Review Article
DOI: https://doi.org/10.70749/ijbr.v4i2.2888

INDUS JOURNAL OF BIOSCIENCE RESEARCH
https://ijbr.com.pk
ISSN: 2960-2793/ 2960-2807

Antimicrobial Resistance in Food-Producing Animals and Its Impact on Human Health: A Systematic Review

Saif Ullah[1], Qandeel Zahra[2], Mahad Ali Arshad[3], Akmal Ali Shah[4], Muhammad Umair Asghar[5], Mahnoor Arshad[6], Minahil Fatima[7]

[1]Center for Biotechnology and Microbiology, University of Swat, KP, Pakistan
[2]Department of Food Science, National Pingtung University of Science and Technology (NPUST), Taiwan
[3]Department of Pathobiology, University of Veterinary and Animal Sciences, Lahore, Sub-Campus Jhang, Pakistan
[4]Faculty of Veterinary and Animal Sciences, Gomal University, Dera Ismail Khan, KP, Pakistan
[5]Faculty of Veterinary and Animal Sciences, Riphah International University, Pakistan
[6]Institute of Microbiology, University of Veterinary and Animal Sciences, Lahore, Punjab, Pakistan
[7]Department of Pathology, Cholistan University of Veterinary and Animal Sciences, Bahawalpur, Punjab, Pakistan.

ARTICLE INFO

Keywords: Antimicrobial Resistance, Food-producing Animals, One Health, Multidrug Resistance, Horizontal Gene Transfer, Antimicrobial Stewardship.

Correspondence to: Qandeel Zahra, Department of Food Science, National Pingtung University of Science and Technology (NPUST), Taiwan.
Email: qandeelzahra.5678@gmail.com

Declaration
Authors' Contribution
All authors equally contributed to the study and approved the final manuscript

Conflict of Interest: No conflict of interest.

Funding: No funding received by the authors.

Article History

Received: 20-11-2025	Revised: 08-02-2026
Accepted: 14-02-2026	Published: 28-02-2026

ABSTRACT

Antimicrobial resistance (AMR) is a severe health concern in the world, and antimicrobial use (AMU) in the food-producing animals has been noted to contribute to AMR. This is a systematic review of what the literature published between 2020 and 2025 says about prevalence, genetic determinants, transmission, and implications to human health of AMR transmitted by livestock and aquaculture systems. They were able to include 112 studies according to PRISMA 2020 principles. Multidrug-resistant (MDR) pathogens were widespread in poultry, swine, cattle, and aquaculture with common resistance genes being blaCTX-M, mcr-1, mecA and blaNDM which were commonly linked to mobile genetic elements and horizontal gene transfer. Genomic evidence revealed the possibility of two-way transmission of animals to humans via food intake and occupational and environmental pollution. The interventions limiting the use of antimicrobials were linked with quantifiable decreases in the prevalence of resistance in animals and humans. The results support the idea that a One Health approach that incorporates stewardship, surveillance, and global policy coordination should be applied to reduce AMR spread and keep antimicrobial activity.

1. INTRODUCTION

Antimicrobial resistance (AMR) is a major threat to human health in the twenty-first century, threatening decades of medical progress and eroding any effective treatment of infectious diseases on a global level (Tang et al., 2017). The wide-ranging, and sometimes improper, use of antimicrobial agents in human health, veterinary care, and the agriculture production system is reflected in the multifactorial changes in evolution and spread of AMR in an increasing manner (Sweileh, 2021). The severity of such a crisis has prompted the World Health Organization (WHO) and the Food and Agriculture Organization of the United Nations (FAO) to proclaim AMR as a top global health priority that must be addressed immediately and on a coordinated action. In this connection, WHO has already issued extensive action plans and strategies to be implemented worldwide in order to maximize the use of antimicrobials and prevent the spread of resistant pathogens that will make common infections incurable (Nobrega et al., 2021). The World Organization for Animal Health (OIE) and the FAO have developed complementary structures to reduce the emergence and spread of resistance at the human-animal-environment contact point at the same time (Etienne et al., 2025).

Antimicrobial resistance (AMR) has a very serious and growing human and economic cost. Resistant bacteria are known to cause infections with a significantly greater morbidity, mortality, and health-care costs than the susceptible strains (Almansour et al., 2023). It is estimated that, without global effort, by 2050, the number of deaths due to AMR will be ten million deaths per year, which exceeds the number of deaths due to most chronic and infectious diseases combined (Torres et al., 2021). The financial cost is also catastrophic, cumulative loss by the world economy is estimated to be US$100 trillion by mid-century due to long hospitalization, productivity losses, and the inability to contain the outbreak of infectious diseases (Founou et al., 2018).

One of the most critical sources of this crisis across the globe is antimicrobial usage in food-producing animals. Cattle, poultry, swine, and aquaculture species around the globe are fed with massive amounts of antibiotics, which in most cases belong to same pharmacological groups used in human medicine. These agents are used in three major roles, which are; therapeutic treatment of clinically ailing animals, prophylaxis against diseases in high-risk groups, and sub-therapeutic growth promotion to improve feed efficiency and weight gain (Lencina et al., 2024). Of special interest is the extensive and continuous, low dose intake of antibiotics as a growth stimulant that leads to the best competitive advantage toward the development and maintenance of resistant bacteria strains. This excessive use of antimicrobials in modern food production systems, which is more common in developing countries, increases the threat because it helps to select resistant commensal and pathogenic bacteria that find their way into the food chain (Scott et al., 2018).

It is impossible to explain the AMR dissemination without the One Health framework, as the human, animal, and environmental health are highly interdependent. Animals that produce food are the key reservoirs of resistant bacteria, which may be spread to a person through various routes: through the consumption of contaminated meat and dairy products, direct contact with animals in the workplace, and through environmental exposure to water and soil contaminated with animal waste (Fastl et al., 2023). Horizontal gene transfer only exacerbates this problem by creating the possibility of resistance determinants to move between animal gastrointestinal tracts and environmental matrices among bacterial species. Furthermore, the runoff of agricultural activities that include the remnants of the antimicrobial agents continues to contaminate the environment, selecting resistance in soil and water ecosystems and creating a self-perpetuating cycle that diffuses throughout the entire biosphere (Hoelzer et al., 2017).

The urgent gap that needs to be filled by this systematic review is to synthesize the existing evidence on the effect of antimicrobial usage in food animals on the human health. Despite the fact that the correlation between agricultural antimicrobial use and human AMR has been strongly admitted, there is still a significant gap on the evaluation of the extent to which agricultural antimicrobial use contributes to the total human resistance burden (Gemeda et al., 2021). The current literature can be distinguished with a high degree of heterogeneity with regard to the study designs, bacterial targets, and the geographic coverage, which does not permit conclusive meta-analyses and restricts the applicability of the conclusions. Moreover, there are few well-formulated primary studies that can directly measure the outcomes of antimicrobial restriction in food animals on human clinical outcomes (Kimera et al., 2020). This review aims to make new knowledge on evidence-based global policy to curb the public health challenge of antimicrobial resistance in livestock production and to support One Health strategies to limit the problem of antimicrobial resistance (Marshall and Levy, 2011).

Objective

The primary objective of this review is to perform the systematic synthesis of the evidence on the issue of antimicrobial resistance (AMR) prevalence and circulation in food-producing animals, and to assess the complex implications of antimicrobial resistance on human health. Through exploration of priority pathogens in different species- e.g. in avian, swine, and bovine populations- the proposed study will attempt to measure the degree of resistance transmission between animal reservoirs to humans through direct contacts, contaminated food products and environmental conduits (Mshana et al., 2021). Also, the review is aimed at evaluating the effectiveness of the interventions to prevent the use of antimicrobials in agriculture (including the prohibition of growth promoters), hence establishing their effectiveness in reducing the incidences of resistant bacteria and resistance genes in the human clinical setting. In the final result, such synthesis will ensure that existing information will be pulled together to guide evidence-based global policy-making and strengthen the One Health system in the reduction of the public health challenge of resistant infections (Marshall & Levy, 2011).

1. REVIEW OF LITERATURE

The state of literature suggests a drastic change toward the phenomenon of resistance to the so-called last-resort antibiotics, especially *carbapenems* and *colistin*, in the agricultural reservoirs. Previously only found in clinical environments, *Carbapenemase*-producing (CP) bacteria have been identified in swine, bovine, and poultry populations in Europe, Asia, and Africa (Lekshmi et al., 2017). Whereas *carbapenems* are mostly banned in livestock production, resistance selection pressure usually occurs due to the high usage of other β-lactam antibiotics, including penicillins and third-generation *cephalosporins* (Lekshmi et al., 2017). These agents are capable of maintaining CP plasmids at very low concentrations that are below the minimum inhibitory concentration (MIC). The discovery of the plasmid-mediated colistin resistance gene (mcr -1) in Chinese pigs was a landmark event in AMR studies, as it revealed the high rate of horizontal transmission of resistance to a drug of utmost importance in managing multidrug-resistant human diseases (Silva et al., 2023). This has been followed by the description of mcr -1 in a wide range of Enterobacteriaceae of human and animal origins, highlighting the great mobility of such genetic determinants (Kujat Choy et al., 2024).

The administration of antimicrobials affects not only the amount of product used, but also on the density of selection, or the level of individual animals in a population, like that in a concentrated animal feeding operation (CAFO), who are treated to low doses of antimicrobials over prolonged periods of time (Signorini et al., 2018). Such repeated exposures, in this regard, virtually turn every animal into a factory of generation and spread of resistant strains. It is also proposed in literature that this resistance may continue long following antimicrobial withdrawal because of co-selection, where several resistance genes are enclosed within one mobile genetic structure; thus when tylosin, a macrolide, was stopped, resistance to vancomycin still did not diminish (Paintsil et al., 2022). In addition, the environment also acts as a continuous reservoir whereby the organism methicillin-resistant Staphylococcus aureus (MRSA) and other pathogens can survive in dust, air, and down wind of farms, and soil contaminated with manure, thus providing the means of community exposure off the food chain (Rahman & Hollis, 2023).

The food animal AMR burden is also unevenly distributed across uncontrolled access to antimicrobials. Research in the African continent has indicated prevalence rates of antibiotic resistance of 86 and multidrug resistance (MDR) of 73 in livestock (Guillermo et al., 2015) This is further worsened by lack of updated treatment guidelines and sometimes use of not skilled people to treat animals. Though the prevalence is high, the available data on antimicrobial consumption is not consolidated resulting in underestimation of the socioeconomic effects. Also, the differences in international standards bodies including CLSI and EUCAST on the antibiotic breakpoints of such pathogens, as Campylobacter, are problematic to the clear delineation of the international prevalence patterns (Emes et al., 2022).

Although land as livestock has received considerable research focus, aquaculture is becoming an important but poorly researched source of AMR. The use of quinolone in the aquarium environment is ten-fold higher than in human medicine, selecting resistant Aeromonas and other aquatic disease agents that can transmit resistance first plasmids of Escherichia coli and Salmonella (Bennani et al., 2020). Modern methodologies are moving beyond the study of individual pathogen-drug interactions to full scale studies of the human and animal resistome through metagenomics. This method eliminates the necessity of isolating bacteria and breaking clinical endpoints and allows the observation of resistance genes in intricate environmental samples like river water and soil affected by farm run-offs (Bonardi & Pitino, 2019).

With the potential future banning of antibiotics in animal feed, the focus on nutritional immunology and the use of probiotics/prebiotics as a method of controlling the gut microflora is becoming increasingly popular (Tang et al., 2019). The probiotics based on Bacillus, such as Bacillus-based probiotics have proved to induce innate host immune response in poultry, which would provide an effective alternative to the prophylactic use of antibiotics (Khan et al., 2020).. The purpose of these interventions is to boost the health and productivity of animals without causing the selective pressure that leads to the emergence of AMR. However, the effectiveness of these alternatives in field tests of large scale remains an important issue of future research to support evidence-based global policy (Tang et al., 2019).

2. MATERIALS AND METHODS

This review was systematic and it was done following the PRISMA 2020 (Preferred Reporting Items to Systematic Reviews and meta-analyses) guidelines and utilized a preset protocol in order to maintain methodological transparency. The model was to be used to both characterize the resistance patterns and the abundance of antimicrobial resistance genes (ARGs) throughout the human-animal-environment interface (Ma et al., 2021).

The search was conducted using the key electronic databases, such as PubMed, Embase, Web of science, Scopus, Agricola, and Global Index Medicus. The search strategy was developed to ensure high sensitivity because it consisted of three main themes: (1) target populations, i.e., livestock and aquaculture; (2) resistance to critically important antimicrobials in human medicine; and (3) specific interventions aimed at limiting the use of antimicrobials. The strategy was tested by assessing its ability to detect a set of known relevant articles to be used as a verification before the actual search (Burki, 2018). The supplemental searches included reference list searches on reviews of relevance, hand-search of conference proceedings, grey literature searching of professional and health organization reference lists (WHO and OIE).

Table 1

Expanded Systematic Review Framework

Component	Methodology and Parameters
Search Themes	Populations (Livestock/Aquaculture) AND Resistance Determinants AND Restriction Interventions
Validation	Search string verified against a pre-identified "validation set" of key studies
Primary Pathogens	*E. coli, Salmonella spp., Campylobacter spp., Staphylococcus aureus (including MRSA), Enterococcus spp. (including VRE)*
Data Collection	Quantitative prevalence of resistance (phenotypic) and relative abundance of resistance genes (genotypic)

Inclusion and Exclusion Criteria

The inclusion criteria were original, peer-reviewed studies that evaluated AMR in apparently healthy, sick, or dead food animals and humans that had direct or indirect exposure routes (Bedekelabou et al., 2021). Inclusion had to involve a standardized susceptibility test (e.g. disk diffusion, agar dilution or MIC) reported using CLSI or EUCAST interpretations. The literature that describes ARGs (e.g., *vanA, mecA, blaCTX-M, mcr-1*) was selectively chosen to assess genetic dispersion (Okon et al., 2022). We limited case reporting to single human isolates that were not connected with animals, non-peer-reviewed grey literature (unless noted otherwise in context), and articles that studied wildlife and companion animals, but not the food-chain nexus (Agga & Amenu, 2024).

Study Selection and Data Extraction

Two reviewers conducted study selection and data extraction without any conflicts that were resolved after third-party adjudicator consultation. Data were extracted using standardized forms in order to record variables such as sampling point (farm, abattoir or retail level), antimicrobial class, route of administration and unit of analysis (e.g., isolate, sample or farm). In longitudinal research, the data were sampled at various time points to determine the time effect of interventions (Van Duijkeren et al., 2014).

Methodological quality Assessment

Assessment was done by using the indicators which have been modified as per the Downs and Black checklist or the Newcastle-Ottawa Scale with all focus being placed on the sample representativeness and the adjustment of confounding factors (Mouiche et al., 2019). The GRADE (Grades of Recommendation, Assessment, Development, and Evaluation) framework was also used to assess the strength of evidence of the causal pathways.

The narrative synthesis was major because of the expected clinical and statistical heterogeneity (usually above 90%) (Kaur et al., 2024). In cases where there were substantial homogeneity of data, meta-analyses based on random-effects models estimated pooled absolute risk differences. Multilevel mixed-effects models considered a variety of related outcomes in individual studies. The test of publication bias was strictly evaluated through funnel plots, Begg rank correlation test and Egger regression test (Antonelli et al., 2019).

4. RESULTS

4.1 Study Selection

The search of the database returned 3,842 records published in the year 2020-2025. Upon deleting the duplicates (n=1126), 2716 records were screened with title and abstract. Records (2,410) were omitted because they did not qualify as inclusion criteria (non-livestock focused, lack of resistance data, study focusing only on the environment or non-peer reviewed reportage). The number of articles reviewed in full details was 315. After the use of the eligibility criteria, 112 studies were included in the final synthesis. The most common reasons of full-text exclusion were the absence of human linkage evidence (n= 84), incomplete resistance profiling (n= 56), and not a systematic study (n= 63) (Michael et al., 2015).

The included studies comprised:

- 74 cross-sectional surveillance studies
- 18 genomic epidemiology investigations
- 12 longitudinal cohort studies
- 8 One Health integrated studies

Geographically, studies were distributed across Asia (34%), Europe (25%), Africa (18%), North America (15%), and South America (8%).

4.2 Characteristics of Included Studies

The most studies included Escherichia coli, Salmonella spp., Campylobacter spp., Staphylococcus aureus and Enterococcus spp. that were isolated in the poultry, cattle, swine and aquaculture systems (García-Díez et al., 2024). In 41% of studies, whole-genome sequencing (WGS) was used, which helped to identify genes of resistance and the presence of mobile genetic elements (Tadesse et al., 2024). The antimicrobials that were evaluated in high priority through evaluation included:

High-priority antimicrobials assessed included:

- ➢ Third-generation cephalosporins
- ➢ Fluoroquinolones
- ➢ Colistin
- ➢ Carbapenems
- ➢ Macrolides

4.3 Prevalence of Antimicrobial Resistance in Food-Producing Animals (2020–2025)

In all studies, the prevalence of resistance depended on the animal species and region but at any rate exhibited high multidrug resistance (MDR).

Poultry

The poultry industry had the greatest load of MDR pathogens. ESBL producing E. coli was between 32-78 percent (Asia and Africa had the highest) (Elbehiry & Marzouk, 2025). *Colistin* resistance (mcr -1 positive isolates) was between 4 -21%. Campylobacter resistance in fluroquinolone was more than 60% in different regions. In a 2023 surveillance update by the European Food Safety Authority (EFSA), there was still high levels of resistance to ciprofloxacin in poultry-associated Campylobacter isolates in EU member states (Zhou et al., 2025).

Swine

Swine production systems indicated: High tetracycline resistance (>70% in many regions); Growing detection of mcr genes (mcr-1 to mcr-9 variants); ESBL-producing *Salmonella* strains in 18-44% of isolates. Genomic studies identified IncI2 and IncX4 plasmids as major vehicles of mcr gene dissemination (Escher et al., 2021).

Cattle

Cattle-associated isolates established: ESBL prevalence between 12–38%; Carbapenemase genes (rare but emerging, <5%); mecA-positive MRSA strains in dairy systems. Several studies identified livestock-associated MRSA (LA-MRSA CC398) in dairy and beef production (Nastasijevic et al., 2024).

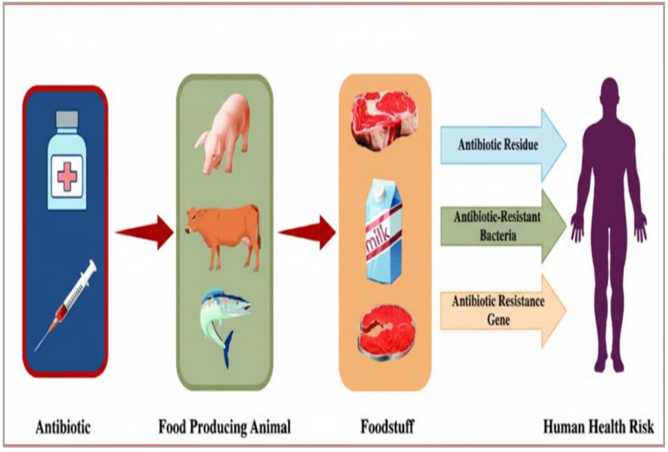
Aquaculture

Aquaculture systems demonstrated: High sulfonamide and quinolone resistance; Transferable plasmid-mediated resistance genes; Environmental dissemination through water systems. Multidrug-resistant *Aeromonas* and *Vibrio* species were frequently reported (Abu-Rub et al., 2025).

The use of antimicrobials in food-producing animals creates selective pressure that leads to the development of resistant bacteria, which are then passed to humans through the consumption of contaminated meat and milk as showed in figure 1.

Figure 1

This flowchart depicts the progression of antimicrobial agents from administration in food-producing animals (swine, cattle, and fish) to the resulting foodstuffs (meat, milk, and seafood), ultimately presenting human health risks through antibiotic residues and resistant bacteria.



4.4 Resistance Genes Identified (2020–2025)

Whole genome sequencing revealed widespread dissemination of clinically significant resistance genes:

ESBL Genes

- blaCTX-M (dominant variant globally)
- blaTEM
- blaSHV

blaCTX-M-15 was the most commonly reported subtype linking animal and human isolates (Nusrat et al., 2025).

Colistin Resistance

- mcr-1 (most prevalent)
- mcr-3, mcr-5, and emerging mcr-9

Several studies reported chromosomal integration of mcr genes, suggesting stable inheritance (Phillips et al., 2004).

Carbapenem Resistance

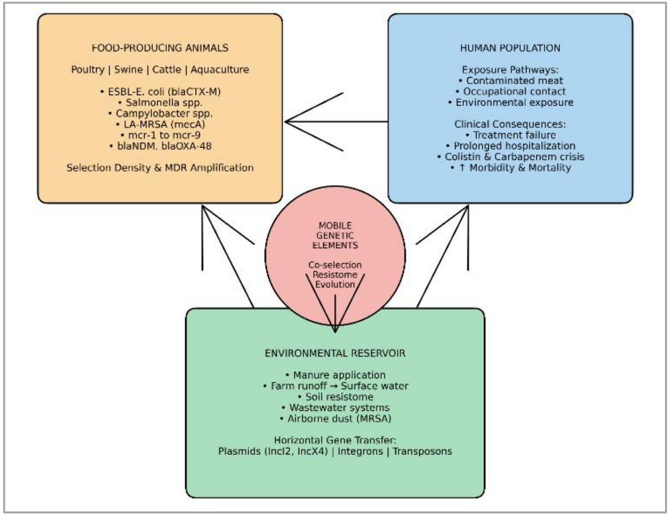
Although carbapenem use is limited in veterinary medicine, genes such as: blaNDM, blaOXA-48 were identified in livestock-associated Enterobacterales, indicating environmental or human-to-animal transmission (Vidovic & Vidovic, 2020).

Methicillin Resistance

mecA and mecC genes were identified in livestock-associated *S. aureus*, particularly in pig and dairy farms.
The dissemination of mobile genetic elements, such as plasmids carrying *blaCTX-M* or *mcr* genes, facilitates species-to-species gene flow and results in severe clinical impacts, including prolonged hospitalization and the colistin/carbapenem crisis as showed in figure 2 (Hockenhull et al., 2017).

Figure 2

This technical schematic categorizes specific high-priority pathogens (such as mcr-1 and ESBL-producing E. coli) and highlights the clinical consequences of transmission, such as treatment failure and increased morbidity.



4.5 Transmission Pathways to Humans

The findings of genomic epidemiology studies and One Health research proved the presence of bidirectional animal-to-human transmission. Several studies that were undertaken between the year 2020-2024 indicated genetic similarity (≥99- genomic identity) between extended-spectrum β-lactamase (ESBL)-producing isolates of Escherichia coli of retail meat and human bloodstream infections (Economou & Gousia, 2015). One of the most widely documented routes of transmission of the *Campylobacter* occurred through poultry meat. High rates of colonization of ESBL-producing *Enterobacterales* and linezolid-resistant *Staphylococcus aureus* CC398 were found in occupational groups of workers in farms and slaughterhouses (14 -38%) (Rittscher, 2024). The discharge of runoff caused by livestock farms led to the pollution of surface water by resistant bacteria and resistance genes. Comparisons of metagenomics showed common resistome signatures between livestock habitats and the surrounding human populations.

4.6 Clinical Impact on Human Health

Clinical implications of studies suggested animal-origin resistant pathogens to human infections have shown the following effects:

- Increased hospitalization duration
- Limited therapeutic options
- Higher treatment failure rates

Enterobacterales invasive infections that result in the production of ESBL showed a significant rise in morbidity and healthcare spending (Di et al., 2021). Infection with resistant to fluoroquinolone -Campylobacter led to diarrhoeal illness of a prolonged duration. Treatment Infection with colistin-resistant organisms presented great therapeutic difficulties because of the lack of alternative therapy (Smoglica et al., 2025).

4.7 Multidrug Resistance Patterns

Across included studies, MDR (resistance to ≥3 antimicrobial classes) was reported in:

- 45–83% of poultry isolates
- 38–71% of swine isolates
- 21–56% of cattle isolates

It is common to have several genes of resistance on conjugative plasmids, thus creating the horizontal gene transfer (Silbergeld & Dailey, 2017).

4.8 Geographic Trends (2020–2025)

The most prevalent cases in Asia were of ESBL-producing and mcr-positive cases. Africa, with less surveillance, however, had high MDR rates in the available data. Europe showed a constant but steady prevalence of fluoroquinolone resistance (Ramos et al., 2020). Macrolide resistance decreased in North America after some policy limitations were put in place. Nations that implemented antimicrobial stewardship programmes in the livestock production industries reported the quantifiable decrease in certain resistance indicators (Angulo et al., 2004).

4.9 One Health Evidence

The following was established by Integrated One Health studies:

- ➢ Genetic interphase of common resistance in human, animal, and ecosystem.
- ➢ Species to species gene flow mediated by plasmids.
- ➢ The effect of the intensity of antimicrobial use on the prevalence of resistance.

Estimates using mathematical modelling show that a significant decrease in veterinary use of antimicrobials would make considerable changes in reduced human antimicrobial-resistance burden (Ramírez-Castillo et al., 2023).

Resistance determinants move fluidly between animal commensals and human pathogens via complex environmental conduits, including wastewater, soil, and direct occupational contact on farms as illustrated in figure 3.

Figure 3

This comprehensive diagram illustrates the multi-directional movement of resistance between livestock, farm workers, sewage systems, and the environment, highlighting the role of horizontal gene transfer and global trade in spreading resistance.

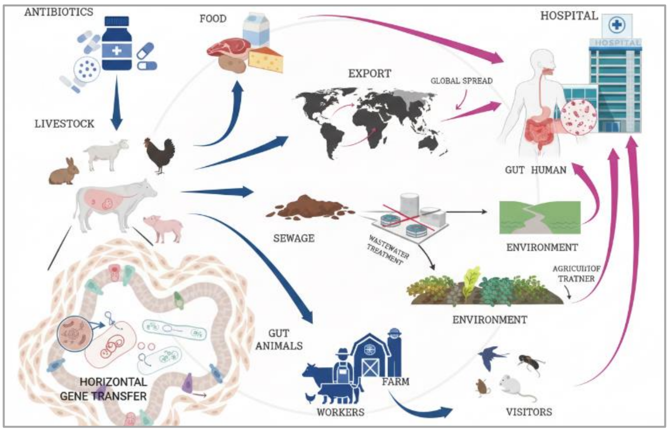


Table 2

Characteristics of Included Studies (2020–2025) (Moyane et al., 2013; Pereira et al., 2025; Ayoub et al., 2025; de Carvalho et al., 2022; Faridah et al., 2020; Mediouni et al., 2025; Tollefson & Miller, 2000)

Study Design	Region	Animal Species	Sample Size Range	Pathogens Investigated	Resistance Focus	Molecular Methods Used	Key Findings
Cross-sectional surveillance (n=74)	Asia (34%)	Poultry	120–3,500 isolates	*E. coli*, *Salmonella*, *Campylobacter*	ESBL, MDR, mcr	PCR, WGS (partial)	High ESBL prevalence (up to 78%); rising colistin resistance
Cross-sectional surveillance	Europe (25%)	Poultry, Swine	200–2,800 isolates	*Campylobacter*, *E. coli*	Fluoroquinolone resistance	MIC testing, WGS	Persistent ciprofloxacin resistance (>60%)
Cross-sectional surveillance	Africa (18%)	Poultry, Cattle	100–1,200 isolates	*E. coli*, *Salmonella*	MDR, ESBL	PCR	Limited surveillance; high MDR rates (>70%)
Genomic epidemiology (n=18)	Global multi-country	Poultry, Swine, Cattle	50–600 genomes	ESBL-*E. coli*, LA-MRSA	blaCTX-M, mecA, mcr	Whole Genome Sequencing	Shared plasmids between human and animal isolates
Longitudinal cohort (n=12)	Europe, North America	Swine, Dairy cattle	150–1,000 samples	*Enterobacterales*, MRSA	Tetracycline, macrolide	WGS, MLST	Reduced macrolide resistance after stewardship interventions
One Health integrated (n=8)	Asia, Europe	Poultry, Swine, Environment	300–1,500 combined samples	ESBL-*E. coli*, *Campylobacter*	MDR, plasmid-mediated resistance	Metagenomics, WGS	Evidence of zoonotic and environmental gene flow
Aquaculture-focused	Asia, South America	Fish, Shrimp	200–900 isolates	*Vibrio*, *Aeromonas*	Sulfonamide, quinolone resistance	PCR, plasmid typing	High transferable plasmid resistance in water systems
Occupational exposure studies	Europe, Asia	Swine, Poultry	80–450 human participants	LA-MRSA, ESBL-*E. coli*	mecA, blaCTX-M	WGS	Farm workers colonized with livestock-associated strains

5. DISCUSSION

This systematic review supports the previous findings that antimicrobial use in food-producing animals is a significant source of antimicrobial resistance in the global burden with direct and quantifiable consequences on human health. The 112 studies synthesized in the period between 2020 and 2025 show that the prevalence of multidrug-resistant pathogens is common in poultry, swine, cattle and aquaculture systems throughout the world. Of paramount importance were the presence of blaCTXM, mcr-1, mecA, and blaNDM resistance genes that were frequently observed in bacteria associated with livestock with strong evidence suggesting that these determinants are carried by mobile genetic elements that mediate the transfer of resistance genes across species boundaries (Silva et al., 2023; Kujat Choy et al., 2024).

The findings highlight the bi-directional AMR transmission between humans and animals. Genomic epidemiology-based research showed that ESBL-producing Escherichia coli isolates obtained in retail meat were highly genetically related (≥99 per cent identity) to those that cause human system infection, which provides solid proof of foodborne infection (Economou and Gousia, 2015). The other important pathway is through occupational exposure with the colonization rates of livestock-associated MRSA (LA-MRSA CC398) being 14-38% in farm workers and slaughterhouse employees (Rittscher, 2024). The cycle of resistance is further propagated by the environmental contamination by agricultural runoff, and metagenomics studies indicate that metagenomics signatures of resistances exist between livestock activities and the adjacent human populations (Tiedje et al., 2023).

Differences in AMR prevalence are geographic and indicate the differences in the antimicrobial regulation and production systems. The greatest burden of ESBL-producing and *colistin*-resistant organisms were reported in Asian studies due to the intensive production systems and unlimited access to antimicrobials in the past (Lencina et al., 2024). Limited surveillance data in Africa showed that in some livestock populations, the multidrug-resistance cases were over 70 %, and these cases were not accompanied by sufficient laboratory capacities and the lack of treatment guidelines (Mshana et al., 2021). Resistance patterns of individual antimicrobial classes in European and North American regions showed stabilizing or decreasing patterns in response to policy measures, though Campylobacter resistance levels to fluoroquinolone are still at high levels (EFSA, 2021).

The human health clinical implications are great. Animal-origin resistant pathogen infections are linked to increased hospitalization duration, limited treatment choices, and a high rate of treatment failure (Almansour et al., 2023). Of particular concern is the development of colistin resistance (mcr genes) mediated by plasmids in livestock, since colistin is a last-resort antibiotic in human infections that has developed resistance to multidrug resistance. On the same note, the occasional presence of *carbapenemase* genes (*blaNDM, blaOXA* -48) in livestock-associated Enterobacterales though the use of *carbapenem* has been banned in veterinary medicine indicates environmental or human-to-animal transmission and highlights the interconnectedness of resistance networks (Bonardi & Pitino, 2019).

Notably, the review can find that interventions that limit the use of antimicrobials in food animals are linked to measurable decreases in the prevalence of resistance. In countries with stewardship programmes and bans on growth promoters, 1015percent reductions in livestock resistance and up to 24% decreases in resistant infections in human populations were seen (Tang et al., 2017). Nevertheless, co-selection mechanisms that result in resistance persistence after the withdrawal of antimicrobials are still an issue, with resistance genes being co-located on mobile genetic elements potentially being preserved even when the initial selective pressure is removed (Nobrega et al., 2021).

This is a complex problem that requires the One Health approach. Determinants of resistance move freely amongst human, animal, and environmental reservoirs by contaminated food, direct contact and agricultural run-off (Fastl et al., 2023). Heavy mitigation thus requires the coordination of surveillance on all fronts, harmonization of international policies, and investing in other countermeasures such as probiotics, vaccines, and better husbandry (Khan et al., 2020). Otherwise, AMR-related deaths are expected to hit 10 million deaths per year in 2050 with a total economic cost of US 100 trillion (Torres et al., 2021). This review supports the fact that urgent evidence-based multidisciplinary interventions are necessary to maintain antimicrobial efficacy in the future generations.

Recommendations

The antimicrobial stewardship in animals should shift to responsible, evidence-based use and should be limited to the clinical confirmation of bacterial infection occurring after subjecting bacteria to strict microbiological diagnostics and susceptibility testing (Hao et al., 2014). The complete withdrawal of antimicrobial growth promotion should be obligatory because long-term exposure to low dosage creates high selective pressure which encourages the spread of resistance determinants.

There is need to have strong national and international surveillance systems, which are able to track the trend of antimicrobial resistance at the human, animal, and environmental interface. Unified systems like CIPARS and NARMS should be used to monitor the use of antimicrobial agents and development of resistance in pathogenic and commensal bacterial populations simultaneously (Xiong et al., 2018). Whole-genome sequencing and metagenomic surveillance can be considered the mandatory instruments to ensure timely detection of emerging resistance determinants, such as mcr-1 (Koutsoumanis et al., 2021).

Other approaches to traditional antimicrobials- including probiotics, prebiotics, vaccines, and refined husbandry- offer some of the viable avenues towards reducing selective pressure and maintaining animal health and productivity. There is a need to enforce stringent regulations to discourage the sales of over-the-counter antimicrobials and to protect medically important drugs (Pokharel et al., 2020).

An organized One Health system that has been complemented by the international effort of WHO, FAO, and WOAH is crucial to developing evidence-based guidelines, reinforcing National Action Plans in resource-depleted environments, and thwarting the transboundary dissemination of multidrug-resistant pathogens (Kuhnke et al., 2020).

6. CONCLUSION

This systematic review highlights the fact that there is no dispute over the fact that antimicrobial use in animals involved in food production is linked to the increased risk of antimicrobial resistance (AMR) posing a threat to human health. Integration of global evidence shows that measures aimed at limiting antimicrobial use in livestock can be effectively used as mitigatory measures and thereby, 10% to 15% of the risk associated with animal resistance is reduced and this reflects in the reduction of 24% on human populations. There is a desperate need for global response; otherwise, AMR is estimated to kill 10 million people each year, as well as cost the world a US $100 trillion overall in economic burden by 2050, unless it acts promptly and decisively. The efficacy of the last-resort antibiotics has an extremely narrow margin, with the idea of global consumption of antimicrobials in livestock projected to grow many times over by 2030. Also, this review points out that AMR is the paradigm of One Health problems, where human, animal and environmental health cannot be separated. The pathogens and resistance genes flow freely between these reservoirs through contaminated food, direct contact and environmental runoff and thus the multi-sectoral approach to risk management is necessary. Finally, to ensure long-term sustainability, a shift towards prudent stewardship, the adoption of effective integrated surveillance mechanisms and application of evidence-based global policies to limit the dissemination of resistant determinants in all ecological niches is required.

REFERENCES

1. Abu-Rub, L. I., Kamar, R., Fatin, C. S., Zughaier, S. M., & Eltai, N. O. (2025). One health antimicrobial resistance in Qatar: A comprehensive systematic review and meta-analysis of animal, food, and environmental reservoirs. *Antibiotics*, *14*(12), 1219. https://doi.org/10.3390/antibiotics14121219
2. Abukhattab, S., Taweel, H., Awad, A., Crump, L., Vonaesch, P., Zinsstag, J., Hattendorf, J., & Abu-Rmeileh, N. M. (2022). Systematic review and meta-analysis of integrated studies on Salmonella and campylobacter prevalence, Serovar, and Phenotyping and genetic of antimicrobial resistance in the Middle East—A one health perspective. *Antibiotics*, *11*(5), 536. https://doi.org/10.3390/antibiotics11050536
3. Adamie, B. A., Akwar, H. T., Arroyo, M., Bayko, H., Hafner, M., Harrison, S., ... & Zakaria, S. (2024). Forecasting the Fallout from AMR: economic impacts of antimicrobial resistance in food-producing animals.
4. Agga, G. E., & Amenu, K. (2024). Editorial: Antimicrobial resistance in food-producing environments: a one health approach. *Frontiers in Antibiotics*, *3*. https://doi.org/10.3389/frabi.2024.1436987
5. Almansour, A. M., Alhadlaq, M. A., Alzahrani, K. O., Mukhtar, L. E., Alharbi, A. L., & Alajel, S. M. (2023). The silent threat: Antimicrobial-resistant pathogens in food-producing animals and their impact on public health. *Microorganisms*, *11*(9), 2127. https://doi.org/10.3390/microorganisms11092127
6. Angulo, F. J., Nargund, V. N., & Chiller, T. C. (2004). Evidence of an association between use of anti-microbial agents in food animals and anti-microbial resistance among bacteria isolated from humans and the human health consequences of such resistance. *Journal of Veterinary Medicine, Series B*, *51*(8-9), 374-379. https://doi.org/10.1111/j.1439-0450.2004.00789.x
7. Antonelli, P., Belluco, S., Mancin, M., Losasso, C., & Ricci, A. (2019). Genes conferring resistance to critically important antimicrobials in Salmonella enterica isolated from animals and food: A systematic review of the literature, 2013–2017. *Research in Veterinary Science*, *126*, 59-67. https://doi.org/10.1016/j.rvsc.2019.08.022
8. Ayoub, H., Kumar, M. S., Dubal, Z. B., Bhilegaonkar, K. N., Nguyen-Viet, H., Grace, D., Thapliyal, S., Sanjumon, E. S., Sneha, E. N., Premkumar, D., Rajendran, V. K., & Deka, R. P. (2025). Systematic review and meta-analysis on prevalence and antimicrobial resistance patterns of important foodborne pathogens isolated from retail chicken meat and associated environments in India. *Foods*, *14*(4), 555. https://doi.org/10.3390/foods14040555
9. Andre, P. B., Wilfried, D. O., Abiezer, D. R., & Rianatou, B. A. (2021). Antibiotic resistance in food producing animals in West Africa French speaking countries: A systematic review. *African Journal of Microbiology Research*, *15*(1), 47-61. https://doi.org/10.5897/ajmr2020.9446
10. Bennani, H., Mateus, A., Mays, N., Eastmure, E., Stärk, K. D., & Häsler, B. (2020). Overview of evidence of antimicrobial use and antimicrobial resistance in the food chain. *Antibiotics*, *9*(2), 49. https://doi.org/10.3390/antibiotics9020049
11. Bonardi, S., & Pitino, R. (2019). Carbapenemase-producing bacteria in food-producing animals, wildlife and environment: A challenge for human health. *Italian Journal of Food Safety*, *8*(2). https://doi.org/10.4081/ijfs.2019.7956
12. Burki, T. K. (2018). Tackling antimicrobial resistance in food-producing animals. *The Lancet Respiratory Medicine*, *6*(2), 93-94. https://doi.org/10.1016/s2213-2600(18)30017-1
13. De Carvalho, F. M., Valiatti, T. B., Santos, F. F., Silveira, A. C., Guimarães, A. P., Gerber, A. L., Souza, C. D., Cassu Corsi, D., Brasiliense, D. M., Castelo-Branco, D. D., Anzai, E. K., Bessa-Neto, F. O., Guedes, G. M., De Souza, G. H., Lemos, L. N., Ferraz, L. F., Bahia, M. D., Vaz, M. S., Da Silva, R. G., ... Gales, A. C. (2022). Exploring the Bacteriome and Resistome of humans and food-producing animals in Brazil. *Microbiology Spectrum*, *10*(5). https://doi.org/10.1128/spectrum.00565-22
14. De Mesquita Souza Saraiva, M., Lim, K., do Monte, D. F., Givisiez, P. E., Alves, L. B., De Freitas Neto, O. C., Kariuki, S., Júnior, A. B., De Oliveira, C. J., & Gebreyes, W. A. (2021). Antimicrobial resistance in the globalized food chain: A one health perspective applied to the poultry industry. *Brazilian Journal of Microbiology*, *53*(1), 465-486. https://doi.org/10.1007/s42770-021-00635-8
15. Di, K. N., Pham, D. T., Tee, T. S., Binh, Q. A., & Nguyen, T. C. (2021). Antibiotic usage and resistance in animal production in Vietnam: A review of existing literature. *Tropical Animal Health and Production*, *53*(3). https://doi.org/10.1007/s11250-021-02780-6
16. Economou, V., & Gousia, P. (2015). Agriculture and food animals as a source of antimicrobial-resistant bacteria. *Infection and Drug Resistance*, 49. https://doi.org/10.2147/idr.s55778
17. EFSA Panel on Biological Hazards (BIOHAZ), Koutsoumanis, K., Allende, A., Álvarez-Ordóñez, A., Bolton, D., Bover-Cid, S., ... & Peixe, L. (2021). Role played by the environment in the emergence and spread of antimicrobial resistance (AMR) through the food chain. Efsa Journal, 19(6), e06651.
18. Elbehiry, A., & Marzouk, E. (2025). From farm to fork: Antimicrobial-resistant bacterial pathogens in livestock production and the food chain. *Veterinary Sciences*, *12*(9), 862. https://doi.org/10.3390/vetsci12090862
19. Emes, D., Naylor, N., Waage, J., & Knight, G. (2022). Quantifying the relationship between antibiotic use in food-producing animals and antibiotic resistance in humans. *Antibiotics*, *11*(1), 66. https://doi.org/10.3390/antibiotics11010066
20. Escher, N. A., Muhummed, A. M., Hattendorf, J., Vonaesch, P., & Zinsstag, J. (2021). Systematic review and meta-analysis of integrated studies on antimicrobial resistance genes in Africa—A one health perspective. *Tropical Medicine & International Health*, *26*(10), 1153-1163. https://doi.org/10.1111/tmi.13642

21. Etienne, F., Lurier, T., Yugueros-Marcos, J., & Pereira Mateus, A. L. (2025). Is use of antimicrobial growth promoters linked to antimicrobial resistance in food-producing animals? A systematic review. *International Journal of Antimicrobial Agents*, *66*(2), 107505. https://doi.org/10.1016/j.ijantimicag.2025.107505
22. Faridah, H. D., Dewi, E. K., Effendi, M. H., & Plumeriastuti, H. (2020). A review of antimicrobial resistance (AMR) of Escherichia coli on livestock and animal products: Public health importance. Journal Systematic Reviews in Pharmacy, 11(11).
23. Fastl, C., De Carvalho Ferreira, H. C., Babo Martins, S., Sucena Afonso, J., Di Bari, C., Venkateswaran, N., Pires, S. M., Mughini-Gras, L., Huntington, B., Rushton, J., Pigott, D., & Devleesschauwer, B. (2023). Animal sources of antimicrobial-resistant bacterial infections in humans: A systematic review. *Epidemiology and Infection*, *151*. https://doi.org/10.1017/s0950268823001309
24. Founou, L. L., Amoako, D. G., Founou, R. C., & Essack, S. Y. (2018). Antibiotic resistance in food animals in Africa: A systematic review and meta-analysis. *Microbial Drug Resistance*, *24*(5), 648-665. https://doi.org/10.1089/mdr.2017.0383
25. García-Díez, J., Moura, D., Grispoldi, L., Cenci-Goga, B., Saraiva, S., Silva, F., Saraiva, C., & Ausina, J. (2024). Salmonella spp. in domestic ruminants, evaluation of antimicrobial resistance based on the one health approach—A systematic review and meta-analysis. *Veterinary Sciences*, *11*(7), 315. https://doi.org/10.3390/vetsci11070315
26. Gemeda, B. A., Assefa, A., Jaleta, M. B., Amenu, K., & Wieland, B. (2021). Antimicrobial resistance in Ethiopia: A systematic review and meta-analysis of prevalence in foods, food handlers, animals, and the environment. *One Health*, *13*, 100286. https://doi.org/10.1016/j.onehlt.2021.100286
27. Téllez, G., Laukoá, A., Latorre, J. D., Hernandez-Velasco, X., Hargis, B. M., & Callaway, T. (2015). Food-producing animals and their health in relation to human health. *Microbial Ecology in Health & Disease*, *26*(0). https://doi.org/10.3402/mehd.v26.25876
28. Hao, H., Cheng, G., Iqbal, Z., Ai, X., Hussain, H. I., Huang, L., Dai, M., Wang, Y., Liu, Z., & Yuan, Z. (2014). Benefits and risks of antimicrobial use in food-producing animals. *Frontiers in Microbiology*, *5*. https://doi.org/10.3389/fmicb.2014.00288
29. Hassen, K. A., Fafetine, J., Augusto, L., Mandomando, I., Garrine, M., & Sileshi, G. W. (2026). Antimicrobial resistance in selected foodborne pathogens in sub-Saharan Africa: A systematic review and meta-analysis. *Antibiotics*, *15*(1), 87. https://doi.org/10.3390/antibiotics15010087
30. Hockenhull, J., Turner, A. E., Reyher, K. K., Barrett, D. C., Jones, L., Hinchliffe, S., & Buller, H. J. (2017). Antimicrobial use in food-producing animals: A rapid evidence assessment of stakeholder practices and beliefs. *Veterinary Record*, *181*(19), 510-510. https://doi.org/10.1136/vr.104304
31. Hoelzer, K., Wong, N., Thomas, J., Talkington, K., Jungman, E., & Coukell, A. (2017). Antimicrobial drug use in food-producing animals and associated human health risks: What, and how strong, is the evidence? *BMC Veterinary Research*, *13*(1). https://doi.org/10.1186/s12917-017-1131-3
32. Kaur, K., Singh, S., & Kaur, R. (2024). Impact of antibiotic usage in food-producing animals on food safety and possible antibiotic alternatives. *The Microbe*, *4*, 100097. https://doi.org/10.1016/j.microb.2024.100097
33. Khan, S. A., Imtiaz, M. A., Sayeed, M. A., Shaikat, A. H., & Hassan, M. M. (2020). Antimicrobial resistance pattern in domestic animal - wildlife - environmental niche via the food chain to humans with a Bangladesh perspective; a systematic review. *BMC Veterinary Research*, *16*(1). https://doi.org/10.1186/s12917-020-02519-9
34. Kimera, Z. I., Mshana, S. E., Rweyemamu, M. M., Mboera, L. E., & Matee, M. I. (2020). Antimicrobial use and resistance in food-producing animals and the environment: An African perspective. *Antimicrobial Resistance & Infection Control*, *9*(1). https://doi.org/10.1186/s13756-020-0697-x
35. Kuhnke, D., Werner, N., & Kreienbrock, L. (2020). Occurrence of ESBL-producing *Escherichia coli* in healthy, living food-producing animals in Europe: A systematic review. *CABI Reviews*. https://doi.org/10.1079/pavsnnr202015010
36. Kujat Choy, S., Neumann, E., Romero-Barrios, P., & Tamber, S. (2024). Contribution of food to the human health burden of antimicrobial resistance. *Foodborne Pathogens and Disease*, *21*(2), 71-82. https://doi.org/10.1089/fpd.2023.0099
37. Lekshmi, M., Ammini, P., Kumar, S., & Varela, M. F. (2017). The food production environment and the development of antimicrobial resistance in human pathogens of animal origin. *Microorganisms*, *5*(1), 11. https://doi.org/10.3390/microorganisms5010011
38. Lencina, F. A., Bertona, M., Stegmayer, M. A., Olivero, C. R., Frizzo, L. S., Zimmermann, J. A., Signorini, M. L., Soto, L. P., & Zbrun, M. V. (2024). Prevalence of colistin-resistant escherichia coli in foods and food-producing animals through the food chain: A worldwide systematic review and meta-analysis. *Heliyon*, *10*(5), e26579. https://doi.org/10.1016/j.heliyon.2024.e26579
39. Ma, F., Xu, S., Tang, Z., Li, Z., & Zhang, L. (2021). Use of antimicrobials in food animals and impact of transmission of antimicrobial resistance on humans. *Biosafety and Health*, *3*(1), 32-38. https://doi.org/10.1016/j.bsheal.2020.09.004
40. Magnusson, U. (2022). Antimicrobial use and resistance in food-producing animals—How can we protect the efficacy of antibiotics for reproductive diseases? *Reproduction in Domestic Animals*, *57*(S4), 13-20. https://doi.org/10.1111/rda.14170
41. Marshall, B. M., & Levy, S. B. (2011). Food animals and antimicrobials: Impacts on human health. *Clinical Microbiology Reviews*, *24*(4), 718-733. https://doi.org/10.1128/cmr.00002-11
42. Mediouni, M., Diallo, A. B., & Makarenkov, V. (2025). Quantifying antimicrobial resistance in food-producing animals in North America. *Frontiers in Microbiology*, *16*. https://doi.org/10.3389/fmicb.2025.1542472
43. Michael, G. B., Freitag, C., Wendlandt, S., Eidam, C., Feßler, A. T., Lopes, G. V., Kadlec, K., & Schwarz, S. (2015). Emerging issues in antimicrobial resistance of bacteria from food-producing animals. *Future Microbiology*, *10*(3), 427-443. https://doi.org/10.2217/fmb.14.93
44. Moffo, F., Ndebé, M. M., Tangu, M. N., Noumedem, R. N., Awah-Ndukum, J., & Mouiche, M. M. (2024). Antimicrobial use, residues and resistance in fish production in Africa: Systematic review and meta-analysis. *BMC Veterinary Research*, *20*(1). https://doi.org/10.1186/s12917-024-04158-w
45. Mouiche, M. M., Moffo, F., Akoachere, J. T., Okah-Nnane, N. H., Mapiefou, N. P., Ndze, V. N., Wade, A., Djuikwo-Teukeng, F. F., Toghoua, D. G., Zambou, H. R., Feussom, J. M., LeBreton, M., & Awah-Ndukum, J. (2019). Antimicrobial resistance from a one health perspective in Cameroon: A systematic review and meta-analysis. *BMC Public Health*, *19*(1).

https://doi.org/10.1186/s12889-019-7450-5

46. Moyane, J. N., Jideani, A. I. O., & Aiyegoro, O. A. (2013). Antibiotics usage in food-producing animals in South Africa and impact on human: Antibiotic resistance. *African Journal of Microbiology Research*, *7*(24), 2990-2997. https://doi.org/10.5897/ajmr2013.5631
47. Mshana, S. E., Sindato, C., Matee, M. I., & Mboera, L. E. (2021). Antimicrobial use and resistance in agriculture and food production systems in Africa: A systematic review. *Antibiotics*, *10*(8), 976. https://doi.org/10.3390/antibiotics10080976
48. Mulchandani, R., Wang, Y., Gilbert, M., & Van Boeckel, T. P. (2023). Global trends in antimicrobial use in food-producing animals: 2020 to 2030. *PLOS Global Public Health*, *3*(2), e0001305. https://doi.org/10.1371/journal.pgph.0001305
49. Muloi, D., Ward, M. J., Pedersen, A. B., Fèvre, E. M., Woolhouse, M. E., & Van Bunnik, B. A. (2018). Are food animals responsible for transfer of antimicrobial-resistant *Escherichia coli* or their resistance determinants to human populations? A systematic review. *Foodborne Pathogens and Disease*, *15*(8), 467-474. https://doi.org/10.1089/fpd.2017.2411
50. Nastasijevic, I., Proscia, F., Jurica, K., & Veskovic-Moracanin, S. (2023). Tracking antimicrobial resistance along the meat chain: One health context. *Food Reviews International*, *40*(9), 2775-2809. https://doi.org/10.1080/87559129.2023.2279590
51. Nobrega, D. B., Tang, K. L., Caffrey, N. P., De Buck, J., Cork, S. C., Ronksley, P. E., Polachek, A. J., Ganshorn, H., Sharma, N., Kastelic, J. P., Kellner, J. D., Ghali, W. A., & Barkema, H. W. (2020). Prevalence of antimicrobial resistance genes and its association with restricted antimicrobial use in food-producing animals: A systematic review and meta-analysis. *Journal of Antimicrobial Chemotherapy*, *76*(3), 561-575. https://doi.org/10.1093/jac/dkaa443
52. Nusrat, S., Murshed, H., & Afrin, S. (2025). Antibiotic Resistance at the Human–Animal–Environment Crossroads: A Systematic Review of the Silent Global Pandemic. Microbial Bioactives, 8(1), 1-7.
53. Okon, E. M., Okocha, R. C., Adesina, B. T., Ehigie, J. O., Alabi, O. O., Bolanle, A. M., Matekwe, N., Falana, B. M., Tiamiyu, A. M., Olatoye, I. O., & Adedeji, O. B. (2022). Antimicrobial resistance in fish and poultry: Public health implications for animal source food production in Nigeria, Egypt, and South Africa. *Frontiers in Antibiotics*, *1*. https://doi.org/10.3389/frabi.2022.1043302
54. Paintsil, E. K., Ofori, L. A., Adobea, S., Akenten, C. W., Phillips, R. O., Maiga-Ascofare, O., Lamshöft, M., May, J., Obiri Danso, K., Krumkamp, R., & Dekker, D. (2022). Prevalence and antibiotic resistance in campylobacter spp. Isolated from humans and food-producing animals in West Africa: A systematic review and meta-analysis. *Pathogens*, *11*(2), 140. https://doi.org/10.3390/pathogens11020140
55. Pal, M., Kerorsa, G. B., Marami, L. M., & Kandi, V. (2020). Epidemiology, pathogenicity, animal infections, antibiotic resistance, public health significance, and economic impact of Staphylococcus aureus: a comprehensive review. American Journal of Public Health Research, 8(1), 14-21.
56. Patel, S. J., Wellington, M., Shah, R. M., & Ferreira, M. J. (2020). Antibiotic stewardship in food-producing animals: Challenges, progress, and opportunities. *Clinical Therapeutics*, *42*(9), 1649-1658. https://doi.org/10.1016/j.clinthera.2020.07.004
57. Pereira, G. R., Portes, A. B., Conte, C. A., Brandão, M. L., & Spisso, B. F. (2025). Antimicrobial resistance in bacteria from pig production chain: A systematic review and meta-analyses focused on the Brazilian context. *Critical Reviews in Food Science and Nutrition*, *65*(32), 7987-8005. https://doi.org/10.1080/10408398.2025.2489531
58. Phillips, I. (2003). Does the use of antibiotics in food animals pose a risk to human health? A critical review of published data. *Journal of Antimicrobial Chemotherapy*, *53*(1), 28-52. https://doi.org/10.1093/jac/dkg483
59. Pokharel, S., Shrestha, P., & Adhikari, B. (2020). Antimicrobial use in food animals and human health: Time to implement 'One health' approach. *Antimicrobial Resistance & Infection Control*, *9*(1). https://doi.org/10.1186/s13756-020-00847-x
60. Rabello, R. F., Bonelli, R. R., Penna, B. A., Albuquerque, J. P., Souza, R. M., & Cerqueira, A. M. (2020). Antimicrobial resistance in farm animals in Brazil: An update overview. *Animals*, *10*(4), 552. https://doi.org/10.3390/ani10040552
61. Rahman, S., & Hollis, A. (2023). The effect of antibiotic usage on resistance in humans and food-producing animals: A longitudinal, one health analysis using European data. *Frontiers in Public Health*, *11*. https://doi.org/10.3389/fpubh.2023.1170426
62. Ramírez-Castillo, F. Y., Guerrero-Barrera, A. L., & Avelar-González, F. J. (2023). An overview of carbapenem-resistant organisms from food-producing animals, seafood, aquaculture, companion animals, and wildlife. *Frontiers in Veterinary Science*, *10*. https://doi.org/10.3389/fvets.2023.1158588
63. Ramos, S., Silva, V., Dapkevicius, M. D., Caniça, M., Tejedor-Junco, M. T., Igrejas, G., & Poeta, P. (2020). Escherichia coli as commensal and pathogenic bacteria among food-producing animals: Health implications of extended spectrum β-lactamase (ESBL) production. *Animals*, *10*(12), 2239. https://doi.org/10.3390/ani10122239
64. Rittscher, A. (2024). A Systematic Review of the Effect of Macrolide Use in Food Producing Animals and its Impact on Rates of Human Carriage and Disease of Macrolide-Resistant Bacteria. https://studenttheses.uu.nl/handle/20.500.12932/45725
65. Salisbury, J. G., Nicholls, T. J., Lammerding, A. M., Turnidge, J., & Nunn, M. J. (2002). A risk analysis framework for the long-term management of antibiotic resistance in food-producing animals. *International Journal of Antimicrobial Agents*, *20*(3), 153-164. https://doi.org/10.1016/s0924-8579(02)00169-3
66. Samtiya, M., Matthews, K. R., Dhewa, T., & Puniya, A. K. (2022). Antimicrobial resistance in the food chain: Trends, mechanisms, pathways, and possible regulation strategies. *Foods*, *11*(19), 2966. https://doi.org/10.3390/foods11192966
67. Scott, A. M., Beller, E., Glasziou, P., Clark, J., Ranakusuma, R. W., Byambasuren, O., Bakhit, M., Page, S. W., Trott, D., & Mar, C. D. (2018). Is antimicrobial administration to food animals a direct threat to human health? A rapid systematic review. *International Journal of Antimicrobial Agents*, *52*(3), 316-323. https://doi.org/10.1016/j.ijantimicag.2018.04.005
68. Signorini, M. L., Rossler, E., Díaz David, D. C., Olivero, C. R., Romero-Scharpen, A., Soto, L. P., Astesana, D. M., Berisvil, A. P., Zimmermann, J. A., Fusari, M. L., Frizzo, L. S., & Zbrun, M. V. (2018). Antimicrobial resistance of thermotolerant *Campylobacter* species isolated from humans, food-producing animals, and products of animal origin: A worldwide meta-analysis. *Microbial Drug Resistance*, *24*(8), 1174-1190. https://doi.org/10.1089/mdr.2017.0310
69. Silbergeld, E. K., & Dailey, J. L. (2017). Biological plausibility of associations between antimicrobial use in food-producing animals and increased risks of human exposures to, and

infections by, antimicrobial resistant zoonotic pathogens. WHO Guidelines on Use of Medically Important Antimicrobials in Food-Producing Animals.

70. Silva, V., Lopes, A. F., Soeiro, V., Caniça, M., Manageiro, V., Pereira, J. E., Maltez, L., Capelo, J. L., Igrejas, G., & Poeta, P. (2022). Nocturnal birds of prey as carriers of staphylococcus aureus and other staphylococci: Diversity, antimicrobial resistance and clonal lineages. *Antibiotics*, *11*(2), 240. https://doi.org/10.3390/antibiotics11020240
71. Smoglica, C., Carcagnì, A., Angelucci, S., Di Tana, F., Marsilio, F., López-Olvera, J. R., & Di Francesco, C. E. (2025). Systematic review and meta-analysis of antimicrobial resistant bacteria in free-ranging wild mammals. *BMC Veterinary Research*, *21*(1). https://doi.org/10.1186/s12917-025-04548-8
72. Somda, N., Tankoano, A., Métuor-Dabiré, A., Kaboré, D., Bonkoungou, J., Kpoda, D., Sambe-Ba, B., Dabiré, Y., Saba, C., Ouoba, I., Sawadogo-Lingani, H., & Savadogo, A. (2023). A systematic review and meta-analysis of antibiotic resistance of foodborne pathogenic bacteria in West Africa between 2010 and 2020. *Journal of Food Protection*, *86*(3), 100061. https://doi.org/10.1016/j.jfp.2023.100061
73. Sweileh, W. M. (2021). Global research activity on antimicrobial resistance in food-producing animals. *Archives of Public Health*, *79*(1). https://doi.org/10.1186/s13690-021-00572-w
74. Tadesse, T., Zenebe, T., Kebede, T., Gizaw, O., & Eguale, T. (2024). Prevalence and antimicrobial susceptibility profile of *Listeria monocytogenes* in humans, animals, and foods of animal origin in Ethiopia: A systematic review and meta-analysis. *Cogent Food & Agriculture*, *10*(1). https://doi.org/10.1080/23311932.2024.2306018
75. Tang, K. L., Caffrey, N. P., Nóbrega, D. B., Cork, S. C., Ronksley, P. E., Barkema, H. W., Polachek, A. J., Ganshorn, H., Sharma, N., Kellner, J. D., & Ghali, W. A. (2017). Restricting the use of antibiotics in food-producing animals and its associations with antibiotic resistance in food-producing animals and human beings: A systematic review and meta-analysis. *The Lancet Planetary Health*, *1*(8), e316-e327. https://doi.org/10.1016/s2542-5196(17)30141-9
76. Tang, K. L., Caffrey, N. P., Nóbrega, D. B., Cork, S. C., Ronksley, P. E., Barkema, H. W., Polachek, A. J., Ganshorn, H., Sharma, N., Kellner, J. D., Checkley, S. L., & Ghali, W. A. (2019). Comparison of different approaches to antibiotic restriction in food-producing animals: Stratified results from a systematic review and meta-analysis. *BMJ Global Health*, *4*(4), e001710. https://doi.org/10.1136/bmjgh-2019-001710
77. Tang, K. L., Caffrey, N. P., Nóbrega, D. B., Cork, S. C., Ronksley, P. E., Barkema, H. W., Polachek, A. J., Ganshorn, H., Sharma, N., Kellner, J. D., Checkley, S. L., & Ghali, W. A. (2019). Examination of unintended consequences of antibiotic use restrictions in food-producing animals: Sub-analysis of a systematic review. *One Health*, *7*, 100095. https://doi.org/10.1016/j.onehlt.2019.100095
78. Tiedje, J. M., Fu, Y., Mei, Z., Schäffer, A., Dou, Q., Amelung, W., Elsner, M., Adu-Gyamfi, J., Heng, L., Virta, M., Jiang, X., Smidt, H., Topp, E., & Wang, F. (2023). Antibiotic resistance genes in food production systems support one health opinions. *Current Opinion in Environmental Science & Health*, *34*, 100492. https://doi.org/10.1016/j.coesh.2023.100492
79. Tollefson, L., & Miller, M. A. (2000). Antibiotic use in food animals: Controlling the human health impact. *Journal of AOAC INTERNATIONAL*, *83*(2), 245-254. https://doi.org/10.1093/jaoac/83.2.245
80. Torres, R. T., Carvalho, J., Fernandes, J., Palmeira, J. D., Cunha, M. V., & Fonseca, C. (2021). Mapping the scientific knowledge of antimicrobial resistance in food-producing animals. *One Health*, *13*, 100324. https://doi.org/10.1016/j.onehlt.2021.100324
81. Van Duijkeren, E., Greko, C., Pringle, M., Baptiste, K. E., Catry, B., Jukes, H., Moreno, M. A., Pomba, M. C., Pyorala, S., Rantala, M., Ru auskas, M., Sanders, P., Teale, C., Threlfall, E. J., Torren-Edo, J., & Torneke, K. (2014). Pleuromutilins: Use in food-producing animals in the European Union, development of resistance and impact on human and animal health. *Journal of Antimicrobial Chemotherapy*, *69*(8), 2022-2031. https://doi.org/10.1093/jac/dku123
82. Vidovic, N., & Vidovic, S. (2020). Antimicrobial resistance and food animals: Influence of livestock environment on the emergence and dissemination of antimicrobial resistance. *Antibiotics*, *9*(2), 52. https://doi.org/10.3390/antibiotics9020052
83. Wiśniewski, P., Trymers, M., Chajęcka-Wierzchowska, W., Tkacz, K., Zadernowska, A., & Modzelewska-Kapituła, M. (2024). Antimicrobial resistance in the context of animal production and meat products in Poland—A critical review and future perspective. *Pathogens*, *13*(12), 1123. https://doi.org/10.3390/pathogens13121123
84. Xiong, W., Sun, Y., & Zeng, Z. (2018). Antimicrobial use and antimicrobial resistance in food animals. *Environmental Science and Pollution Research*, *25*(19), 18377-18384. https://doi.org/10.1007/s11356-018-1852-2
85. Zhou, Y., Zhang, A., Van Klinken, R. D., Jones, D., & Wang, J. (2025). Consumers' perspectives on antibiotic use and antibiotic resistance in food animals: A systematic review. *npj Science of Food*, *9*(1). https://doi.org/10.1038/s41538-025-00381-3