cultural methods and biochemical tests. A total of 15 types of pathogens were reported: *Salmonella* spp. ($n=14$), *E. coli* ($n=13$), *Staphylococcus* spp. ($n=12$), *Campylobacter* ($n=6$), *Enterococcus* spp. ($n=4$), *Klebsiella* spp. ($n=3$), *Listeria monocytogenes* ($n=3$), *P. aeruginosa* ($n=3$), *Vibrio* ($n=2$), *Citrobacter* ($n=2$), *Clostridioides* spp. ($n=1$), *Shigella* ($n=1$), *Aeromonas* ($n=1$), *Providencia* spp. ($n=1$) and *Enterobacter* spp. ($n=1$). Various antimicrobial agents were tested against these pathogens. Disc diffusion tests were the most commonly used methods to assess antimicrobial susceptibility, followed by dilution tests.

Bias assessment

The funnel plot showed the somewhat asymmetrical distribution of studies, which could indicate potential publication biases or differences in study characteristics. Additionally, Egger's test result revealed statistically significant evidence of publication bias ($p=0.008$) (See Figure 1 in Supplementary File 3). However, when outliers were removed, the result of Egger's test was no longer statistically significant ($b=-0.92$, 95% CI $-2.074-0.233$, $p=0.17$), and the funnel plot showed symmetrical distribution (Figure 2). To address the potential publication bias further, we conducted a subgroup analysis.

Quality of studies

The result indicated that among 40 included studies, 35 studies met all 10 criteria of the quality assessment critical appraisal tool developed by Munn et al. (2014). In contrast, the remaining five studies had limitations such as insufficient methods to address confounding factors and data analyses that did not provide sufficient coverage of the identified sample.

Prevalence of isolated bacterial pathogens from different food sources

In the studies included, the samples collected to isolate bacterial pathogens ranged from 25 to 3,055. All studies reported the prevalence of pathogens isolated from various food sources (animals, animal products, vegetables and fruits), and the prevalence rates ranged from 4% (Supriya et al., 2024) to 100% (Zhou et al., 2024). As shown in Figure 3, the estimated pooled prevalence across the 40 studies was 45% (95% CI [33, 57]).

Subgroup analysis

Because of the high heterogeneity as shown in Figure 3, we conducted a subgroup analysis to explore potential sources of heterogeneity.

Prevalence of food source pathogens based on the study area

As shown in Figure 4, the prevalence of bacterial pathogens isolated from food sources exhibited significant geographic variation. Asia exhibited considerable variation, with prevalence rates ranging from as low as 4% (Supriya et al., 2024) to 100% (Yan et al., 2024; Zhou et al., 2024). A study conducted in India reported that 97.3% of 150 fruit and vegetable samples were positive for foodborne pathogens (Saksena et al., 2020). In Japan, 82% of the analysed samples were found to be positive (Yamagami et al., 2023). The pooled prevalence of foodborne pathogens in Asia was 44% (95% CI [27, 62]). Africa also exhibited

Table 1. Characteristics of included studies.

First author (publication year)	Study area (country)	Study period	Sample size	Sample source	No. of positive samples	Main isolated bacteria species	Prevalence of isolated bacteria species	Resistance patterns of the isolates
Afshari et al. (2022)	Iran	2019–2020	357	Ready-to-eat food	87	<i>Staphylococcus aureus</i> and <i>Enterococcus</i> spp.	<i>S. aureus</i> = 24.37% and MVRSA = 22.98% Enterococci = 15.4 VRE = 21.81%	VRSA was 100% resistant to ampicillin, oxacillin, ceftiofur, erythromycin, clindamycin, gentamicin and trimethoprim-sulfamethoxazole. High prevalence of resistance to quinupristin-dalfopristin (100%), erythromycin (83.33%), tetracycline (83.33%), doxycycline (66.66%) and rifampin (66.66%) antibiotic agents The highest resistance to chloramphenicol and ciprofloxacin followed by tetracycline. High resistance rates for amoxicillin/clavulanic acid (87.7%), tetracycline (82.5%), sulphonamide (57.9%) and chloramphenicol (26.3%). AMR reached 100% towards oxacillin and Penicillin G for both <i>S. aureus</i> and CoNs.
Ahmadi et al. (2025)	Afghanistan	2023	130	Raw meat	16	<i>S. aureus</i>	13.3%	
Ferreira et al. (2021)	Brazil	2018–2020	110	Fish from Supermarkets	46	<i>Salmonella</i> spp.	45.5%	
Benjelloun Touimi et al. (2020)	Morocco	Not mentioned	608	Food samples from the kitchen	Food S. = 122 Utensils = 180 Food H. = 55	<i>Staphylococcus</i> spp. or <i>S. aureus</i> and CoNs	<i>S. aureus</i> = 17.33% and coagulase-negative staphylococci = 23.33%	
Beres et al. (2022)	Romania	2021–2022	192	Pigs	24	<i>Clostridioides difficile</i>	12.5	A significant proportion of the porcine isolates (50%) were resistant to levofloxacin
(Adzitey et al. 2020)	Ghana	Not Men	225	Raw meat	189	<i>E. coli</i>	84%	Isolates were highly resistant to erythromycin (85.00%), tetracycline (73.33%) and ampicillin (71.67%).
Giri et al. (2021)	India	2019	100	Ready-to-eat street food	27 = <i>E. coli</i> 32 = <i>K. pneumoniae</i>	<i>E. coli</i> and <i>K. pneumoniae</i>	25.42%	The isolates showed high resistance to ampicillin (91.5%) followed by erythromycin (88.1%), cefepime (72.9%), imipenem (55.9%), cefotaxime (52.5%), cefoperazone sulbactam (49.2%) and ertapenem (47.5%)
Hadiyan et al. (2022)	Iran	–	380	Raw meat	94	<i>Campylobacter</i> species/ <i>C. jejuni</i> and <i>C. coli</i>	57.44% for <i>C. jejuni</i> and 48.14% <i>C. coli</i>	<i>C. jejuni</i> strains harboured the highest resistance against erythromycin (42.59%), ampicillin (38.88%), ciprofloxacin (33.33%), chloramphenicol (31.48%) and tetracycline (31.48%). <i>C. coli</i> isolates harboured the highest resistance rate against ampicillin (73.07%), ciprofloxacin (73.07%), erythromycin (65.38%) and chloramphenicol (50%).
Hailu et al. (2021)	USA	2016–2020	844	Poultry Farms	163	<i>E. coli</i> O157, <i>Salmonella</i> , <i>L. monocytogenes</i> and <i>Campylobacter</i> spp.	19.3%	Out of the total positive samples, 17.8% (29 of 163) had an MDR pathogen.

(Continued)

Table 1. Continued.

First author (publication year)	Study area (country)	Study period	Sample size	Sample source	No. of positive samples	Main isolated bacteria species	Prevalence of isolated bacteria species	Resistance patterns of the isolates
Tate et al. (2022)	USA	2019	salmon (n = 710) and shrimp (n = 710) and tilapia (n = 214)	Fish	467 = salmon 369 = Shrimp 84 = tilapia	<i>Salmonella</i> spp., <i>Aeromonas</i> spp., <i>Vibrio</i> spp., <i>P.</i> <i>aeruginosa</i> , <i>Staphylococcus</i> spp. and <i>Enterococcus</i> spp.	66% from shrimp, 52% from tilapia and 39% from salmon	Only the <i>vibrio</i> spp. was resistant to Ampicillin (42%) and Azithromycin (43%) but the other isolates were susceptible to most antimicrobials.
Jia et al. (2024)	China	2021	143	Ready-to-eat fruits and vegetables	47	<i>S. aureus</i>	RTE fruits = 34.8% Vegetables = 31.2%.	Isolates were resistant to trimethoprim-sulphamethoxazole, oxacillin and ampicillin.
Abey et al. (2024)	Ethiopia	2020–2021	384	Slaughterhouse (Abattoir worker's hands, carcasses, knives, cattle feces, abattoir water and effluents)	115	<i>E. coli</i>	14.8%	All isolates were resistant to vancomycin and erythromycin but were susceptible to ampicillin, nalidixic acid and norfloxacin.
Marijani (2022)	Tanzania	2021	112	Fish	89	<i>E. coli</i> , <i>Klebsiella</i> spp., <i>Salmonella</i> spp., <i>Staphylococcus</i> , <i>Citrobacter</i> , <i>Shigella</i> spp. and <i>Pseudomonas</i> spp.	96.7%	<i>E. coli</i> isolates demonstrated resistance to erythromycin, penicillin, gentamicin, azithromycin and tetracycline, whereas <i>Salmonella</i> spp. isolates were resistance to gentamicin, penicillin, tetracycline and erythromycin.
Mekhloufi et al. (2021)	Algeria	2019	207	Ready-to-eat foods	48	<i>S. aureus</i> as in the case of methicillin-resistant strains (MRSA)	23.2%	Strains were resistant to benzylpenicillin, ofloxacin, erythromycin, lincomycin, tetracycline, kanamycin, oxacillin and cefotaxim.
Ngai et al. (2021)	Kenya	2019	150	Poultry feed types		<i>Salmonella</i> sp. and <i>E.</i> <i>coli</i>	58% <i>E. coli</i> and 28% <i>Salmonella</i> spp.	The highest resistance was against ampicillin (41%) for <i>Salmonella</i> sp. and (62%) for <i>E.</i> <i>coli</i> isolates.
Nguyen et al. (2021)	Vietnam	2017–2020	3,055	Poultry farms	181	<i>Salmonella</i> spp.	5.92%	Isolates were relatively resistant to chloramphenicol (62.98%), tetracycline (55.80%), ampicillin (54.14%) and sulfamethoxazole/trimethoprim (53.04%).
Poursina et al. (2023)	Iran	2021–2022	550	Raw meat	47	<i>P. aeruginosa</i> strains	8.54%	<i>P. aeruginosa</i> isolates showed the high resistance rate toward penicillin (87.23%), ampicillin (85.10%), tetracycline (85.10%), gentamicin (65.95%) and trimethoprim (57.44%).
Saharan et al. (2020)	India	2016–2029	202	Fish	<i>E. coli</i> = 81 <i>Salmonella</i> spp. = 72 <i>S. aureus</i> = 49	<i>E. coli</i> , <i>Salmonella</i> spp. and <i>S. aureus</i>	<i>E. coli</i> = 51% <i>Salmonella</i> spp. = 45% <i>S.</i> <i>aureus</i> = 31%	In the case of <i>E. coli</i> and <i>Salmonella</i> spp., the highest resistance (>95%) was observed against streptomycin, while for <i>S. aureus</i> , it was observed against trimethoprim.

(Continued)

Table 1. Continued.

First author (publication year)	Study area (country)	Study period	Sample size	Sample source	No. of positive samples	Main isolated bacteria species	Prevalence of isolated bacteria species	Resistance patterns of the isolates
Saksena et al. (2020)	India	2019, but not mentioned	150	Raw fruits and vegetables from retail and wholesale vendors.	146	<i>E. coli</i> , <i>Klebsiella</i> spp., <i>Enterobacter</i> spp., <i>Citrobacter</i> spp., <i>Providencia</i> spp., <i>Acinetobacter</i> spp. and <i>Pseudomonas</i> spp.	97.3%	All isolates were resistant to ceftazidime and cefotaxime
Hassani et al. (2022)	Iran	2022, but not mentioned	100	Raw bovine milk		<i>S. aureus</i> , <i>E. coli</i> , <i>L.</i> <i>monocytogenes</i> and <i>Salmonella</i> spp.	<i>E. coli</i> = 78% <i>L.</i> <i>monocytogenes</i> = 47% <i>S. aureus</i> = 25%, <i>Salmonella</i> spp. = 21%	All isolates demonstrate significant resistance to amoxicillin, chloramphenicol, gentamycin, tetracycline and cefalexin.
Sodagari et al. (2023)	Australia	2023, but not mentioned	100	Eggs sourced from caged and non-caged housing systems	57	<i>E. coli</i>	57%	The highest level of resistance was found against tetracycline (49%), followed by ampicillin (36%), trimethoprim (20%), sulfamethoxazole (18%), ciprofloxacin (2%) and tigecycline (1%).
Supriya et al. (2024)	India	2019–2020	720	Milk supply chains	31	<i>Staphylococcus</i> species	4.3%	Isolates showed resistance to methicillin (32.2%), b-lactam (41.9%) and macrolide-lincosamide-streptogramin B (3.2%).
Taha et al. (2021)	Iraq	2021, but not mentioned	25	Fish farm	19	<i>Aeromonas</i> spp.	76%	Ninety-six percentages of the isolates were resistant to each of the imipenem and gentamicin, followed by doxycycline 92%, ciprofloxacin and trimethoprim-sulfamethoxazole 88%, norfloxacin 58% and ceftriaxone 33%
Tedersoo et al. (2023)	Estonian	2015, 2017 and 2019	229	Pigs	119	<i>Campylobacter</i> spp.	52%	The resistance to streptomycin, tetracycline, ciprofloxacin and nalidixic acid was 74.8%, 54.4%, 34.4% and 31.9%, respectively
Tedersoo et al. (2022)	Estonia	2022, but not mentioned	46 strains of food and 15 strains of patients	Poultry	55	<i>Campylobacter</i> spp.	90.2%	Campylobacter resistance was highest to nalidixic acid (90.2% of strains) and ciprofloxacin (90.2%), followed by tetracycline (57.4%), streptomycin (42.6%) and erythromycin (6.6%).
Thwala et al. (2022)	South Africa	2022, but not mentioned	400	Beef meat	13	<i>S. aureus</i>	3.3%	The strain was resistant to erythromycin (23%), clindamycin (30.77%) and ciprofloxacin (15.3%)
Vázquez-Villanueva et al. (2023)	Mexico.	2023, but not mentioned	336	Slaughterhouse (water, surfaces, carcasses and feces)	280	<i>E. coli</i>	83.3%	The most prevalent phenotypic resistances were for tetracycline (83.3%), Cephalothin (44.2%), streptomycin (35%) and 36.7% for ampicillin.
Vogt et al. (2022)	Canada	2022, but not mentioned	200	Pigs	43	<i>E. coli</i>		Isolates were resistances to streptomycin, ampicillin, sulfisoxazole and trimethoprim/ sulfamethoxazole.

(Continued)

Table 1. Continued.

First author (publication year)	Study area (country)	Study period	Sample size	Sample source	No. of positive samples	Main isolated bacteria species	Prevalence of isolated bacteria species	Resistance patterns of the isolates
Weng et al. (2022)	China	2018–2020	321	Raw meat	216	<i>Salmonella</i> spp.	40.2%	Isolates were resistant to streptomycin (81%), tetracycline (77%), ampicillin (76.9%) and Azithromycin (53%).
Wiśniewski et al. (2022)	Poland	2020–2021	27 = food 13 environments	Purchased food and food processing area		<i>L. monocytogenes</i>	66.7% = food 53.8% = food processing environment	Isolates were resistant immediately resistant to clindamycin (33%) and trimethoprim (23%).
Worku et al. (2022)	Ethiopia	2020	556	Raw meat	36	<i>Salmonella</i> species and <i>E. coli</i>	6.47%	<i>Salmonella</i> spp. were resistant to amoxicillin (65%), cefotaxime (78%), ceftazidime (91%) and gentamycin (100%). <i>E. coli</i> was resistant to cefotaxime (100%) and gentamycin (90%).
Yamagami et al. (2023)	Japan	2018–2020	332	Animal feed	47 = feed samples and	<i>Enterococcus</i> spp.	67/57 = 82.5%	Highest resistance to kanamycin (26.1%), followed by erythromycin (24.6%), tetracycline (6.0%), lincomycin (2.2%), tylosin (1.5%), gentamicin (0.8%) and ciprofloxacin (0.8%).
Yan et al. (2024)	China	2021–2023	43	Ready-to-eat food	43	<i>Salmonella enteritidis</i>	100%	Resistance rates were 100% to nalidixic acid and 90.70% to ampicillin and ampicillin/sulbactam.
Yanestria et al. (2023)	Indonesia	2022	100	Poultry	23	<i>C. jejuni</i>	23%	Phenotypically, 100% (23/23) and 73.9% (17/23) <i>C. jejuni</i> isolates had high resistance to aztreonam and ampicillin, respectively.
Yanestria et al. (2024)	Indonesia	2022	200	Poultry	28	<i>C. Jejuni</i>	14%	These isolates showed high resistance to enrofloxacin (92.9%).
Yang et al. (2024)	China	2011–2019	125 (95 food + 30 human)	Ready-to-eat food	22 form food samples and 21 from human samples	<i>Salmonella</i> spp.	23.2% from food and 70% from patients	Isolates were commonly resistant to tetracycline (55%), ampicillin (49%), chloramphenicol (34%), streptomycin (32%) and sulphonamide (47%).
Ye et al. (2021)	China	2018–2019	724	Pig Farms	92	<i>Salmonella</i> spp.	12.7%	Isolates showed the highest resistance to tetracycline (85.9%), followed by trimethoprim (67.4%), ampicillin (60.9%) and chloramphenicol (51.1%).
Yu et al. (2024)	China	2002–2020		Fish	33	<i>Vibrio scophthalmi</i>	??	All isolates were frequently resistant to penicillins (48.5%), azithromycin (37%), tetracycline (36.36%) and ceftriaxone (57%).
Zhao et al. (2022)	China	2022, but not mentioned	510	Pigs	328	<i>Enterococci</i> spp.	64.3%	The resistance rate to furazolidone was 68.60%, followed by 42.99% to tetracycline, and one vancomycin-resistant <i>E. faecium</i> isolates were isolated from feed origin.
Zhou et al. (2024)	China	2016–2021	102	Retail food	102	<i>Salmonella</i> spp.	100%	Ampicillin had highest resistance rate (69.6%), followed by tetracycline (67.7%) and trimethoprim/sulfamethoxazole (48.0%).

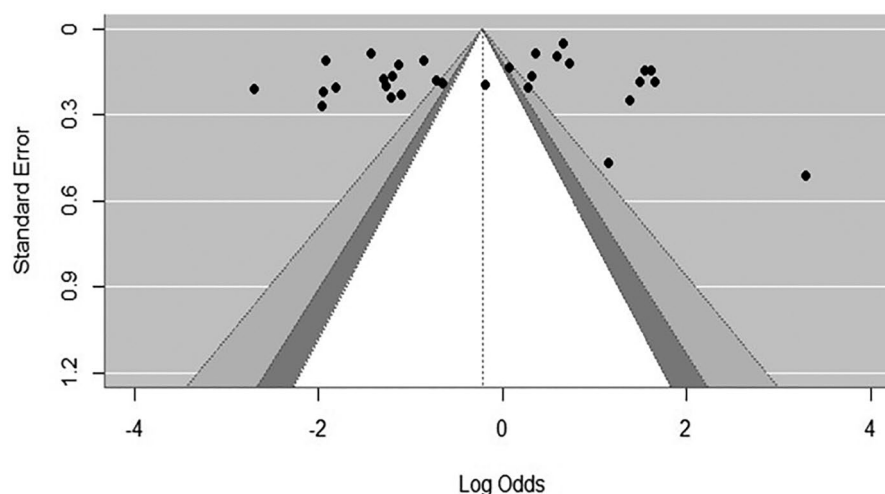


Figure 2. Funnel plot for the prevalence of AMR.

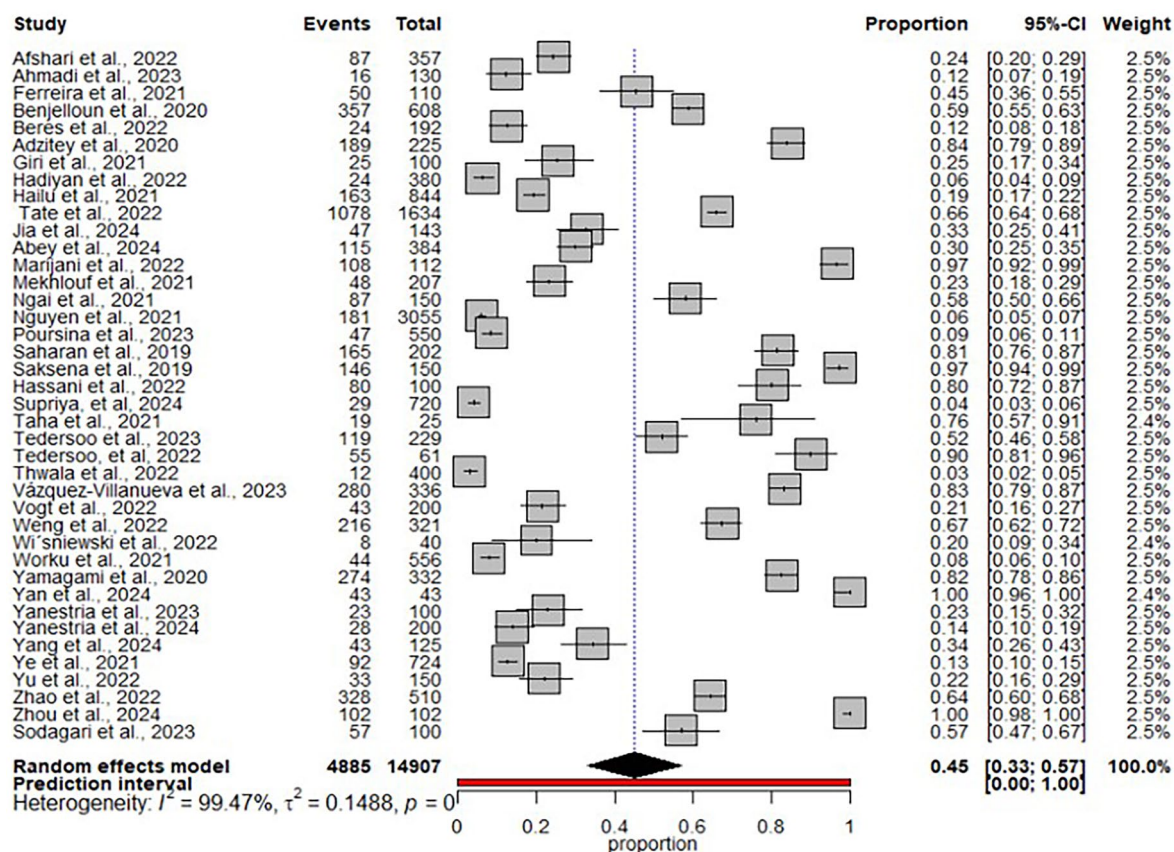


Figure 3. Forest Plot of prevalence of food source bacterial pathogens among in the included studies (event=total sample size; event=number of positive samples).

considerable variation, with Thwala et al. (2022) reporting a low prevalence (3%) and Marijani (2022) reporting a prevalence of 96.7%. A study conducted in Ghana reported that 84% of samples from raw meat tested positive for foodborne pathogens (Adzitey et al., 2020). The pooled prevalence of foodborne pathogens in Africa was 44% (95% CI [18, 72]). In North America, the prevalence rates ranged from 19.3% (Hailu et al., 2021) to 66% (Tate et al., 2022). Europe had a minimum rate of 12.5% (Beres et al., 2022) and a maximum rate of 90%. These differences indicate the influence of regional differences in food safety practices and environmental factors.

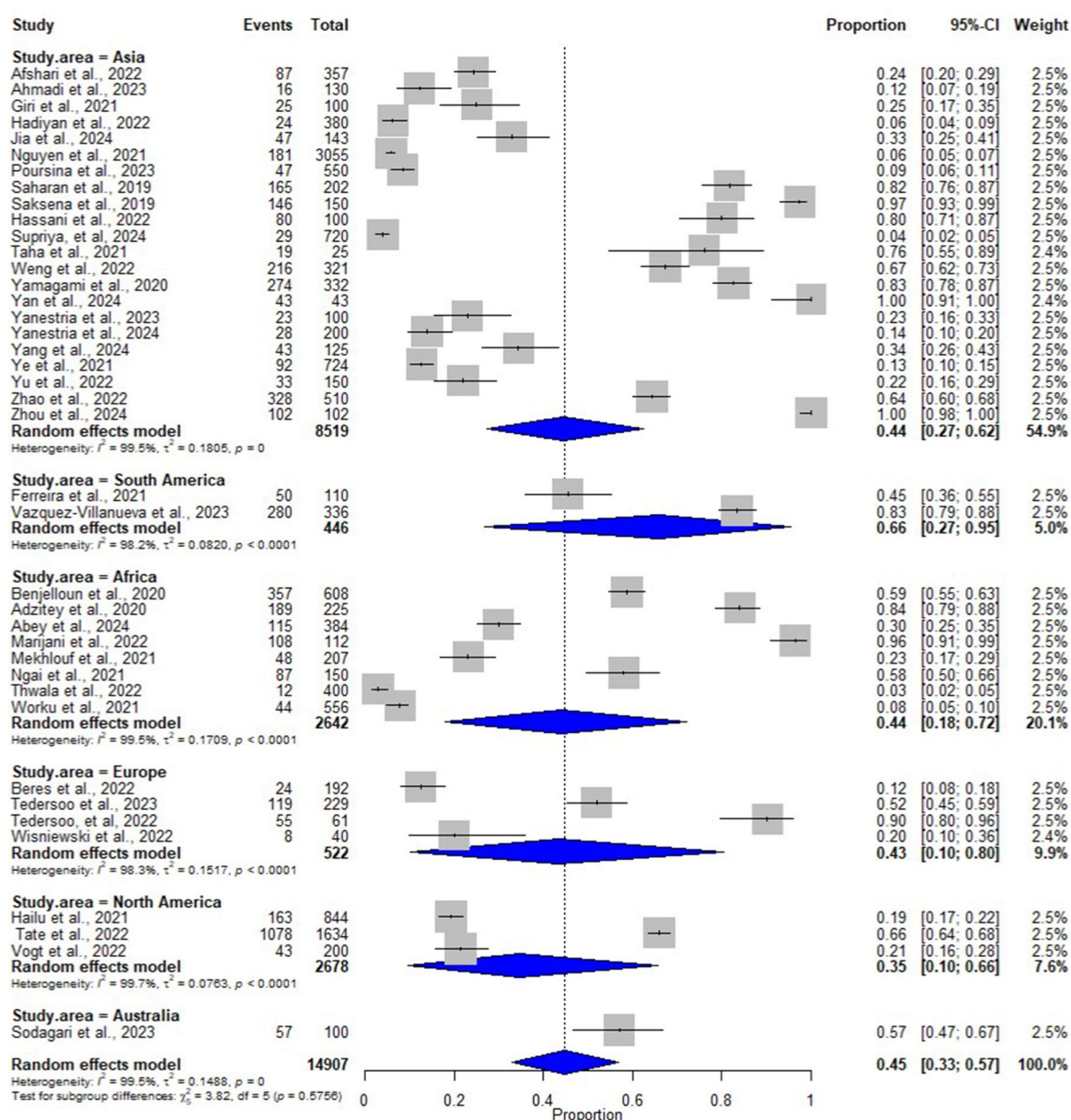


Figure 4. Forest Plot of prevalence of food source bacterial pathogens among in the included studies based on study area (event=total sample size; event=number of positive samples).

Table 2 shows the types of bacteria and their prevalence rates reported in the included studies. Fourteen studies conducted in various countries detected *Salmonella* spp. in different food samples. Of a total of 4,885 samples, 1,050 were positive for *Salmonella* spp., with a pooled prevalence of 36% (95% CI [15, 60]). Studies also reported high prevalence rates of *E. coli* (40%), *Enterococcus* spp. (58%) and *Klebsiella* spp. (33%). The pooled prevalence rates of *Campylobacter* spp., *Staphylococcus* spp. and *Enterococcus* spp. were 20%, 30% and 60%, respectively.

As shown in Table 3, the prevalence of isolated bacterial pathogens varied among food sources. Ready-to-eat food, raw meat and poultry samples were the most commonly tested, yielding the most detections. A total of 657 isolates were obtained from 2,493 raw meat samples, while 820 dairy product samples yielded 203 isolates. Ready-to-eat food samples (1,712) had the most isolates (923). There were also 147 isolates from 1,153 pig samples and 395 isolates from 720 slaughterhouse-related samples (including workers' hands, waters, carcasses and knives). Fruits and vegetables yielded 135 isolates. The prevalence of *Salmonella* spp. was highest in Ready-to-eat food samples (11.3%), raw meat samples (10%) and pig samples (7.98%; Table 3). Lower *Salmonella* spp. prevalence rates were observed in dairy

Table 2. Prevalence of isolated pathogens reported by different studies.

Isolated bacterial	No. of studies	Total sample size	No. of a positive result	No. of positives (%)	Pooled prevalence % (95% CI)	I ² (p-value)
<i>Salmonella</i> spp.	14	4,923	1,050	21.33	36 (15–60)	98 ($p < 0.001$)
<i>Staphylococcus</i> spp.	12	4,306	1,242	28.84	26 (14–40)	97 ($p < 0.001$)
<i>E. coli</i>	13	3,359	1,092	32.51	40 (22–60)	99 ($p < 0.001$)
<i>Enterococcus</i> spp.	4	2,619	1,684	64.3	58 (32–82)	99 ($p < 0.001$)
<i>Clostridioides</i> spp.	1	1,200	24	2	—	—
<i>Klebsiella</i> spp.	3	360	123	34.17	33 (22–44)	82 ($p < 0.001$)
<i>Campylobacter</i> spp.	6	1,814	317	17.48	30 (7–59)	98 ($p < 0.001$)
<i>L. monocytogenes</i>	3	984	121	12.3	23 (5–49)	97 ($p < 0.001$)
<i>Aeromonas</i>	1	1,634	425	26.01	—	—
<i>Vibrio</i>	2	2,144	736	34.33	32 (14–54)	96 ($p < 0.001$)
<i>P. aeruginosa</i>	3	2,446	87	3.56	4 (1–9)	94 ($p < 0.001$)
<i>Shigella</i>	1	112	4	3.57	—	—
<i>Citrobacter</i>	2	262	8	3.05	3 (1–6)	20 ($p < 0.26$)
<i>Providencia</i> spp.	1	150	2	1.33	—	—
<i>Enterobacter</i> spp.	1	400	38	9.5	—	—

product samples (2.56%) and poultry farm samples (5.8%). *Staphylococcus* spp. showed the highest prevalence in ready-to-eat food samples (32.4%) and dairy product samples (6.83%), indicating that these sources are particularly prone to contamination. Fish samples (4.9%) also showed notable *Staphylococcus* spp. contamination, while raw meat samples had a lower rate (0.52%).

E. coli and *Enterococcus* spp. had varying prevalence rates across food sources. For instance, *E. coli* was most frequently reported in eggs (57%), slaughterhouse samples (54.86%), and dairy products (9.5%), while it was less prevalent in ready-to-eat food samples (1.5%) and chicken samples (1.2%; Table 3). Similarly, *Enterococcus* spp. were reported in chicken samples (6.8%), other animal samples (9%) and fruit and vegetable samples (4.5%). *Campylobacter* spp. was also observed in various food sources, with prevalence rates of 5.7% in raw meat samples, 4.8% in pig samples and 4.5% in chicken samples. These findings suggest that certain food sources, particularly seafood, processed foods and slaughterhouse environments, are particularly prone to bacterial contamination.

Antimicrobial resistance profile of isolated bacterial pathogens

As shown in Table 4, resistance to various antimicrobial agents was observed mainly in *Staphylococcus* spp., *E. coli*, *Salmonella* spp., *Klebsiella* spp., *Enterococcus* spp., *Clostridioides* spp., *Campylobacter* spp., *L. monocytogenes* and *Vibrio* spp. The analysed studies used more than 20 antimicrobial panels to assess the AMR patterns of these bacterial pathogens. *Salmonella* spp. showed high pooled rates of resistance to multiple drugs, such as ceftazidime 94% (95% CI [86, 99]), streptomycin 88% (95% CI [78, 94]) and ampicillin 64% (95% CI [52, 75]). *Staphylococcus* spp. isolates exhibited varying resistance to different drugs, with high pooled rates of resistance to clindamycin (75%; 95% CI [12, 90]), amoxicillin (64%; 95% CI [28, 100]) and azithromycin (64%; 95% CI [30, 90]) and a lower rate of resistance to ciprofloxacin (29%; Table 4). *E. coli* also showed considerable resistance, particularly to cefotaxime (62%; 95% CI [24, 100]) and trimethoprim-sulfamethoxazole (60%; 95% CI [5, 90]). *Klebsiella* spp. were particularly resistant to ampicillin (100%) and ceftriaxone (78.2%; 95% CI).

Comparison of antimicrobial resistance of bacterial pathogen across different food sources

Table 5 shows the prevalence of AMR isolates from various food sources across different domains, including animal and food of animal products (representing livestock sectors), vegetable and fruit food origin (representing agricultural impacts) and slaughterhouse (from workers' hand, abattoir water, carcass and knives) to illustrate the human interface and connecting processing and production chains) reflecting One Health. *Salmonella* spp. exhibited high AMR especially in ready-to-eat foods and fish, with pooled prevalence rates of 70% (95% CI [19, 90]) and 43% (95% CI [13, 80]), respectively. *Staphylococcus* spp. also showed high pooled AMR rates: 30% (95% CI [16, 46]) in fish and 27% (95% CI [20–72]) in ready-to-eat foods. Similarly, *E. coli* exhibited considerable AMR, with a pooled prevalence of 62% (95% CI [20–95]) in fish samples. Of the 395 samples collected from slaughterhouses, 321 (81.2%) were positive for *E. coli*,

Table 3. Prevalence of bacterial pathogens in different food sources from the included studies.

Isolated bacteria	No. of studies	Source of sample										Total
		Raw meat (n=2,493)	Dairy products (n=820)	Ready-to-eat food (n=1,712)	Pig (n=1,153)	Eggs (n=100)	Fish (n=2,233)	Slaughterhouse (workers' hand, abattoir water, carcass and knives) (n=720)	Fruits and vegetables (n=293)	Poultry farm (n=4,859)	Other animal farms (n=524)	
<i>Salmonella</i> spp.	14	252 (10%)	21 (2.56%)	193 (11.3%)	92 (7.98%)	—	211 (9.5%)	—	—	281 (5.78%)	—	1,050
<i>Staphylococcus</i> spp.	12	13 (0.52%)	56 (6.83%)	555 (32.4%)	—	—	109 (4.9%)	—	—	—	—	733
<i>E. coli</i>	13	202 (8.1%)	78 (9.51%)	25 (1.5%)	—	57 (57%)	209 (10%)	395 (54.86%)	26 (8.9%)	58 (1.2%)	—	1,050
<i>Enterococcus</i> spp.	4	—	—	82 (4.5%)	—	—	—	—	—	328 (6.8%)	47 (9%)	457
<i>Clostridioides</i> spp.	1	—	—	—	—	—	—	—	—	—	24 (4.58%)	24
<i>Klebsiella</i> spp.	3	—	—	25 (1.5%)	—	—	65 (3%)	—	66 (22.53%)	—	—	156
<i>Campylobacter</i> spp.	6	143 (5.7%)	—	—	55 (4.8%)	—	—	—	—	220 (4.5%)	—	418
<i>L. monocytogenes</i>	3	—	48 (5.8%)	24 (1.4%)	—	—	—	—	—	66 (1.36%)	—	138
<i>Aeromonas</i> spp.	1	—	—	19 (1.1%)	—	—	—	—	—	—	—	19
<i>Vibrio</i> spp.	2	—	—	—	—	—	366 (16.4%)	—	—	—	—	366
<i>P. aeruginosa</i>	3	47 (0.42%)	—	—	—	—	—	—	—	—	—	47
<i>Shigella</i> spp.	1	—	—	—	—	—	4 (0.2%)	—	—	—	—	4
<i>Citrobacter</i> spp.	2	—	—	—	—	—	5 (0.22%)	—	3 (0.57%)	—	—	8
<i>Providencia</i> spp.	1	—	—	—	—	—	—	—	2 (0.06%)	—	—	2
<i>Enterobacter</i> spp.	1	—	—	—	—	—	—	—	38 (13%)	—	—	38

Table 4. Pooled prevalence rate of AMR of different bacterial pathogens.

Isolates bacteria in the studies	Antimicrobial agents	No. of studies	No. of isolates tested	No. of resistant isolates	Resistant isolates (%)	Pooled prevalence of AMR % (95%CI)
<i>Salmonella</i> spp.	Ampicillin	8	775	380	49%	64 (52–75)
	Kanamycin	1	125	30	24%	—
	Tetracycline	10	840	645	76.78%	62 (49–75)
	Chloramphenicol	6	483	321	66.41%	43 (30–58)
	Gentamycin	5	210	100	47.55%	48 (10–89)
	Ciprofloxacin	1	102	12	11.76%	—
	Trimethoprim-sulphamethoxazole	6	520	263	50.6%	65 (30–81)
	Azithromycin	5	499	414	82.9%	56 (17–80)
	Cefazolin	1	102	30	29.4%	—
	Ceftriaxone	3	324	176	54.3%	32 (7–56)
	Cefotaxime	2	138	104	75.5%	25 (20–60)
	Ceftazidime	2	183	171	93.5%	94 (86–99)
	Erythromycin	1	112	14	12.5%	—
	Streptomycin	3	376	320	85.2%	88 (78–94)
	Amoxicillin-clavulanic acid	3	204	116	56.8%	54 (25–80)
<i>Staphylococcus</i> spp.	Ampicillin	2	78	34	42.8%	64 (30–95)
	Tetracycline	5	185	29.23	15.8%	39 (18–63)
	Chloramphenicol	2	116	66	56.4%	44 (9–83)
	Gentamycin	5	525	200	38%	35 (4–75)
	Ciprofloxacin	5	442	162	36.5%	29 (14–50)
	Trimethoprim-sulphamethoxazole	3	544	183	33.6%	53 (2–95)
	Ceftriaxone	1	100	24	24%	—
	Azithromycin	2	457	382	83.6%	64 (30–90)
	Cefazolin	1	357	375	95%	—
	Erythromycin	4	195	76	38.8%	38 (8–90)
	Doxycycline	1	87	56	65%	—
	Clindamycin	3	156	49	31%	75 (12–90)
	Oxacillin	4	465	272	58.4%	55 (7–100)
	Kanamycin	1	48	8	16.9%	—
	Amoxicillin	2	125	54	43%	64 (28–100)
	Levofloxacin	2	63	21	33.1%	33 (30–35)
<i>E. coli</i>	Ofloxacin	1	48	4	8.7%	—
	Ampicillin	5	420	191	45.4%	57 (34–79)
	Tetracycline	5	586	348	59.4%	56 (8–75)
	Chloramphenicol	1	189	158	83.5%	—
	Gentamycin	4	274	205	74.9%	53 (8–85)
	Ciprofloxacin	3	288	126	43.8%	34 (2–80)
	Trimethoprim-sulphamethoxazole	5	542	1,232,381	70.2%	60 (5–90)
	Ceftriaxone	1	189	151	80%	—
	Azithromycin	3	225	128	56.7%	57 (13–77)
	Cefazolin	1	78	64	82%	—
	Cefotaxime	4	179	135	75.4%	62 (24–100)
	Erythromycin	4	375	188	50.3%	58 (15–80)
	Amoxicillin	3	256	124	48.2%	52 (23–60)
<i>Enterococcus</i> spp.	Tetracycline	3	457	205	44.8%	64 (42–80)
	Gentamycin	1	328	109	33.33%	—
	Ciprofloxacin	1	82	27	33.33%	—
	Cefazolin	1	328	104	31.7%	—
	Erythromycin	3	457	224	48.9%	52 (23–78)
	Doxycycline	1	82	55	66.66%	—
	Rifampin	1	82	55	66.66%	—
	Kanamycin	1	47	12	26.2%	—
	Kitasamycin	1	328	142	43.1%	—
	Furazolidone	1	328	225	68.6%	—
<i>Klebsiella</i> spp.	Ampicillin	1	25	25	100%	—
	Ceftriaxone	1	25	20	78.2%	—
	Cefotaxime	2	90	27	30%	35 (5–60)
<i>Campylobacter</i> spp.	Ampicillin	4	190	148	78%	—
	Tetracycline	5	368	326	88.9%	73 (37–82)
	Chloramphenicol	1	24	8	31.5%	—
	Gentamycin	1	68	33	48.6%	—
	Ciprofloxacin	4	276	140	50.5%	64 (32–90)
	Azithromycin	1	68	43	63.5%	—
	Erythromycin	4	225	152	67.7%	39 (3–89)
	Streptomycin	2	174	119	68.3%	62 (41–74)
	Enrofloxacin	1	78	73	92.9%	—

(Continued)

Table 4. Continued.

Isolates bacteria in the studies	Antimicrobial agents	No. of studies	No. of isolates tested	No. of resistant isolates	Resistant isolates (%)	Pooled prevalence of AMR % (95%CI)
<i>L. monocytogenes</i>	Ampicillin	1	67	55	81.5%	—
	Tetracycline	1	47	23	48.9%	—
	Chloramphenicol	2	114	69	60.2%	55 (45–60)
	Gentamycin	2	114	85	74.8%	66 (50–77)
	Ciprofloxacin	1	67	53	79%	—
	Trimethoprim-sulphamethoxazole	2	91	72	79.7%	64 (22–90)
	Ceftriaxone	1	47	17	36.2%	—
	Azithromycin	2	114	79	69%	65 (24–100)
	Clindamycin	1	24	8	33.3%	—
	Amoxicillin	1	47	46	97.8%	—
<i>Vibrio</i> spp.	Ampicillin	1	333	140	42%	—
	Tetracycline	1	33	12	36.4%	—
	Ceftriaxone	1	33	11	33.3%	—
	Azithromycin	2	336	138	41%	41 (35–42)
	Cefazolin	1	33	18	57%	—
	Doxycycline	1	33	10	30.3%	—
	Cefradine	1	33	25	75.6%	—

Table 5. Comparison of AMR in bacterial pathogens based on different food sources.

Bacterial pathogen	Sample source	No. of studies	The total number of isolates tested	No. of resistant isolates	Resistant isolates (%)	Pooled prevalence (%) (95%CI)
<i>Salmonella</i> spp.	Raw meat	3	252	152	60.3%	33 (4–53)
	Ready-to-eat food	3	193	178	92.2%	70 (19–90)
	Dairy products	1	21	6	28.6%	—
	Pig	1	92	79	85.9%	—
	Fish	3	211	168	79.6%	43 (13–80)
	Poultry farm	3	281	171	60.8%	16 (1–57)
<i>Staphylococcus</i> spp.	Raw meat	1	13	5	38.5%	—
	Dairy products (raw milk)	2	56	34	60.7%	13 (10–39)
	Ready-to-eat foods	6	998	535	53.6%	30 (16–46)
	Fish	2	109	58	53.9%	26 (20–72)
<i>E. coli</i>	Fruit and vegetables	1	47	38	80.9%	—
	Raw meat	2	202	170	84.2%	27 (22–88)
	Dairy products	1	78	69	88.5%	—
	Ready-to-eat foods	1	25	23	92%	—
	Pigs	1	43	30	69.8%	—
	Eggs	1	57	28	49%	—
	Fish	2	209	168	80.4%	62 (20–95)
	Slaughterhouse	2	395	321	81.2%	58 (9–98)
<i>Enterococcus</i> spp.	Ready-to-eat foods	1	82	68	83%	—
	Chicken	2	328	225	68.6%	45 (40–78)
	Another animal	1	47	39	84%	—
<i>Clostridioides</i> spp.	Other animals	1	24	22	92%	—
<i>Klebsiella</i> spp.	Ready-to-eat foods	1	25	20	80%	—
	Fish	1	32	23	72%	—
	Fruits and vegetables	1	66	45	68.2%	—
<i>Campylobacter</i> spp.	Raw meat	2	143	55	38.5%	25 (4–77)
	Pigs	1	55	32	58.2%	—
	Chicken	2	119	75	63%	22 (7–70)
<i>L. monocytogenes</i>	Dairy products	1	48	41	85.4%	—
	Chicken	1	66	48	72.7%	—
	Ready-to-eat foods	1	24	4	16.7%	—
<i>Aeromonas</i> spp.	Ready-to-eat foods	1	19	18	96%	—
<i>Vibrio</i> spp.	Fish	2	366	153	42%	35 (30–73)
<i>P. aeruginosa</i>	Raw meat	1	47	41	87.2%	—
<i>Enterobacter</i> spp.	Ready-to-eat foods	1	38	32	84.2%	—
	Fruit and vegetables	1	38	30	79%	—

representing a pooled prevalence of 58% (95% CI [9–98]). Regarding *Enterococcus* spp., 225 (68.6%) of the 328 isolates from chicken samples were resistant to various drugs, with a pooled prevalence of 45% (95% CI [40–78]). Among the *Campylobacter* spp. isolates from raw meat samples, 38.5% showed AMR, with a pooled prevalence of 25% (95% CI [4–77]).

Table 6. Multidrug pattern of isolated bacteria pathogens from different food sources.

Isolated bacterial pathogen	No. of studies	Total number of isolated tested	No. of multidrug isolates	Multidrug-resistant isolates (%)	Pooled prevalence % (95% CI)	I ² (p-value)
<i>Salmonella</i> spp.	11	1013	668	65.9	64 (41–84)	96 (p < 0.001)
<i>Staphylococcus</i> spp.	6	275	95	34.5	36 (8–69)	97 (p < 0.001)
<i>E. coli</i>	8	1,049	544	51.9	59 (33–82)	97 (p < 0.001)
<i>Campylobacter</i> spp.	8	482	50	10.4	24 (12–39)	93 (p < 0.001)
<i>Klebsiella</i> spp.	1	235	30	12.8	—	—
<i>Vibrio</i> spp.	1	33	6	18.2	—	—
<i>Enterococcus</i> spp.	3	1,296	164	12.7	18 (15–45)	92 (p < 0.001)
<i>Pseudomonas</i> spp.	1	47	33	70.2	—	—
<i>L. monocytogenes</i>	2	210	94	44.8	62 (45–65)	99 (p < 0.001)

Prevalence of multidrug resistance patterns

Of the 40 studies included in this review, 28 (70%) reported isolates with multidrug resistance (MDR). Of the 4,885 isolates, 1,865 (38.2%) were resistant to three or more antimicrobial agents. MDR patterns were reported for nine bacterial pathogens: *Salmonella* spp., *Staphylococcus* spp., *Shigella* spp., *E. coli*, *Klebsiella* spp., *Enterococcus* spp., *Vibrio* spp., *Pseudomonas* spp. and *L. monocytogenes*. The pooled MDR rates of *Salmonella* spp., *Staphylococcus* spp. and *E. coli* were 64% (95% CI [41, 84]), 36% (95% CI [8, 69]) and 59% (95% CI [33, 82]), respectively (Table 6). *Enterococcus* spp. had an MDR rate of 18% (95% CI [15, 45]).

Discussion

The One Health concept is a strategy for expanding collaboration in all aspects of health management for humans, animals and the environment (Overgaauw et al., 2020). Despite One Health's goal of achieving sustainable health by addressing human, animal and environmental problems, AMR remains a serious public health issue that requires significant efforts by policymakers and other stakeholders (Tweldemedhin et al., 2022). Increasing evidence indicates that the extensive use of antimicrobials in food-related sources could contribute to the development of resistance to antimicrobials commonly used in human treatment (Huemer et al., 2020). These pathogens can contaminate food products during processing or storage. This highlights the necessity of a One Health approach, which emphasises the interconnectedness of human health, food safety, animal health and the environment. Thus, this study aimed to provide an overall picture of the extant evidence on the AMR of pathogens in food-related sources, along with a One Health perspective.

Our study revealed the high prevalence of AMR pathogens from various food-related sources and the high prevalence of MDR in low- and middle-income countries. The estimated pooled prevalence of bacterial pathogens in food-related sources was 45%. This is higher than previously reported rates, for example, 30% in Thailand (Jasmina Vidic et al., 2023) and 32.9% in Egypt (Gunjan et al., 2023). This higher AMR prevalence estimate in our study likely reflects the broader geographic scope, as these two studies only compare prevalence between two countries regarding their One Health strategies. A study conducted by Smith et al. (2020) also reported a prevalence of 42%. According to a European Union report, in 2017, bacterial agents caused 33.7% of all foodborne disease outbreaks, with *Salmonella* spp. accounting for 21.8% and *Campylobacter* spp. accounting for 21.8% (Bintsis, 2017). This raises significant concerns regarding food safety, including production, processing, storage and distribution, which can lead to contamination. This highlights the limitations of One Health's emphasis on multifaceted collaboration among various professions (Aenishaenslin et al., 2021).

The inconsistent prevalence of pathogens in food-related sources across study areas reflects variations in food safety and pathogen control practices. Our study shows that, in Asian countries, nearly half of the studies reporting a prevalence of more than 50%, for example, the reported prevalence rates ranged from as low as 4% (Supriya et al., 2024) to as high as 100% (Yang et al., 2024; Zhou et al., 2024). This may be due to Asian countries' varying implementation of food safety regulations, surveillance systems and enforcement of hygiene standards in food production and handling (Gandra et al., 2020; Jean & Hsueh, 2011). Uncontrolled antibiotic use has also been indicated as a reason for developing antimicrobial-resistant foodborne strains in these countries (Thapa et al., 2020). Since nearly 90% of the antibiotics given to livestock are excreted with urine and stool and widely dispersed through fertilisers

and groundwater (Killewo et al., 2023). Similarly, studies in Africa showed similar variations in the prevalence of foodborne pathogens, with the highest reported rates being 96.7% (Marijani, 2022), 84% (Adzitey et al., 2020), 59% (Benjelloun Touimi et al., 2020) and 58% (Ngai et al., 2021). Thus, low- and middle-income countries lag behind in terms of containing the spread of foodborne pathogens. The burden of AMR on food animals is partially documented or unknown, and its threat to the food-related sources is poorly understood (Founou et al., 2016). Consequently, there is no data or knowledge on the spill-over of AMR in food-related sources (Murray et al., 2022). Despite the expectation that high-income countries would implement effective AMR control measures, this study indicates that the prevalence of foodborne pathogens remains high in these countries. This may be because our study analysis incorporated fewer studies in high-income countries compared to other regions, which could explain the higher prevalence of AMR. In North America, for instance, the rate varied between 19.3% (Hailu et al., 2021) and 66% (Tate et al., 2022). This indicates that the wide variability in AMR prevalence across regions highlights disparities in food safety infrastructure, antimicrobial stewardship, and surveillance capacity, emphasising the urgent need for coordinated, multidisciplinary One Health interventions globally to control AMR transmission through the food-related sources effectively.

In terms of specific food-related sources, *Salmonella* spp. was mostly identified in ready-to-eat foods and fish, with pooled prevalence rates of 70% and 43%, respectively. These pathogens were found to be highly resistant to antimicrobials such as ceftazidime, streptomycin, and ampicillin. Our result showed that Ready-to-eat food and fish were also typical sources of *Staphylococcus* spp., with pooled prevalence rates of 30% in fish and 27% in ready-to-eat food. *Staphylococcus* spp. was highly resistant to clindamycin, amoxicillin and azithromycin. These findings are consistent with another review of studies on the prevalence of pathogens in Ready-to-eat foods (Mengistu et al., 2022), which estimated a pooled *Staphylococcus* spp. prevalence of 30.24%. Another study reported that *S. aureus* had the highest rates of resistance, particularly to penicillin, clindamycin, erythromycin and gentamycin (Molineri et al., 2021). This might be the result of consuming raw foods with no processing or treatment that could greatly reduce microbial loads. Consuming foods contaminated with pathogenic bacteria remains a major public health concern and a common cause of illness and death worldwide (Kirk et al., 2014). High *E. coli* AMR was observed in fish samples (62%) and slaughterhouses (58%). This pathogen was resistant to cefotaxime and trimethoprim-sulfathiazole. Antimicrobial-resistant *Enterococcus* spp. was frequently observed in chicken samples. This is in line with evidence showing that cattle and poultry production account for the highest consumption of antimicrobials in Africa (Mshana et al., 2021). *Campylobacter* spp. was isolated from raw meat samples. Foodborne *Campylobacter* spp. has also been reported as a common problem (Hlashwayo et al., 2021). A previous study identified *S. aureus*, *E. coli*, *Acinetobacter baumannii*, *K. pneumoniae*, *Streptococcus pneumoniae*, and *P. aeruginosa* as the six leading pathogens implicated in deaths associated with AMR (Murray et al., 2022), which cause an estimated 3.57 million deaths linked to AMR and 929,000 deaths attributable to AMR. These findings indicate that ready-to-eat foods, fish and poultry-related sources serve as significant reservoirs for highly antimicrobial-resistant pathogens, posing a considerable risk for transmission of AMR to humans through the food-related sources. The high prevalence and resistance patterns of key pathogens such as *Salmonella*, *Staphylococcus*, *E. coli* and *Enterococcus* underscore the urgent need for improved food safety measures, targeted antimicrobial stewardship in food production, and enhanced surveillance to mitigate the public health impact of AMR globally.

Another common issue was MDR, which was reported in 28 of the analysed studies. MDR was observed in *Salmonella* spp., *Staphylococcus* spp., *Shigella* spp., *E. coli*, *Klebsiella* spp., *Enterococcus* spp., *Vibrio* spp., *Pseudomonas* spp. and *L. monocytogenes*. *Salmonella* spp. had a particularly high MDR rate (64%), followed by *E. coli* (59%). These findings are consistent with several previous studies. For example, Syed Abu Thahir et al. (2023) reported that 66.7% of *Salmonella* spp. isolates from animals in Malaysia were MDR, with an MDR index of 0.42, indicating high-risk antibiotic contamination. A study conducted in China reported even higher MDR rates of *Salmonella* spp. isolated from chicken meat (81.1%) and pork meat (73.2%) at retail markets (Zhang et al., 2018). Overall, these findings underscore the extent of the spread of MDR pathogens and the urgent need for improved antimicrobial stewardship and surveillance across sectors, including agriculture and healthcare. The presence of MDR pathogens in food animals and retail food products poses a significant risk to consumers. Moreover, infections with MDR bacteria in hospital settings have adverse clinical outcomes, such as prolonged hospital stays and mortality, and create

significant financial burdens (Madrazo et al., 2021; Serra-Burriel et al., 2020). Better-managed mitigation strategies and systematic One Health-based AMR surveillance can narrow knowledge gaps and facilitate comprehensive MDR risk computations (Himanshu et al., 2022).

The findings of this study underscore the critical importance of a One Health approach to combat AMR in food-related sources effectively. The interconnectedness of human, animal and environmental health is evident in the widespread prevalence of AMR pathogens and MDR across diverse food sources. Variability in AMR prevalence across regions reflects disparities in food safety practices, antimicrobial use and regulatory enforcement, particularly in low- and middle-income countries, where unregulated antimicrobial use in agriculture and inadequate surveillance exacerbate the spread of resistance.

Strengths and limitations

The main strength of this systematic review and meta-analysis lies in the comprehensive search strategies employed, and the rigorous analysis performed. However, this study also has certain limitations. First, there was considerable heterogeneity among the included studies, possibly due to differences in methodologies and sample sizes, which may have affected the pooled prevalence rates. A subgroup analysis was performed to determine whether the high heterogeneity could be explained by differences in study characteristics. Additionally, the potential for publication bias exists, as the analysis included only published studies, which may overrepresent positive findings and underestimate negative results; this could impact the overall conclusion. Second, only studies focusing on AMR in bacteria found in food sources were included. AMR patterns in other pathogens, such as parasites and fungi, were not considered. Third, only studies published online from 2020 to 2024 were included. Including recent studies is beneficial, given that AMR patterns can change rapidly due to evolving practices, interventions, or environmental factors. Fourth, fewer studies from European data were included in this analysis due to limited studies meeting the inclusion criteria. Similarly, the low number of studies on vegetables and fruits suggests that research has focused more on meat and RTE foods, possibly due to higher AMR risks or better surveillance. These gaps highlight the need for broader research and reporting across regions and food types to support comprehensive AMR monitoring. Finally, some studies lacked details about AMR patterns, specifically which pathogens were resistant to antimicrobials.

The implication of the results for practice, policy and future research

The findings of this study have important implications for practice, policy and future research. The high prevalence of antimicrobial-resistant pathogens in food sources highlights the need for stronger food safety measures, particularly in low- and middle-income countries, where food safety regulations and surveillance systems may be insufficient. The observed high prevalence of multidrug-resistant pathogens in various food sources suggests that policymakers should prioritise the development and implementation of robust antimicrobial stewardship programs in the agricultural, food production and environmental sectors and strengthen international collaborations to reduce the spread of antimicrobial-resistant bacteria through globalised food-related sources. Future research should focus on issues not covered in this study, such as multidrug-resistant pathogen transmission pathways, implementing comprehensive antimicrobial stewardship programs throughout the entire food value chain, ensuring responsible use of antibiotics in agriculture and veterinary practice combined with surveillance for AMR in animals, food products and the environment. The One Health approach should be enhanced by incorporating standardised monitoring to better assess the efficacy of interventions against AMR for human, animal and environmental health.

Conclusion

Our study provides the burden of AMR in food sources, emphasising the critical interconnectedness of humans, animals and the environment and the need to adopt a One Health approach to prevent the spread of resistant bacteria globally. This study highlights significant geographic variations in the prevalence of AMR among pathogenic bacteria from various food sources, and it showed the highest in Asian

and African countries. *Salmonella* spp., *Staphylococcus* spp., *E. coli*, *Campylobacter* spp. and *Enterococcus* spp. are the bacteria most commonly detected in this review from different food sources, with high rates observed across several antimicrobial agents. Common sources include ready-to-eat food, fish, poultry, raw meat and slaughterhouses. Pathogens such as *Salmonella* spp., *E. coli* and *Staphylococcus* spp. exhibit considerable multidrug resistance, posing substantial public health risks. The presence of highly resistant pathogens in the food-related sources highlights the urgent need for integrated interventions that encompass improved antimicrobial stewardship, strengthened food safety measures and coordinated surveillance systems across human health, veterinary, agricultural and environmental sectors. Addressing AMR through a holistic One Health framework will not only reduce the transmission of resistant pathogens through food but also mitigate the broader public health impacts, including difficult-to-treat infections and increased healthcare burdens, thereby promoting sustainable and effective control of AMR globally.

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Ethical approval

Not applicable.

Authors' contributions

GE and AM developed the conceptual focus, reviewed and analysed the literature, and wrote the original draft; SR and DT developed the conceptual focus, contributed to data analysis and data curation, and reviewed the manuscript; MSI and NJ supervised the team and contributed to conceptualisation, data curation, validation, visualisations, review and editing. All authors approved the final version to be published.

Availability of data and material

All data generated or analysed during the current study are included in this published article and its supplementary information files.

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ORCID

Md Shahidul Islam  <http://orcid.org/0000-0001-8984-8689>

Daniel Teshome Gebeyehu  <http://orcid.org/0000-0002-3325-4571>

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