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REVIEW ARTICLE

A SYSTEMATIC REVIEW AND META-ANALYSIS OF THE BACTERIAL PREVALENCES AND RESISTANCE PROFILES IN SELECTED FOOD-PRODUCING ANIMALS AND ANIMAL-DERIVED PRODUCTS IN NIGERIA (2000–2025)

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Ethical considerations: When reporting experiments on animals Observation of the ARRIVE guidelines 2.0: Updated guidelines for reporting animal research, published on July 14, 2020 (DOI: 10.1371/journal.pbio.3000410), is applied. The authors ensure that all procedures were performed in compliance with the guidelines for animal care of their institutions or with national/international guidelines.

ABSTRACT

Bacterial pathogens such as *Escherichia coli* and *Salmonella* spp. are widely reported in food-producing animals in Nigeria and contribute to animal disease, food contamination, and public health risk. However, evidence on their prevalence and antimicrobial resistance (AMR) patterns remains fragmented. This study systematically reviewed and meta-analyzed studies published between January 2000 and March 2025 on bacterial prevalence and resistance profiles in food-producing animals and related products in Nigeria. Data on pathogen type, host species, sample source, and antimicrobial susceptibility were extracted. Pooled prevalence estimates were calculated using random-effects meta-analysis (REML), and heterogeneity was assessed using Cochran's Q and I^2 statistics. Thirty-two studies met the inclusion criteria. *E. coli* and *Salmonella* spp. were the most frequently reported pathogens and exhibited substantial multidrug resistance (resistance to ≥3 antimicrobial classes), particularly to tetracyclines, fluoroquinolones, sulphonamides, and *β*-lactams. The pooled prevalence of bacterial detection was 25% (95% CI: 14%–41%), with high heterogeneity (I^2 = 96.9%). Higher prevalence was observed in poultry systems, and meta-regression indicated that sample size significantly influenced prevalence estimates. These findings highlight a substantial burden of resistant bacteria in food-animal systems and underscore the need for strengthened antimicrobial stewardship, improved surveillance, and coordinated One Health interventions in Nigeria.

Key words: antimicrobial resistance; *Escherichia coli*; food animals; meta-analysis; One Health; *Salmonella*; surveillance

INTRODUCTION

Bacterial pathogens of major importance to food-animal production in Nigeria—particularly *Salmonella* spp., *Escherichia coli*, *Campylobacter* spp. and several others—have been widely reported in poultry, cattle, swine, and small ruminants across diverse regions of the country [1–7]. These organisms contribute not only to poor animal health, reductions in productivity, and increased economic losses for farmers but also to substantial challenges in veterinary clinical management [1, 3]. Rising antibiotic resistance has made the treatment of these infections increasingly difficult, with multiple studies documenting resistance to commonly used antibiotics, such as tetracyclines, fluoroquinolones, β-lactams, and aminoglycosides [2, 3, 5, 8]. Reports from several parts of Nigeria have consistently described multidrug-resistant *E. coli* and *Salmonella* serovars, including extended-spectrum β-lactamase (ESBL)-producing isolates, recovered from farm environments, slaughter facilities, and retail animal products [2, 6, 8, 9]. These findings underscore the growing clinical complexity of treating bacterial infections in livestock and the broader concerns for animal health systems in Nigeria.

A variety of structural and systemic factors contribute to the emergence and persistence of antimicrobial-resistant (AMR) bacteria in Nigerian food animals—antibiotics are widely accessible, frequently purchased without prescription, and commonly used for routine prophylaxis, metaphylaxis, or empirical mass treatment, particularly within commercial livestock operations [8–9]. These practices are often accompanied by inconsistent observance of withdrawal periods, insufficient veterinary oversight, and limited laboratory infrastructure for routine antibiotic susceptibility testing [2, 9]. Such conditions not only facilitate the development of antibiotic resistance but also hinder the generation of reliable data to guide antibiotic stewardship. As injudicious antibiotic use increases and production systems continue to expand, the challenges of understanding the national AMR landscape have become more pressing.

Despite the growing body of primary research, the existing evidence remains highly fragmented, as many studies focus on specific states, isolated production systems, or single pathogens, and their findings vary widely in methodology, sample size, and reporting standards [7]. Several narrative reviews have addressed aspects of AMR in Nigeria, but these are generally limited in analytical depth and have not provided formal meta-analytic estimates. Crucially, there is no comprehensive synthesis covering the entire 21st-century evidence base that integrates prevalence and resistance data across bacterial pathogens, regions, animal species, time periods, and antibiotic classes. In a country with a rapidly expanding livestock sector and significant public health concerns around antibiotic effectiveness, this gap has restricted the ability of policymakers, veterinary authorities, and public health practitioners to identify consistent national trends or to understand the magnitude and distribution of antibiotic-resistant bacteria [7, 8].

This systematic review and meta-analysis were undertaken to address these limitations by collating and rigorously synthesizing published evidence from 2000 to 2025. By bringing together data from multiple regions, animal hosts and animal-derived food products and applying standardized analytical methods, this study provides a comprehensive national assessment of bacterial pathogen prevalence and resistance patterns in Nigerian food-producing animals and animal-derived products. Beyond producing pooled estimates, the review evaluates the extent of heterogeneity across studies and explores the antibiotic resistance patterns of the bacteria identified. In doing so, it offers critical insights into the epidemiology of AMR in Nigeria's livestock sector, identifies gaps in surveillance and reporting, and highlights areas where targeted investment and policy interventions may have the greatest impact. The review represents a more detailed and methodologically robust synthesis of its kind for Nigeria and contributes essential evidence to guide antibiotic stewardship. Also, it improves surveillance frameworks and supports One Health–aligned strategies that safeguard the efficacy of antibiotics across both human and animal health.

METHODS

This systematic review and meta-analysis were conducted and reported in accordance with the PRISMA 2020 statement and followed methodological guidance for prevalence reviews and meta-analyses. The review protocol was developed using the PRISMA-P checklist [10]. The methods described below summarize the stepwise approach used for literature identification, study selection, data extraction and validation, risk-of-bias assessment, quantitative and qualitative synthesis, and sensitivity anal-

yses to ensure a rigorous and transparent approach for prevalence reviews and meta-analyses.

Eligibility criteria

Studies were eligible if they reported primary data on bacterial pathogens isolated from food-producing animals in Nigeria (including but not limited to chickens, cattle, pigs, ducks, and quails) or from animal-derived products from these animals (including eggs, milk, and meat) and presented prevalence estimates or sufficient numerator/denominator data to calculate prevalence. Eligible studies also included those that reported detailed antibiotic susceptibility results for isolates, using phenotypic or molecular methods, because a principal aim was to synthesize resistance patterns. We included observational studies (cross-sectional surveys, surveillance reports, and cohort studies) and peer-reviewed articles as well as grey literature if primary data were available. We limited the search to publications in English between 1 January 2000 and 30 March 2025 and excluded reviews, editorials, commentaries and conference abstracts (without primary data), experimental infection (challenge) studies, studies of companion or wild animals that did not include food animals, studies not conducted in Nigeria, and reports that duplicated data published elsewhere. Studies reporting only antibiotic residue concentrations without isolates or organism-level susceptibility data were also excluded.

Search strategy and information sources

A comprehensive search was performed on 30 March 2025 in PubMed, Web of Science, ScienceDirect, and African Journals Online (AJOL) and supplemented by screening the reference lists of included studies and relevant reviews. The PubMed search combined Medical Subject Headings and free-text terms and used Boolean operators; a representative query was: ("food animals" OR livestock OR poultry OR cattle OR swine OR goats OR sheep) AND (Nigeria) AND ("*Salmonella*" OR "*Campylobacter*" OR "*Escherichia coli*" OR "*Listeria*" OR "*Staphylococcus*") AND ("antimicrobial resistance" OR "antibiotic resistance" OR "AMR") AND (prevalence OR occurrence OR epidemiology). The same conceptual search was adapted to other databases to match their syntax and filters; for example, MeSH terms were omitted in AJOL, and search fields were adjusted in Web of Science to search within Title/Abstract/Keywords. Where databases supported it, searches were limited by publication date (2000–2025) and language (English). Search logs were maintained, documenting the exact query used in each database and the number of records retrieved.

Study selection and data management

All retrieved records were exported to Microsoft Excel for Office 2019 (Microsoft Corp.) and then imported into a reference manager for de-duplication. After removal of duplicates, three reviewers (MMH, FAO, TGO) independently screened titles and abstracts against the eligibility criteria and subsequently reviewed full texts for inclusion. The reviewers used a pilot-tested screening form to ensure consistency, and discrepancies at either stage were resolved by discussion and, where necessary, adjudication by four other reviewers (AML, OML, BSA, and VIA). This multi-reviewer approach ensured consistency and minimized selection bias during study inclusion. The process of identification, screening, eligibility assessment, and inclusion was documented using a PRISMA flow diagram.

Data extraction and validation

Data were extracted using a standardized, pilot-tested abstraction form. Extracted variables included study characteristics (author, year, location), animal host, sample type, bacterial organism(s) identified, and prevalence data. Animal-derived samples (e.g., milk, eggs, and meat) were retained where studies explicitly linked them to food-producing animals, as these represent important points along the production-to-consumption continuum. Where reported, antimicrobial susceptibility testing (AST) methods and interpretive standards were recorded; however, due to inconsistent reporting, these variables were not included in quantitative synthesis. Antimicrobial resistance (AMR) was defined as resistance to any antimicrobial agent, including antibiotics and non-antibiotic agents such as sulphonamides. Information on resistance assessment approaches (phenotypic or genotypic) was noted where reported in the included studies. Phenotypic resistance was generally determined using antimicrobial susceptibility testing (AST) methods, including disk diffusion and minimum inhibitory concentration (MIC)-based approaches, although reporting of these methods and associated interpretive standards (e.g., CLSI or EUCAST) was inconsistent. Given this variability and incomplete reporting across

studies, AST methodologies were not analyzed as part of the synthesis, so the review focused on the reported antimicrobial resistance patterns.

Risk-of-bias assessment

The methodological quality of included studies was assessed using the Joanna Briggs Institute (JBI) Critical Appraisal Checklist for Prevalence Studies [11]. This tool evaluates sampling methods, population representativeness, measurement reliability, and completeness of reporting. Studies were classified as having low, moderate, or high risk of bias, and disagreements were resolved through consensus.

Statistical analysis

Quantitative analyses were conducted in R (version 4.3.2) using the *meta* and *metafor* packages [12]. Study-level prevalence was calculated as the proportion of samples yielding the bacterial organism(s) of interest. The primary outcome was the bacterial pooled prevalence and the resistance profiles of the bacterial isolates. Proportions were logit-transformed prior to pooling, and random-effects meta-analysis was performed using restricted maximum likelihood (REML) to estimate between-study variance (τ^2). Heterogeneity was assessed using Cochran's Q and quantified with the I^2 statistic. Subgroup analyses were conducted by host species, reclassified sample types, and geographic regions. Meta-regression was used to assess the influence of study-level variables, including sample size, study year, and host category, on prevalence estimates. Given the expected methodological and epidemiological variability across studies, pooled estimates were interpreted cautiously in the presence of substantial heterogeneity.

Publication bias was evaluated using funnel plots and Egger's regression test. Sensitivity analyses were performed to assess robustness by excluding high-risk studies and examining the influence of individual studies. In addition to quantitative synthesis, a qualitative analysis of AMR patterns was conducted. Resistance profiles across bacterial species and antimicrobial classes were summarized and visualized using a heatmap generated in *ggplot2*, with antimicrobial classes and organism names standardized to ensure comparability.

RESULTS

Literature search outcome

The database search identified 281 records across PUBMED, AJOL, and Web of Science, with 10 additional studies located through grey literature and manual searches. After removing 85 duplicates, 206 records were screened by title and abstract, and 169 were excluded for lacking extractable data or presenting duplicated datasets. Of the 37 studies assessed at full text, five were excluded due to unclear or undefined sampling procedures, resulting in thirty-two studies meeting all eligibility criteria for inclusion in the review and meta-analysis (Fig. 1; Table 1).

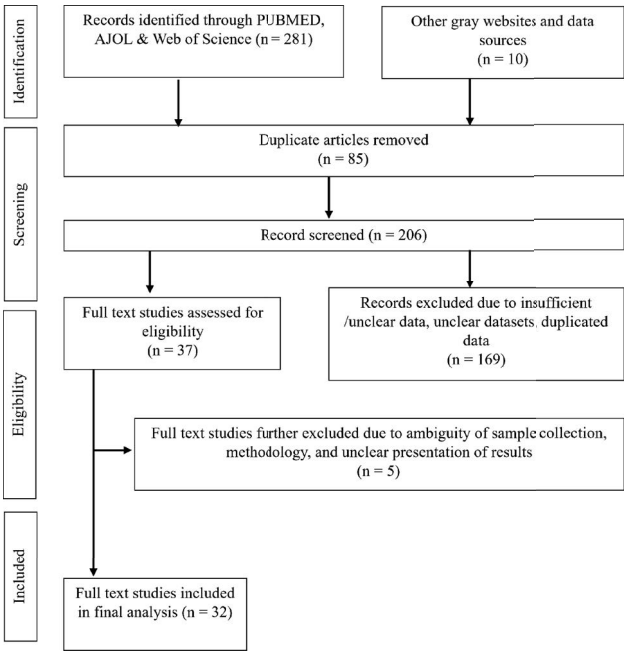

Fig. 1. PRISMA flowchart of the selection of eligible studies

Descriptive characteristics of included studies

The 32 included studies covered food-producing animals and animal-derived samples across all geopolitical zones of Nigeria. In total, 9,811 samples were analyzed, of which 1,865 tested positive for the bacterial organism(s) reported in the studies (19.01%; 95% CI: 18.24%–19.8%). Chickens were the most frequently investigated host species, followed by cattle, pigs, and mixed avian populations. The South-west (27.1%) and South-south (20%) zones contributed the largest proportion of samples.

Across bacterial groups, studies focusing on single organisms reported moderate prevalence estimates. *Escherichia coli* was the most frequently isolated organism, with

Table 1. Characteristics of eligible studies reporting the prevalence of resistant bacteria in food-producing animals and animal-derived products in Nigeria

Year	State	Geographic region	Animal/sample source	Positive samples	Reported bacterial prevalence (%)	No of isolates	Bacteria found	References
2010	Ogun	South-west	Dead chickens	5	100.0	5	*Salmonella* spp.	[32]
2010	Plateau	North-central	Dead-in-shell embryos, dead chicks, sick chicks and eggshells	45	9.0	45	*Salmonella* spp.	[34]
2010	Oyo	South-west	Live chickens	70	10.9	70	*Salmonella* spp.	[19]
2011	Osun	South-west	Live chickens	2	1.3	2	*Arcobacter butzleri*, *Arcobacter cryaerophilus*	[40]
2014	Oyo and Borno	South-west and North-east	Live chickens	45	7.0	45	*Salmonella* spp.	[26]
2014	Borno	North-east	Dead fishes	23	11.5	23	*Salmonella* spp.	[41]
2017	Ogun	South-west	Live quails	14	3.5	14	*Salmonella* spp.	[33]
2018	Ebonyi	South-east	Live cattle	48	40.0	48	*Escherichia coli*	[29]
2018	Oyo, Ondo, Ogun, Ekiti and Osun	South-west	Live chickens and pigs	240	100.0	350	*Klebsiella pneumoniae*, *Morganella morganii*, *Leclercia adecarboxylata* and *Citrobacter freundii*	[38]
2018	Enugu	South-east	Live chickens and pigs	20	3.9	18	*Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter asburiae* and *Providencia* spp.	[39]
2019	Kwara	North-central	Live chickens	58	6.4	58	*Salmonella* spp.	[31]
2020	Kwara	North-central	Live and dead chickens	42	11.8	58	*Salmonella* spp.	[35]
2021	Enugu and Ebonyi	South-east	Live and dead chickens and cattle	55	18.3	55	*Escherichia coli*, *Klebsiella* spp. and *Pseudomonas* spp.	[17]
2021	Kwara	North-central	Live pigs	16	2.7	16	*Salmonella* spp.	[18]
2021	Nasarawa	North-central	Cattle meat (suya samples)	40	13.3	40	*Escherichia coli*	[27]
2021	Oyo	South-west	Live cattle	53	21.2	56	*Escherichia coli*	[21]
2021	Ogun	South-west	Egg samples	14	14.0	14	*Salmonella* spp.	[3]
2021	Kwara	North-central	Dead chickens and ready-to-eat gizzards	43	8.6	43	*Salmonella* spp.	[37]
2021	Oyo	South-west	Milk samples from live cattle	40	23.8	40	*Escherichia* coli, *Enterobacter amnigenus* and *Pseudomonas aeruginosa*	[42]
2022	Ogun	South-west	Live chickens	32	80.0	32	*Escherichia coli*	[13]
2022	Plateau	North-central	Live and dead chickens and cattle	132	28.0	132	*Campylobacter* spp.	[14]
2022	Abuja and Lagos	North-central and South-west	Dead cattle	44	16.2	43	*Escherichia coli*	[15]
2022	Nasarawa	North-central	Live chickens	120	100.0	120	*Escherichia coli*, *Salmonella* spp., *Klebsiella* spp. and *Pseudomonas* spp.	[16]
2022	Kwara	North-central	Dead chickens	73	40.3	73	*Escherichia coli*	[23]
2022	Oyo	South-west	Live chickens	77	21.4	77	*Salmonella* spp.	[1]
2022	Oyo	South-west	Live chickens and ducks	156	83.9	156	*Escherichia coli* and *Salmonella* spp.	[30]
2023	Edo and Delta	South-south	Live chickens	10	20.0	10	*Salmonella* spp.	[21]
2023	Sokoto, Kebbi and Zamfara	North-west	Day-old chickens	32	10.7	32	*Salmonella* spp.	[23]
2023	Kwara	North-central	Dead chickens	37	10.5	37	*Escherichia coli*	[24]
2024	Plateau	North-central	Live chickens	178	99.4	178	*Escherichia coli*	[20]
2025	Ebonyi	South-east	Dead pigs	24	32.0	24	*Escherichia coli*	[28]
2025	Oyo	South-west	Live ducks and pigeons	78	22.9	30	*Escherichia coli*	[36]

a prevalence of 28.7% (606/2,111), while *Salmonella* spp. showed a lower prevalence of 8.9% (494/5,554). A subset of studies reported multiple bacterial organisms, commonly combinations of *E. coli*, *Salmonella* spp., *Klebsiella* spp., and *Pseudomonas* spp. with higher reported prevalence values, typically based on smaller sample sizes (Supplementary Table 2).

To enhance comparability, sample types were reclassified into four categories: live, dead, products (dead-derived), and others (live-derived). Live samples accounted for the largest proportion (5,895 samples; 60.1%), followed by dead samples (3,216 samples; 32.8%). Products derived from dead animals comprised 300 samples (3.0%), while other live-derived samples accounted for 400 samples (4.1%).

Meta-analysis

Random-effects meta-analysis of the 32 studies yielded a pooled prevalence of bacterial detection of 25% (95% CI: 14%–41%), with substantial heterogeneity observed across studies (Q = 999.21, p < 0.0001; I^2 = 96.9%; τ^2 = 4.29) (Fig. 2).

Subgroup analysis showed variation in bacterial pooled prevalence across host species; among chickens, the pooled prevalence was 35% (95% CI: 13%–66%) based on 18 studies (n = 5,618). In cattle, the pooled prevalence was 22% (95% CI: 15%–31%) from five studies (n = 1,110). Other host categories showed a wide range of estimates, including pigs (10%; 95% CI: 1%–65%), Japanese quails (4%; 95% CI: 2%–6%), chickens and ducks (84%; 95% CI: 78%–89%), ducks and pigeons (23%; 95% CI: 19%–28%), and chickens and pigs (4%; 95% CI: 2%–96%) (Fig. 3A and B).

Meta-regression analysis indicated that total sample size significantly influenced reported prevalence estimates (β = −0.0051, p = 0.0012), with larger studies reporting lower prevalence values. Residual heterogeneity remained high after adjustment (τ^2 = 3.1; I^2 = 98.9%). The model explained 27.9% of between-study variability.

Publication bias and sensitivity analysis

Funnel plot inspection showed a broadly symmetrical distribution of studies around the pooled estimate (Fig. 4). Egger's regression test did not indicate significant small-study effects (p = 0.3109). Sensitivity analyses, including exclusion of studies with high risk of bias or extreme estimates, yielded pooled estimates comparable to the primary analysis.

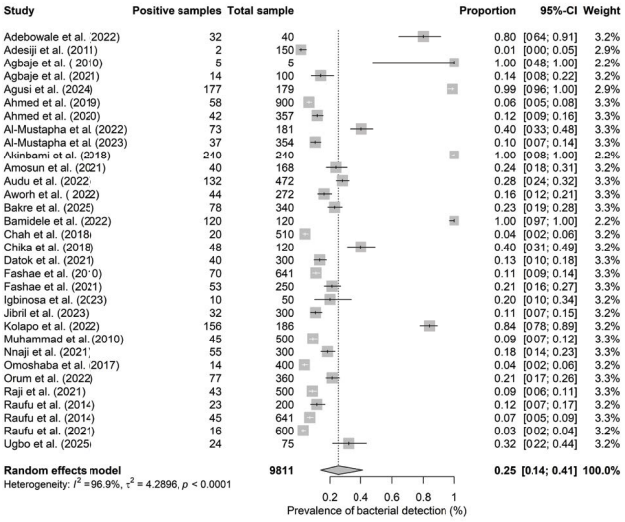

Fig. 2. Forest plot showing the estimated pooled prevalence of bacterial detection/isolation among sampled food animals and related products

Resistance profiles of bacteria detected in studies included in the systematic review

Across the included studies, AMR was frequently reported among *Escherichia coli*, *Salmonella* spp., and other enteric bacteria isolated from food animals and related samples. *E. coli* isolates demonstrated particularly broad antibiotic resistance profiles, with high resistance to tetracyclines, sulphonamides, and *β*-lactams (Fig. 5), and many studies reported multidrug resistance (MDR) rates above 70% [13, 20, 28]. Extended-spectrum *β*-lactamase (ESBL)-producing and cefotaxime-resistant *E. coli* were also widely documented [15, 21, 23].

Similarly, *Salmonella* spp. exhibited notable resistance to multiple antimicrobial classes, including *β*-lactams, fluoroquinolones, and sulphonamides, with several studies reporting multidrug-resistant phenotypes [18, 24, 30]. Other bacterial species, including *Klebsiella* spp., *Pseudomonas* spp., and *Enterobacter* spp., also demonstrated resistance to commonly used antimicrobials, particularly *β*-lactams and tetracyclines, although the magnitude of resistance varied across studies [17, 26, 31]. Molecular analyses further identified key resistance determinants, including *tetA*, *tetB*, *sul1*, *ampC*, and *qnr* genes, as well as mutations in *gyrA* and *parC*, supporting the observed phenotypic resistance patterns and indicating the circulation

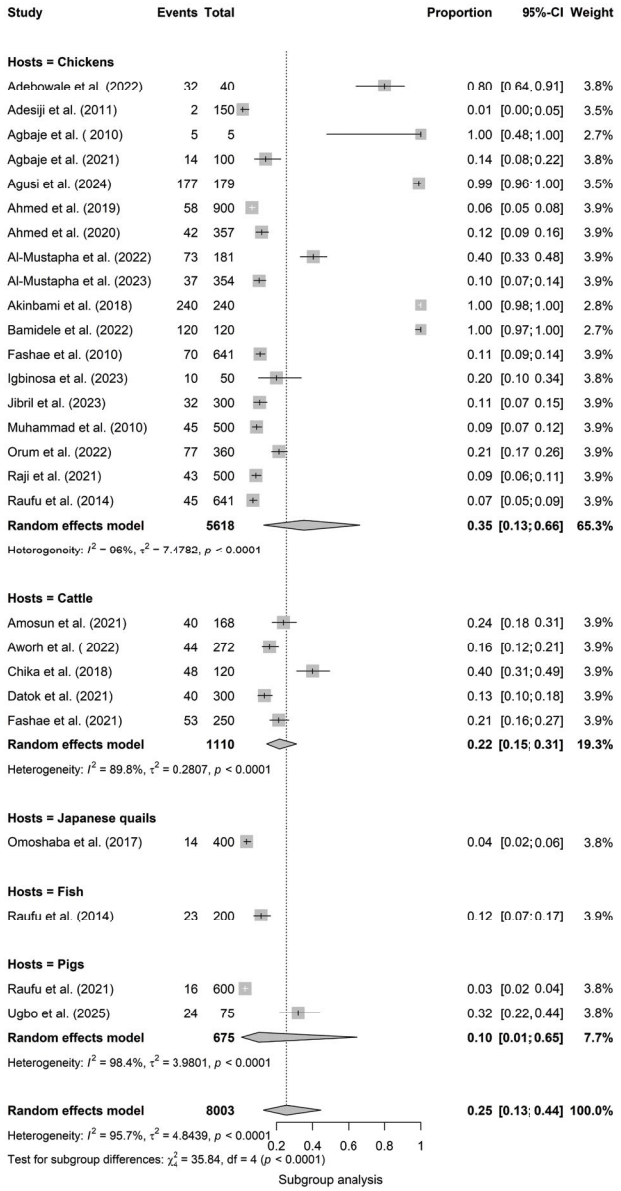

Fig. 3A. Forest plot showing pooled bacterial prevalence in studies of isolates recovered from single-host categories (chicken, cattle, pigs, Japanese quails, and fishes)

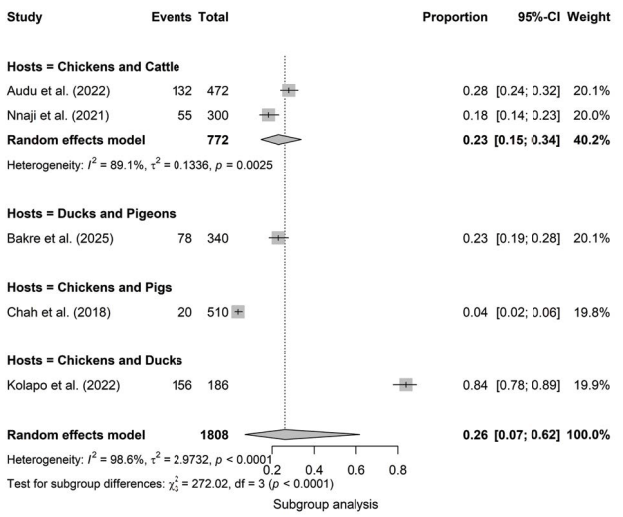

Fig. 3B. Forest plot showing pooled bacterial prevalence in studies involving multiple-host categories (including ducks and pigeons, chickens and pigs, and chickens and ducks)

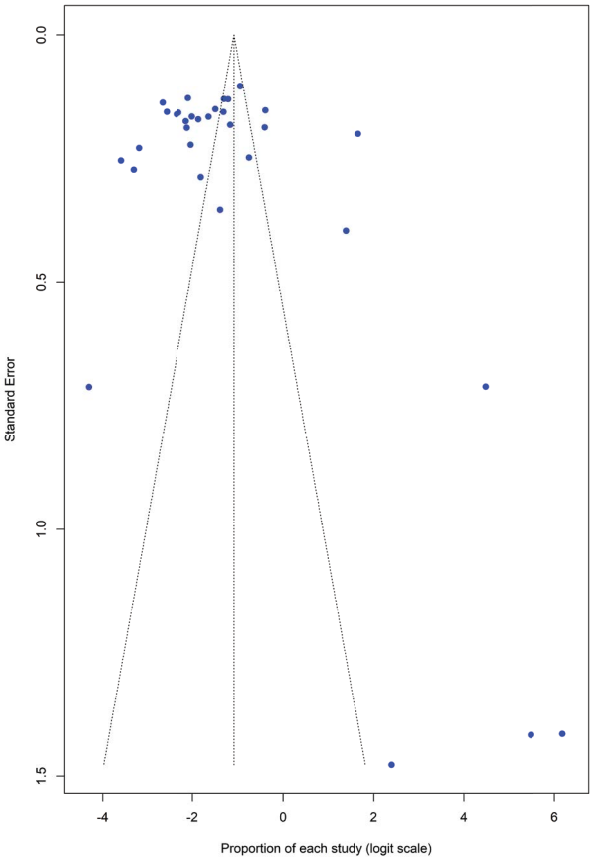

Fig. 4. Funnel plot displaying the proportion of each study against the standard error of each study

of resistant bacterial lineages within food-animal production systems [15, 21, 23, 25, 42].

DISCUSSION

The studies included in this review provide a contemporary synthesis of bacterial prevalence and antimicrobial resistance (AMR) in food-producing animals and related samples in Nigeria. The pooled prevalence of the bacteria identified and resistance patterns observed are consistent with earlier reports from Nigeria [43–44] and other African countries, including Ghana, Kenya, and Ethiopia [45–47], confirming that antimicrobial-resistant bacteria in livestock remain a significant and persistent public health concern across the continent.

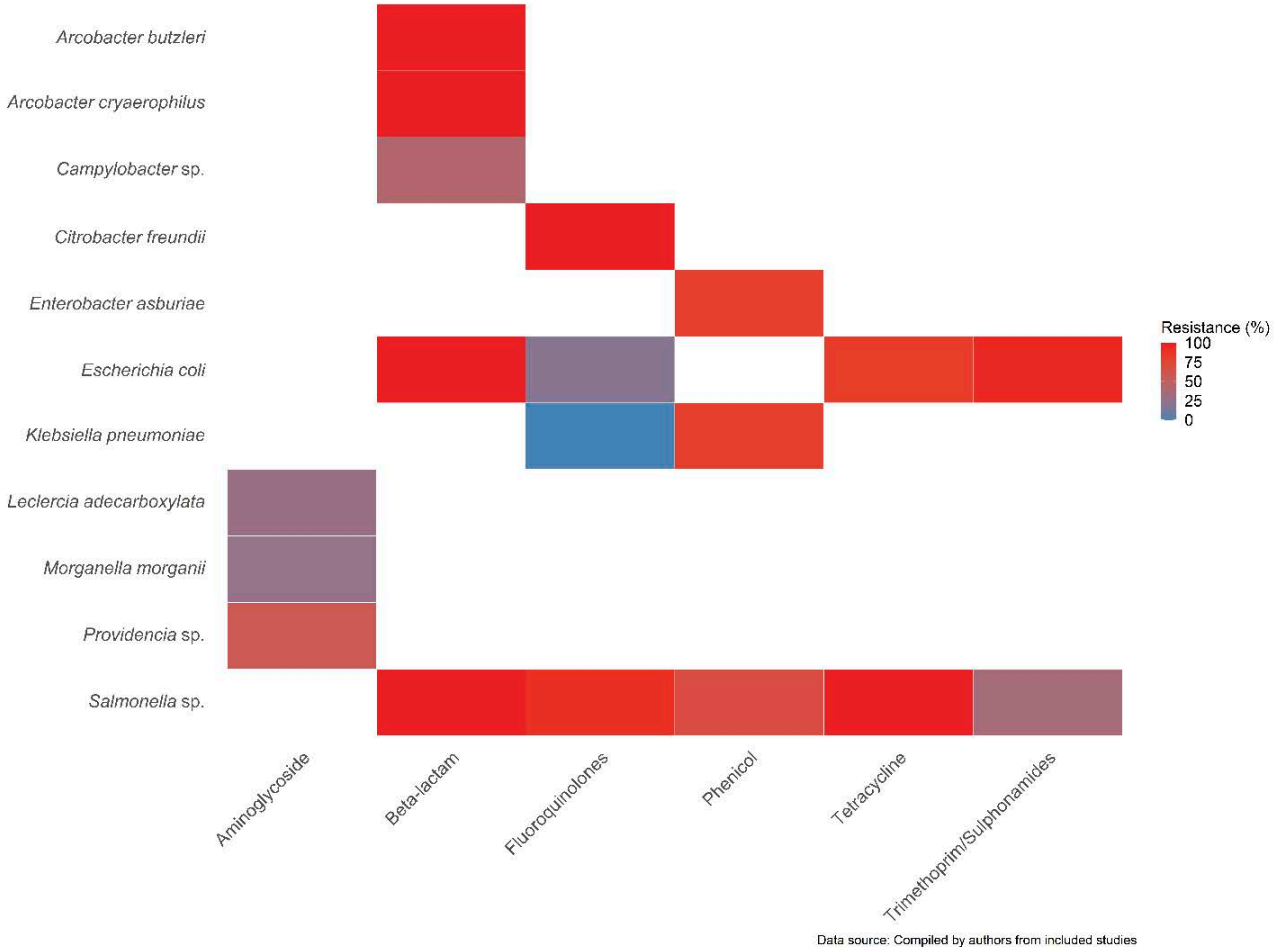

Fig. 5. Resistance patterns of microorganisms isolated from food-producing animals and animal-derived products in Nigeria (2000–2025)

Comparable trends are also reported globally. In Europe and other high-surveillance settings, AMR in food-producing animals continues to be driven by the emergence of multidrug-resistant (MDR) bacteria, defined as resistance to three or more antimicrobial classes, and the widespread occurrence of extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli*. The detection of such organisms in this review highlights the continued relevance of food animals as reservoirs of resistance and underscores the potential movement of resistant bacteria and resistance determinants along the farm-to-fork continuum.

Geographical variation in bacterial prevalence was evident, with higher levels observed in the South-west and North-central regions. These areas are characterized by intensive livestock production, dense market networks, and informal slaughter systems, which may increase opportunities for bacterial transmission and environmental contamination. Similar spatial clustering has been reported in East African production systems with comparable intensification patterns [48–49].

Across host species, poultry, particularly chickens and ducks, demonstrated the highest burden of bacterial detection and AMR. This finding aligns with global evidence indicating that poultry systems, often associated with high stocking densities and frequent antimicrobial exposure, act as major reservoirs of resistant bacteria [50–51]. The predominance of *E. coli* and *Salmonella* spp. across studies is consistent with their recognized role as indicator organisms in AMR surveillance and their capacity to acquire and disseminate resistance determinants [52]. The detection of resistant bacteria in meat, milk, and eggs further reflects contamination risks along the production chain, as reported in other African settings [53–54].

Host-specific differences were also observed, with higher prevalence in poultry compared with cattle. This likely reflects differences in production systems and antimicrobial-use practices, a pattern consistently reported across African livestock systems [49, 55]. The high prevalence observed in mixed chicken–duck systems may be associated with increased opportunities for cross-species

transmission, whereas lower prevalence in quail populations may reflect differences in management practices and stocking density [56].

Substantial between-study heterogeneity was observed, indicating marked variability in prevalence estimates across studies. This variability is likely influenced by differences in production systems, sampling strategies, antimicrobial use, and laboratory methodologies [57]. The inverse relationship between sample size and reported prevalence observed in meta-regression suggests a small-study effect, whereby smaller studies, often conducted in localized or higher-risk settings, report higher prevalence estimates, while larger studies provide more conservative and representative estimates, and this pattern is well documented in epidemiological and AMR meta-analyses [58].

Despite the absence of significant publication bias based on funnel plot symmetry and Egger's test, these findings should be interpreted with caution in the context of high heterogeneity. Furthermore, the limited explanatory power of included moderators suggests that key drivers of AMR, such as antimicrobial usage patterns, farm-level biosecurity, and environmental conditions, remain insufficiently reported in primary studies [59].

The resistance profiles observed across bacterial species in this review are consistent with regional and global trends. High resistance to tetracyclines, fluoroquinolones, sulphonamides, and *β*-lactams was frequently reported, alongside the detection of ESBL-producing *E. coli* and resistance to third-generation cephalosporins. The presence of resistance determinants such as *tetA*, *sul1*, *qnr*, and mutations in *gyrA* and *parC* reflects the circulation of resistant bacterial lineages within animal production systems and aligns with patterns described in global AMR surveillance studies [60–62].

Study limitations

This review has several limitations that should be considered when interpreting the findings. First, the included studies varied widely in design, sampling strategies, laboratory methods, antimicrobial susceptibility testing approaches, and antibiotic testing panels, which contributed to substantial heterogeneity and limited the comparability of resistance estimates across settings. Differences in AST methodology, including the use of disk diffusion versus MIC-based methods, as well as variation in breakpoint interpretation and reporting standards such as CLSI or EUCAST, may have influenced the classification of susceptibility results across studies. In addition, some studies did not clearly report quality-control procedures, breakpoints, or interpretive criteria, raising the possibility of misclassification or inconsistency in resistance reporting. Furthermore, most included studies relied on phenotypic susceptibility testing, while only a limited number reported genotypic resistance determinants, which constrained direct comparison between phenotypic and molecular resistance findings across studies.

Additionally, several studies reported incomplete metadata, such as host species, sample type, production system, or antibiotic exposure history, which constrained the depth of subgroup and meta-regression analyses. Publication bias is also likely, as studies with high antibiotic resistance levels may be more readily published than those reporting low or null findings, although statistical tests for asymmetry were inconclusive due to underlying heterogeneity. Finally, the reliance on phenotypic data in most included studies limited our ability to link AMR patterns to specific genetic determinants comprehensively, and the scarcity of molecular analyses restricted inferences about transmission pathways and the emergence of extensively resistant bacterial pathogens. Despite these limitations, the synthesis provides a robust and regionally relevant overview of bacterial prevalence and antibiotic resistance patterns across the animal, food, and environmental interface.

CONCLUSION AND RECOMMENDATIONS

This review demonstrates that antibiotic resistance is widespread across animal, food, and environmental reservoirs, with particularly high burdens of MDR *Escherichia coli*, *Salmonella* spp., and other enteric pathogens among food animals in Nigeria. The consistency of these patterns across diverse hosts, sample types, and geographic settings underscores the extent to which AMR has become entrenched within livestock production systems and along the broader One Health interface. The high prevalence of resistance to critically important antibiotic classes—including *β*-lactams, fluoroquinolones, and tetracyclines—signals a growing threat to both animal health and public health, especially in regions where surveillance capacity and regulatory enforcement remain limited. The substantial heterogeneity observed across the 32 studies in this work further

highlights the fragmented nature of AMR monitoring in Nigeria and the urgent need for more standardized, coordinated, and longitudinal data to capture trends over time.

Considering these findings, strengthening integrated AMR surveillance should be a priority, with emphasis on harmonized laboratory protocols, routine reporting of both phenotypic and genotypic data, and improved geographic representativeness. Policies aimed at reducing inappropriate antibiotic use in livestock, including restrictions on non-therapeutic use, improved access to veterinary oversight, and promotion of vaccination, biosecurity, and hygiene—are essential to prevent the emergence and spread of antibiotic-resistant bacteria. Investment in laboratory capacity, data management systems, and intersectoral collaboration will be critical to operationalizing effective One Health AMR control strategies. Finally, future research should focus on filling existing data gaps, characterizing antibiotic resistance genes and transmission pathways, and evaluating intervention effectiveness to inform evidence-based policy and practice.

Data Availability Statement

The raw data of this article will be made available by the authors, without undue reservation.

Ethical Statement

No ethical approval was necessary for this study.

Conflict of Interest

Authors declare that no conflicts of interest are directly or indirectly related to the work submitted for publication.

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Authors' Contributions

Agbajelola VI conceived and designed the study. Hamman MM, Oluwadare FA, and Orum TG worked on data screening and selection. Agbajelola VI, Lateef AM, Ogunbadewa AJ, Agbajelola BS, and Lateef OM validated the method and reviewed the manuscript. Agbajelola VI carried out the analysis and drafted the initial version of the manuscript. All the authors read and approved the final manuscript.

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