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Exploring the prevalence of antibiotic resistance patterns and drivers of antibiotics resistance of *Salmonella* in livestock and poultry-derived foods: a systematic review and meta-analysis in Bangladesh from 2000 to 2022

Rezaul Karim Ripon[1]*, Umma Motahara[1], Ayesha Ahmed[1], Nishrita Devnath[1], Fatema Akter Mahua[1], Rubaiya Binthe Hashem[1], Kifayat Sadmam Ishadi[1], Adiba Alam[1], Md. Safaet Hossain Sujan[1] and Md Samun Sarker[2]

[1]Department of Public Health and Informatics, Jahangirnagar University, Savar, Dhaka, Bangladesh; [2]Antimicrobial Resistance Action Center (ARAC), Bangladesh Livestock Research Institute (BLRI), Savar, Dhaka, Bangladesh

*Corresponding author. E-mail: riponrezaul5@gmail.com

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Background: Antimicrobial resistance (AMR) is a severe public health problem that Bangladeshis are dealing with nowadays. However, we wanted to investigate the pooled prevalence of *Salmonella* and AMR in *Salmonella* strains isolated from livestock- and poultry-derived foods between 1 January 2000 and 31 August 2022.

Methods: The metafor and metareg packages in the R programming language were used to conduct all analyses. We used a random-effect or fixed-effect model for pooled prevalence of *Salmonella* and AMR to *Salmonella*, depending on the heterogeneity test for each antibiotic. The heterogeneity was examined using stratified analyses, the meta-regression approach and sensitivity analysis.

Results: The combined prevalence of *Salmonella* in livestock and poultry-derived food in Bangladesh is 37%, according to the 12-research considered (95% CI: 23%–52%). According to subgroup analysis, neomycin had the lowest prevalence of resistance (4%, 95% CI: 1%–13%), whereas tetracycline had the highest prevalence of resistance (81%, 95% CI: 53%–98%). According to univariate meta-analysis and correlation analysis, the prevalence of *Salmonella* increased with the study period ($\beta = 0.0179$; 95% CI: 0.0059–0.0298, $P = 0.0034$; $R^2 = 46.11\%$) and without this, none of aforementioned variables was significantly associated with the detected heterogeneity and there was a positive relationship ($r = 0.692$, $P = 0.001$) between the *Salmonella* prevalence and study period.

Conclusions: AMR is rising alarmingly in Bangladesh by livestock-derived food consumption. However, monitoring and evaluating antibiotic sensitivity trends and developing effective antibiotic regimens may improve *Salmonella* infection inhibition and control in Bangladesh. Policymakers should be concerned about food handling practices. Doctors should be concerned when using prescribing antibiotics.

Introduction

Salmonella is one of the most commonly recognized pathogens that cause gastroenteritis,[1,2] which results in significant morbidity, mortality and economic loss.[3,4] In 2010, the World Health Organization (WHO) reported 153 million cases of non-typhoidal *Salmonella* (NTS) enteric infections worldwide, of which 56 969 were fatal and 50% were foodborne.[5] *Salmonella* was the second foodborne epidemic in some regions' illness monitoring reports from 2006 to 2010.[6] Among the 2600 *Salmonella* serotypes discovered, NTS serovars such as Typhimurium and Enteritidis are the most common worldwide.[7,8] Poultry has been identified as the one cause of human salmonellosis, and avian salmonellosis affects the poultry business and can infect humans when infected poultry meat and eggs are consumed.[9] Eggs are the principal source of salmonellosis and other foodborne illnesses[10–13] *Salmonella* that grows in animal farms may contaminate eggs and meat during the slaughtering process before being transmitted to people via the food chain. Indeed, multiple earlier investigations have reported the isolation of *Salmonella* from animal and human diets.[14–17] Human *S.* Enteritidis is commonly associated with the intake of infected eggs and chicken meat, whereas *S.* Typhimurium is commonly associated with the consumption of pork, poultry and beef.[18,19] In addition, *Salmonella* enterica serovars have been found in varying concentrations in animal products and by-products worldwide.[18,20,21] The most often-reported serovars connected with human foodborne diseases are *Salmonella* Typhimurium and Enteritidis.[22] However, untyped *Salmonella* of animal origin is becoming more common in Bangladesh.[23,24]

However, domestic chickens in developing countries live close to humans in urban and rural communities and are frequently housed overnight in the family home.[25] As soon as a chicken becomes infected, it sheds faeces into the environment. Additionally, interacting with employees in poultry farms and slaughterhouses, the main route of human *Salmonella* infections, involves contaminated meat and eggs.[26] One of the primary reasons for animal management is the risk of antimicrobial resistance (AMR) in humans and animals.[27]

AMR is a worldwide public health issue.[28,29] AMR can be caused by one of three fundamental processes: (i) antibiotic modification by lowering absorption or enhancing efflux of the antibiotic via their enzymes; (ii) alteration in the antibiotic's target site and (iii) gaining the capacity to break or change the antibiotic.[30] Several lines of evidence showed that using antimicrobial agents in food animals contributes to the emergence and spread of AMR in foodborne *Salmonella*.[31] AMR has recently been a significant issue in treating *Salmonella* infections.[32,33] *Salmonella* infections in food animals are essential in public health and, in particular, food safety because food products of animal origin are thought to be the most common source of human *Salmonella* infections.[34] Contamination by healthy food handlers is also assessed during food processing. In recent years, it has been estimated that animals and their products can account for up to 96% of all *Salmonella* infections in humans.[35,36] AMR is expected to increase by 70% in Asia, posing a national and global threat.[37] The WHO estimates that *Salmonella* infections cause 93.8 million instances of gastroenteritis worldwide each year and that *Salmonella* infections cause 155 000 fatalities.[38]

Moreover, according to a recent Shanghai study, just 1.1% of strains were responsive to all 16 medications, and AMR rates for third and fourth-generation cephalosporins (cefotaxime and cefepime) were 10% and 8.1%, respectively.[39] Furthermore, according to a study conducted in Guangzhou, annual resistance rates of ampicillin are reasonably consistent. However, resistance rates of NTS to ceftazidime in 2015 (31.43%) were significantly greater than in 2014 (16%). Furthermore, AMR to ampicillin was considerably higher in serotype Typhimurium and Enteritidis isolates than in other serotypes.[40] *Salmonella* drug resistance rates to cephalosporin and cefepime were 22.3% and 13.1%, respectively, in four hospitals in Shenzhen,[41] which were all higher than the results of earlier Chinese investigations.[42,43] This phenomenon demonstrates that the outlook for AMR is bleak. Regarding AMR mechanisms, the corresponding resistance genes are usually found on plasmids, transposons, gene cassettes or variants of the *Salmonella* genomic islands SGI1 and SGI2.[44]

However, this study revealed a prevalence of *Salmonella* in poultry and livestock-derived foods. In this regard, this meta-analytical study will be evidential for assessing the prevalence of *Salmonella* in livestock and poultry-derived food and AMR in livestock and poultry-derived foods and comprehensively investigate the whole scenario of Bangladesh. We hypothesize that *Salmonella* pooled prevalence and antibiotic resistance are increasing in Bangladesh.

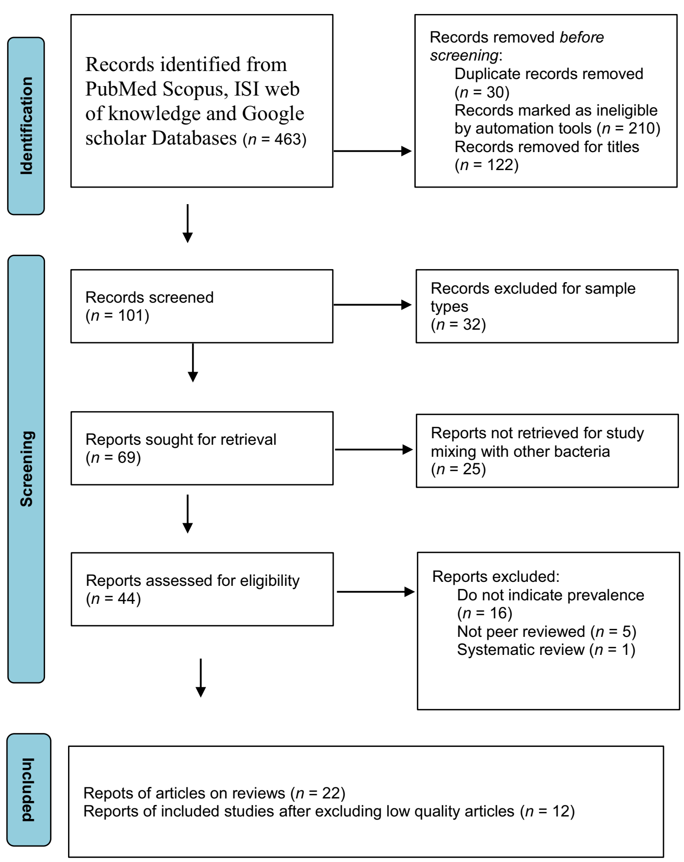

Figure 1. PRISMA flow diagram for this study.

Materials and methods

Data sources and systematic search strategy

We looked for research focused on investigating the prevalence of *Salmonella* and AMR in livestock and poultry-derived food in both English and Bangla. In English and Bangla, an attempt was made to locate grey and published scientific literature. From 2000 to August 2022, search engines such as Google Scholar, Scopus, ISI Web of Knowledge and PubMed were used to identify published literature, with reference lists of pertinent articles manually searched. We did not find any article on Bangla. The screening of titles and abstracts to find relevant publications was followed by full-text scanning of the relevant articles in a two-step approach.

Additionally, we were concerned with resolving any conflicts that developed during the data extraction to eliminate selection bias. '*Salmonella*' AND 'antibiotic resistance OR antimicrobial resistance OR

Table 1. Lists the explanatory factors for study regarding *Salmonella* that were retrieved from the investigations

Author, year	Study year	Location	Host	Sample no.	Positive no.	Sample type	AST method	AST standard	Quality of articles	Resistance antibiotics
Fatema *et al.*, 2014	2013	Dhaka	Chicken	20	10	Meat	Disc diffusion	CLSI	4	Ampicillin, Tetracycline, Nalidixic acid, Ciprofloxacin Gentamicin, Erythromycin, Rifampicin, Streptomycin, Kanamycin, zithromycin
Mahmud *et al.*, 2016	2013	Chittagong	Chicken	240	71	egg shell surface, egg content	Disc diffusion, Broth	CLSI	7	Enrofloxacin
Khan *et al.*, 2000	2004	Mymensingh, Feni, Dhaka	Chicken	24	24	Meat	Disc diffusion	CLSI	4	Ampicillin, Cloxacillin, Nalidixic acid, Erythromycin
Hosain *et al.*, 2012	2012	Mymensingh	pigeon	112	40	Clocal swab, Foot pad Faeces	Disc diffusion	CLSI	4	Ampicillin, Amoxicillin, Tetracycline, Chloramphenicol, Nalidixic acid, Gentamicin, Erythromycin, Kanamycin
Akond *et al.*, 2012	2010	Dhaka	Chicken	210	71	Cloacal swab, Intestinal fluid, Egg surface	Agar	CLSI	4	Ampicillin, Penicillin, Tetracycline, Chloramphenicol, Nalidixic acid, Ciprofloxacin, Erythromycin, Norfloxacin, Rifampicin, Cefixime, Cephalexin
Saifullah *et al.*, 2016	2015	Mymensingh	Pigeon	50	17	Cloacal swab, Pharyngeal swab	Disc diffusion	CLSI	4	Ampicillin, Nalidixic acid, Gentamicin, Azithromycin, Cephalexin
Rahman *et al.*, 2018	2017	Mymensingh, Gazipur	Chicken, Cow	169	37	Chicken meat, Milk, Beef	Disc diffusion	CLSI	6	Amoxicillin, Oxytetracycline, Doxycycline, Sulpha/Trimetho/Cotri, Ciprofloxacin, Gentamicin, Erythromycin, Neomycin, Amikacin, Azithromycin
Islam *et al.*, 2018	2017	Dhaka	Chicken	200	148	Egg	Disc	NCCLS	7	Ampicillin, Amoxicillin, Tetracycline, Chloramphenicol, Nalidixic

Continued

Table 1. *Continued*

Author, year	Study year	Location	Host	Sample no.	Positive no.	Sample type	AST method	AST standard	Quality of articles	Resistance antibiotics
										acid, Ciprofloxacin, Gentamicin, Kanamycin, Azithromycin, Ceftriaxone
Khan *et al.*, 2019	2018	Sylhet	Cattle	200	24	Milk	Agar	CLSI	7	Amoxicillin, Tetracycline, Sulpha/Trimetho/Cotri, Erythromycin, Streptomycin
Sobur *et al.*, 2019	2018	Mymensingh	Cattle	100	60	Cow dung, Milk	Disc	CLSI	4	Tetracycline, Oxytetracycline, Chloramphenicol, Ciprofloxacin, Gentamicin, Erythromycin, Neomycin, Kanamycin, Azithromycin, Ertapenem, Meropenem, Imipenem
Islam *et al.*, 2018a	2017	Jamalpur, Netrokona, Tangail, Kishoreganj	Chicken	20	14	Meat	Disc	CLSI	8	Ampicillin, Amoxicillin, Tetracycline, Ciprofloxacin, Erythromycin Azithromycin
Rahman *et al.*, 2019	2017	Dhaka	Chicken	50	50	Egg	Disc	CLSI	4	Ampicillin, Tetracycline, Gentamicin
Hassan *et al.*, 2014	2012	Chittagong	Chicken	30	13	Liver, Spleen	Disc	NCCLS	9	Amoxicillin, Tetracycline, Doxycycline, Colistin, Ciprofloxacin, Pefloxacin, Kanamycin, Enrofloxacin
Alam *et al.*, 2020	2017	Mymensingh	Chicken	100	35	Cloacal swab	Disc		4	Ampicillin, Tetracycline, Chloramphenicol, Ciprofloxacin, Streptomycin, Ertapenem
Jahan *et al.*, 2018	2017	Mymensingh	Quails	75	10	Cloacal swab	Disc	CLSI	4	Amoxicillin, Tetracycline, Colistin, Erythromycin, Neomycin
Joy *et al.*, 2017	2017	Sylhet	Chicken	320	46	Gut materials	Disc	CLSI	4	Ampicillin, Tetracycline, Sulpha/Trimetho/Cotri, Ciprofloxacin, Erythromycin, Neomycin

Islam *et al.*, 2022	2019–2020	Chattogram	Poultry Chickens	16	8	Chicken meat, Liver	Disc	CLSI	9	Not clear
Rabby *et al.*, 2021	2020	Dhaka	Poultry	52	7	Meat	Disc	CLSI	7	Erythromycin; Cloxacillin; Ampicillin; Trimethoprim; Nitrofurantoin; Ciprofloxacin; Cefotaxime; Ceftriaxone; Levofloxacin; Co-Trimoxazole
Rahman *et al.*, 2022	2020–2021	Barishal	Poultry	40	13	Chicken meat, Frozen milk	Disc	CLSI	8	Amikacin, Streptomycin, Gentamicin, Azithromycin, Oxytetracycline, Amoxicillin, Oxacillin, Sulfamethoxazole-Trimethoprim, Ceftriaxone, Ciprofloxacin
Matubber *et al.*, 2021	Not clear	Barishal, Pirojpur and Bhola	Chicken, Cattle, Goat	205	19	Chicken meat, Cattle meat, Buffalo meat and Goat meat	Disc	CLSI	6	Amoxicillin, Penicillin, Chloramphenicol, Erythromycin, Cefradine, Oxytetracycline, Enrofloxacin, Penicillin, Erythromycin, Cotrimoxazole, Cefradine, Amoxicillin, Penicillin, Cefradine
Rahman *et al.*, 2018a	2017	Dhaka	Chicken	189	82	Meat	Disc	CLSI	7	Amoxicillin, Penicillin, Chloramphenicol, Erythromycin, Cefradine, Oxytetracycline,
Begum *et al.*, 2007	2006	Dhaka	Chicken	50	35	Meat	Disc	CLSI	7	Penicillin, Chloramphenicol, Erythromycin, Cefradine, Oxytetracycline

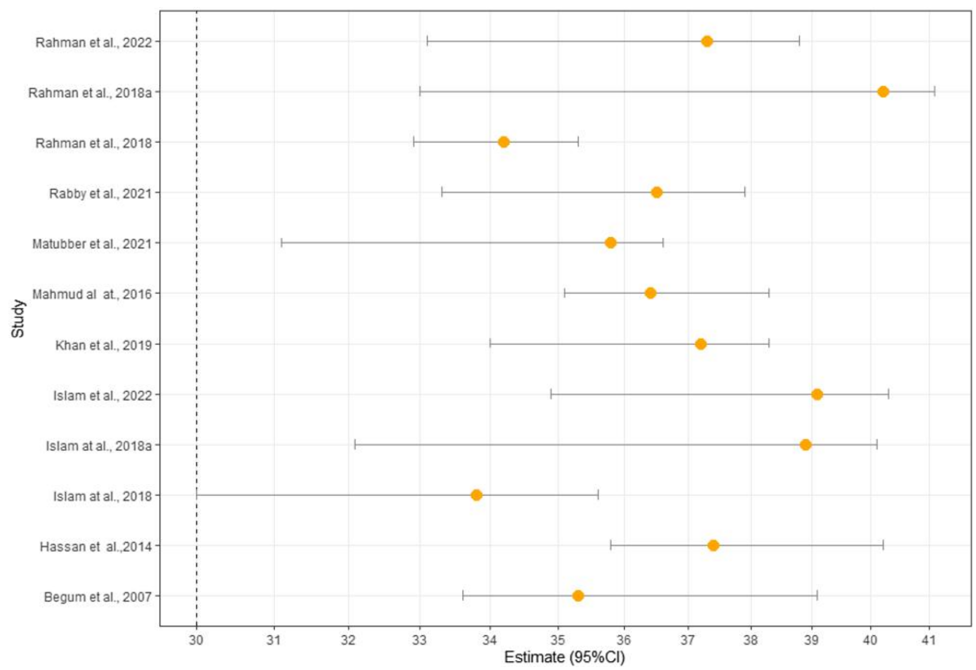

Figure 2. Sensitivity analysis for individual studies.

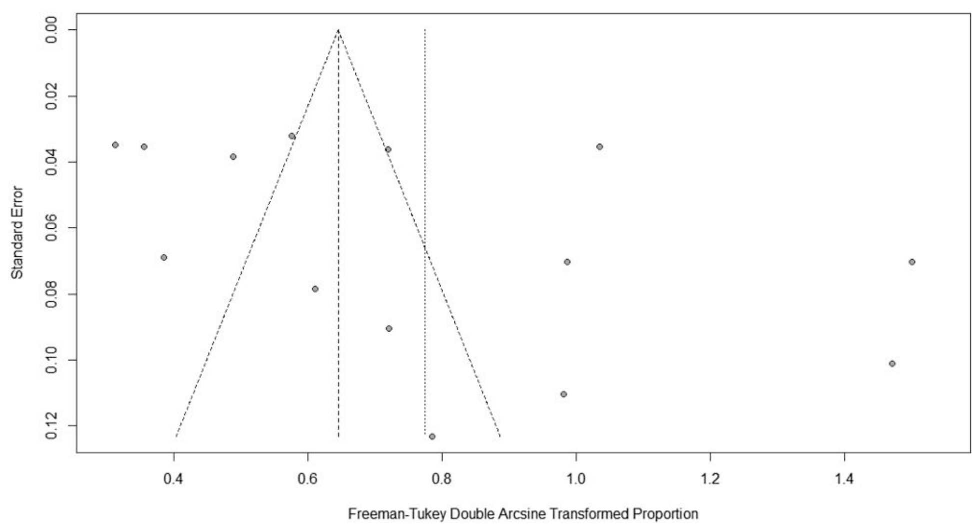

Figure 3. Funnel plot for study bias.

drug resistance OR AMR' AND 'prevalence OR incidence OR morbidity OR odd ratio OR risk ratio OR confidence interval OR *P* value OR rate' AND 'antibiotic resistance OR antimicrobial resistance OR drug resistance' AND 'Bangladesh'. Studies conducted on livestock and poultry were chosen using the Species filters in PubMed and Google Scholar. Because there was no sorting filter for species in the Web of Science and Cochrane Library, new search phrases were added to select species. The articles found during the search were exported to EndNote to be checked for duplicates. The unique hits were then uploaded to the Rayyan QCRI website for data extraction and screening. The title and abstract were screened first, followed by the complete content of the article.

Data collection process and data items

As a result of our search approach, all items were exported to the EndNote program. Duplicated articles were removed from the database. One neutral reviewer (A.A.) examined the titles and abstracts of the discovered papers. The whole texts of qualifying papers were obtained and appropriately evaluated for eligibility. The records were examined for legitimacy by the second examiner (M.S.S.). In the event of a disagreement between the two reviewers (A.A. and M.S.S.), the reviewer was then consulted by F.A.M. and A.M.S. Then, the article information was included by the three reviewers (N.D., K.S.I. and R.B.G.).

Table 2. Overall result in meta-analysis

Antibiotic name	Tau^2	I^2	χ^2	Random/fix effect of resistance prevalence, % [95% CI]	*P* for H	*P* for Egger
Erythromycin	0.13	94%	27.40	84[53–99]	<0.001	0.424
Ciprofloxacin	0.01	95%	143.4	20[4–42]	<0.001	0.523
Gentamicin	0.05	90%	71.82	11[2–24]	<0.001	0.242
Oxytetracycline	0.0097	65%	5.57	52[39–66]	0.06	0.654
Sulpha/Trimetho/Cotri	0.15	97%	144.29	42[11–70]	<0.001	0.524
Tetracycline	0.1	93%	60.48	80[53–98]	<0.001	0.525
Neomycin	0.1	60%	7.45	4[1–13]	0.06	0.131
Doxycycline	0.122	95%	35.63	51[12–89]	<0.001	0.354
Overall *Salmonella* prevalence	0.105	97%	558.13	37[23–52]	<0.001	0.636

Table 3. Univariate meta-regression analysis

Covariates	Beta [β] [95%CI]	*P* value	R^2 [%]
Study year	0.0179 [0.0059 −0.0298]	0.0034	46.11%
Location	−0.0073 [−0.0199 −0.0053]	0.2557	Nil
Host	−0.0085 [−0.0363 −0.0193]	0.5497	Nil
Sample number	0.0024 [−0.0017 −0.0064]	0.2623	20.98%
Positive sample	−0.0069 [−0.0230 −0.0093]	0.4037	Nil
AST method	−0.0106 [−0.0274 −0.0061]	0.2125	Nil
AST standard	0.0028 [−0.0016 −0.0072]	0.2140	15.22%
Quality of articles	−0.0384 [−0.1333 −0.0565]	0.4280	Nil
Resistance antibiotic	0.0097 [−0.0313 −0.0119]	0.3796	Nil

Furthermore, the Final was checked by one reviewer (R.K.R.). Next, statistical analysis was performed by R.K.R. and U.M. The search strategy was depicted in a PRISMA flow chart, which showed which studies were included and excluded and the reasons for exclusion (Figure 1).

Data extraction and quality assessment

We choose studies on the following criteria: (i) reported AMR in livestock and poultry-derived foods in Bangladesh; (ii) published between 2000 and August 2022; (iiii) samples indicated poultry and livestock-derived foods and (iv) were scientifically reported on location, number of samples and outcomes. The analysis did not cover the detection of *Salmonella* and the resistance pattern of sample types of faeces, faecal, cloacal, intestinal and rectal. In Bangladesh, there were no restrictions on when the study might be published.

Reporting bias assessment

Data quality was assessed according to the Joanna Briggs Institute.[45–47] Appropriate sample frame, study participants sampled, sample size, description of study subjects and setting, sample size justification, power description or variance and effect estimates, valid methods for condition identification, a standard and reliable condition measured appropriate statistical analysis, and adequate response rate were among the nine factors used to assess the risk of bias. The phrases 'yes', 'no', 'unclear' and 'not available' were used to convey the risk assessment criteria. They received a one-point score, while the others received a zero. The total score was 0 to 9. The likelihood of bias was considered low when the overall score was greater than 70%, moderate when it was 50%–69% and high when it was 0%–49% (Table 1).[45,47]

Statistical analysis

After reviewing the entire article for quality, the authors independently extracted data using purpose-built forms that specified the pertinent factors. Disagreements were settled by debating the articles and coming to an agreement. The significant dependent variable was a binary categorization of study results on the basis of whether the article supported the prevalence of *Salmonella* and antibiotic resistance to *Salmonella* or not. The proportion for the study based on the standardized effect size was the dependent variable in the meta-analysis. The statistical analysis was carried out with the help of the R programming language. The metafor and metareg in the R programming language were used to determine the pooled prevalence after excluding low-quality articles.[40,45,46] Metafor uses inverse-variance weights from a random-effects model to pool proportions and offers a weighted subgroup and overall pooled estimate. It entailed a meta-analysis of the prevalence values of each publication, weighted by sample size and allowing for potential heterogeneity across studies in this context. Before the random-effects model, the Freeman–Tukey transformation produced a proportional meta-analysis. Prevalence estimates were merged using a random-effects meta-analysis for accounting for between-study heterogeneity. The statistical heterogeneity was assessed using the chi-square test on the Q (H, I^2) statistic, which was quantified by the I^2 values under the assumption that I-square values of 25%, 50% and 75% were nominally assigned as low, moderate and high estimates, respectively.[40,45] The following grouping variables were used in stratified analyses and meta-regression for covariates to examine potential sources of heterogeneity. To establish whether one or more studies had an impact on the outcomes by being excluded one at a time, a sensitivity analysis was also performed. The distribution of the observed studies was visually inspected on a funnel plot to determine publication bias. Egger's linear regression and Begg's rank correlation test were then used to measure the level of bias.[40,45,46] The significance threshold was kept at <0.05.

Results

Search result and eligible studies

PRISMA was used to outline the specific steps of the systematic review and meta-analysis method, and Figure 1 outlines the process of selecting relevant papers. We identified 463 new studies via PubMed, Google Scholar, Scopus, ISI and Web of Knowledge databases. Owing to duplicate records, ineligible by automation tools, titles, sample types and study had mixing with other bacteria, 419 articles were removed. Twenty-two studies were removed for not indicating prevalence, being systematic and not being peer-reviewed. According to the quality assessment standards, two studies received a score of 9, two got an 8, six got a 7, two got a 6 and 10 got a 4. According to the quality scores, the studies were generally deemed to be of acceptable quality (scores more than or equal to 6)[47,48]. Ten articles were also removed for methodological quality. For that, we included 12 studies in this meta-analysis.

Characteristics of eligible studies

Table 1 included the characteristics of eligible studies The study sample included Chittagong, Mymensingh, Sylhet, Chittagong and Barisal divisions. The hosts were chickens, cattle and goats. These three are the most commonly used livestock for a portion of food in Bangladesh. According to the included study, 1411 livestock-derived food were used as a study sample, and the review found 471 samples to be *Salmonella* positive and resistant to some antibiotics. Most samples were identified by the disc diffusion method, and the CLSI method was used as an AST method. Tetracycline, oxytetracycline, doxycycline, sulpha/trimetho/cotri, ciprofloxacin, gentamycin and neomycin have frequently shown resistance against *Salmonella* in many reviewed studies.

Systematic review and meta-analysis results

A higher level of multi-drug resistance was present in Bangladesh. In Bangladesh, the combined prevalence of *Salmonella* isolated from livestock and poultry-derived foods (sample types faeces, faecal, cloacal and rectal excluded) was 37% of the sample. Overall, 37% of the sample had *Salmonella* in livestock and poultry-derived foods [95% CI: (23%–52%), $P \leq 0.001$, $R^2 = 97\%$]. A high prevalence was seen for some of the commonly prescribed antibiotics like tetracycline 81% [(95% CI:53–98), $P \leq 0.001$, $R^2 = 93\%$], oxytetracycline 52% [(95% CI: 38%–66%), $P = 0.06$, $R^2 = 65\%$], doxycycline 51% [(95% CI: 12%–86%), $P \leq 0.001$, $R^2 = 95\%$], sulpha/trimetho/cotri 42% [(95% CI: 11%–77%), $P \leq 0.001$, $R^2 = 97\%$], ciprofloxacin 20% [(95% CI: 4–43), $P \leq 0.001$, $R^2 = 95\%$], gentamycin 11% [(95% CI: 2%–25%), $P \leq 0.001$, $R^2 = 90\%$] and neomycin 4% [(95% CI:1%–13%), $P = 0.06$, $R^2 = 60\%$] (Table 2 and Figures S1–S9 (available as Supplementary data at *JAC-AMR* Online)). Among the included covariate in this study, only the study period showed significance in the univariate meta-analysis ($\beta = 0.0179$; 95% CI: 0.0059–0.0298, $P = 0.0034$; $R^2 = 46.11\%$) (Table 3). Sensitivity analysis was carried out by calculating pooled *Salmonella* prevalence once more when any single study was eliminated to verify the meta-analysis's stability and liability. The related pooled *Salmonella* prevalence was shown range from 40.2% (33.0%–48.5%) to 33.8% (30.0%–35.6%) without significantly changing (Figure 2). The statistically identical findings indicated that no single study had an impact on the stability of the overall estimate of the prevalence of *Salmonella* in this meta-analysis. Even though the funnel plot's visual inspection exhibited asymmetry (Figure 3), Egg's test demonstrated substantial value, and there was no chance of publication bias (Table 2).

There was considerable variation between studies. To investigate potential sources of heterogeneity, meta-regression (univariate) was used. The meta-regression method was used to examine the study period, location, host, sample number, positive sample, AST method, AST standard, quality of articles and resistance antibiotic as potential sources of heterogeneity. Table 3 contains the meta-finding on regressions. None of those previously mentioned factors were found to be substantially correlated with the identified heterogeneity through the regression model, except for research study time ($P = 0.004$). Therefore, we conducted additional research to examine the relationship between *Salmonella* prevalence and the study period. The prevalence of *Salmonella* was found to be positively correlated with the research study period ($r = 0.692$, $P = 0.001$) (Table 4).

Evidence-based antibiotic resistance drivers

AMR is an upcoming predicted pandemic for a low-income country such as Bangladesh.[29–33] Bangladesh has limited information on antibiotic use and resistance.[34] Antibiotics were considered able to treat both the physical and social elements of infection, which has severe implications for AMR.[22] AMR has mainly spread throughout the country's hospitals and unregulated pharmacy stores for their widely available antibiotics, overprescribing and selling antibiotics without prescription.[32] People in hospitals are predisposed to developing nosocomial and other infections due to the abuse of antibiotics and a lack of adherence to isolation techniques in these hospitals.[27] In Bangladesh, most antibiotic prescriptions are written by unqualified practitioners.[28,30] Owing to poor health systems, reported paucity of testing facilities, prescribing antibiotics without laboratory tests, using antibiotics for common infections and not finishing the entire course of antibiotics were causes of widespread resistance.[33] Unsafe drinking water, inadequate sanitation, lack of diagnostic facilities growing private practice and excessive demand for antibiotics are all contributing causes of AMR.[30,33] Antibiotic usage before seeking medical help may impair the sensitivity of blood cultures, which has ramifications for patients and doctors.[29] Antibiotics are used in various food animal production and meat systems, such as commercial poultry and aquaculture.[36] They have been discovered to be frequently used to boost food animal production, leading to the growth of antibiotic-resistant bacteria.[33]

Moreover, its use in aquaculture and aquatic ecology has been linked to AMR development.[28] Antimicrobial drugs used in aquaculture have established AMR bacteria reservoirs in fish and other aquatic and non-aquatic animals.[29–32] The long-term use of

Table 4. The correlation between the *Salmonella* prevalence and potential sources

Covariate	Study year	Location	Host	Sample no.	Positive no.	Sample type	AST method	AST standard	Quality of articles	Resistance antibiotics
P	0.001	0.744	0.563	0.785	0.325	0.325	0.563	0.566	0.743	0.774
r	0.692	0.764	0.346	0.633	0.764	0.763	0.567	0.568	0.366	0.852

these antibiotics indiscriminately and unnecessarily increases the prevalence of AMR.[28–31] This also leads to antibiotic residue. Antibiotic residues, other drugs and pollutants are found in high concentrations in Bangladesh's ponds, canals, lakes, rivers and other bodies of water.[36] Higher residues are caused by poor sanitation, hygiene, antibiotic misuse on the farm and inappropriate use.[33] As part of the food production cycle, food animals, seafood and vegetables are regarded significant reservoirs of AMR bacteria by these residues.[26] Some antibiotics may have lost their effectiveness against specific microorganisms due to the misuse of those antibiotics.[30] Antimicrobials are only available on prescription and to pharmacists who devote more time to patients. Antibiotics are sought and used during an emergency health problem.[24] Policy measures such as restrictions on licensing specific antibiotics are vital to human health.[25] In Bangladesh, specific and targeted measures to combat AMR should include teaching about the proper use of antibiotics.[31] There is a significant frequency of AMR in Bangladesh, and major gaps in surveillance and information, and there has been a drop in the rate of new antibiotic development.[23]

Discussion

The present study found a significant prevalence of *Salmonella* from livestock and poultry-derived foods in Bangladesh (sample type faeces, faecal, collocal and rectal exclude). We found that 37% of livestock and poultry food had *Salmonella*. Consequently, livestock and poultry-derived foods appear to be one of the essential *Salmonella* reservoirs in Bangladesh. A meta-analysis of *Salmonella* in Ethiopia indicates that the prevalence of *Salmonella* in slaughterhouse may vary from 7% to 43%,[46] and a worldwide meta-analysis of *Salmonella* prevalence in food indicate that it was less than 1%.[45,49] Therefore, researchers have investigated *Salmonella* prevalence for many years, and different rates have been found in different studies. The reported prevalence of *Salmonella* found in this study matched and differed from the findings of other researchers studying the prevalence of *Salmonella* in poultry.[50–57] Thus, it can be mentioned that the significant amount of *Salmonella* indicates a severe problem for both livestock and poultry-derived food and ensures public health.

Moreover, globally AMR is becoming a significant health issue.[53] Resistant to many drugs, *Salmonella* has become a considerable public health concern worldwide.[57] Our present study findings also revealed that a high percentage of the *Salmonella* isolates were resistant to routinely used antibiotics such as tetracycline, oxytetracycline, doxycycline, sulpha/trimetho/cotri, ciprofloxacin, gentamycin and neomycin and so on. Almost all the isolates tested in this investigation were determined to be multi-drug resistant, which is a concerning finding (Table 1).

However, among these antibiotics, the highest prevalence rate was seen for tetracycline (81%, 95% CI: 53–98). Some studies showed that isolated *Salmonella* was highly resistant to tetracycline in the antimicrobial investigation.[50–52] The present study found the next high prevalence rate for resistance to oxytetracycline that shows 52% from the isolates (95% CI: 38–66), but some studies found a higher prevalence rate of oxytetracycline rather than our findings.[45,46,48,49] According to a couple of studies, *Salmonella* resistance to tetracycline and oxytetracycline was found in layers and broilers in Bangladesh.[58–60] Doxycycline is another antibiotic used in humans and animals to treat various diseases. Investigating multi-drug resistance due to *Salmonella*, our findings showed that a high prevalence for this commonly prescribed antibiotic is 51% (95% CI: 12–86). In addition, a recent study showed that *Salmonella* in poultry in Bangladesh has also been found to have a considerable number of isolates resistant to doxycycline.[46,48,60] Moreover, according to univariate analysis and correlation in this meta-analysis, the prevalence of *Salmonella* increased with every year. Antibiotic resistance creates a severe problem in the treatment of *Salmonella*.

Furthermore, *Salmonella* has been proven to be a significant cause of creating resistance against several commonly prescribed antibiotics. Resistant to many drugs, *Salmonella* isolates were discovered in various food samples, and the gene responsible for multi-drug resistance could be passed on to consumers through food and unhealthy, unhygienic poultry handling systems, posing a severe public health risk. These findings also revealed that multi-drug resistance in *Salmonella* is rising due to the indiscriminate use of antibiotics in the dairy and poultry industries, pet animal usage and human practice in Bangladesh. In the future, rational usage of this antibiotic may help to prevent the formation of *Salmonella*-resistant isolates.

The main strength of this article was the pooled prevalence of *Salmonella* and antibiotic resistance to *Salmonella* from livestock and poultry-derived foods. We solely refer to the antibiotic subgroup. We looked through numerous databases and websites to discover all relevant and grey publications to eliminate database bias, but some databases or websites may be massing. The limitations mentioned before, as well as publication bias and heterogeneity for some of the pooled results, must be considered when interpreting the results.

Conclusions

Antimicrobial agents used in food animal production may lead to the emergence of multi-drug-resistant *Salmonella* strains. The irrational and excessive use of antibiotics in humans and food-producing animals raises the risk of AMR worldwide. To reduce the risk of pathogenic AMR bacteria originating from animal origin foods, raising awareness about the rational use of antibiotics in food animals, safe food handling and safe cooking practices is obligatory. Doctors should take concern when treating with an antibiotic.

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Transparency declarations

None to declare.

Supplementary data

Figures S1 to S9 are available as Supplementary data at *JAC-AMR* Online.

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