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REVIEW ARTICLE

Transmission Dynamics of Antimicrobial Resistance from Farm to Fork

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ABSTRACT

Contemporary animal production systems routinely employ antimicrobials, which significantly contribute to the selection pressure leading to antimicrobial resistance (AMR), a silent pandemic. The global animal-derived food chain along with intricated associated environment is linked with transmission of antibiotic-resistant bacteria (ARB), antibiotic resistance genes (ARGs) and drug residues. Circulation and transmission dynamics of such AMR drivers challenge good health and well-being of humans and animals leading to economic and life losses. The dissemination of resistant pathogens from foods of animal-origin to humans can result in severe clinical consequences limiting antibiotic treatment options as well as causing global trade and economic impacts. The holistic One Health approach can address global health challenge of AMR with innovative research and policy interventions. AMR stewardship, joint action plan, awareness and political commitment can provide evidence-based solutions to achieve sustainability and health resilience. Judicious antimicrobial usage, import and reduced consumption in animal production systems, veterinary practice and implementation of the WHO-FAO-WOAH-UNEP quadripartite guidelines are imperative to curb AMR or superbugs. The review collated data of situation analysis of AMR, antibiotic usage in animal production to treatment, mechanism of drug resistance, economic impact and future global directions to prepare for the silent pandemic of AMR. The One Health joint plan of action (2022-2026) framework for AMR has been elaborated in the context of low- and middle-income countries to implement decisive actions at the animal-human-environment triad.

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INTRODUCTION

Globally, the escalating concern of antimicrobial resistance (AMR) poses a significant health challenge, with an estimated 10 million deaths by 2050 (Price, 2016). The excessive use of antimicrobials in food-producing animals (FPAs) predominantly drives the transmission of AMR and resistance genes to humans through the food chain. This transmission occurs both directly through livestock contact and indirectly through animal waste (manure and slurry), which subsequently contaminates agriculture, aquaculture, and the environment (Abraham *et al.,* 2025). Consequently, there has been a notable dissemination of antimicrobial-resistant pathogens in humans, animals, and environment.

Farm to fork cycle of AMR dissemination, mechanism of resistance development and its consequences are illustrated in Fig. I. Non-judicious use of antibiotics in animal production systems (animal feed to clinical usage), hospital and pharmaceutical waste results in persistence of antibiotic residues in the ecosystem (Fig. I). Antibiotic residues exert selection pressure on microbes resulting in development of mutations and emergence of antibiotic resistance genes/multi-drug-resistant pathogens. The irrigation of agricultural fields and food chain with adulterated water contributes to spread of antibiotic-resistant microbes to consumers through agriculture and animal products. The vectors, animals, and environmental reservoirs contribute to AMR dissemination. Climate change augments transmission dynamics of AMR through persistence of ARGs in the environment and by migratory birds/animals as reservoirs. To circumvent the AMR menace, robust genome-based surveillance programs, infection prevention and control (IPC), WASH implementation, agri-food system improvement, public awareness and AMR stewardship in One Health perspective are quintessential (Fig. I).

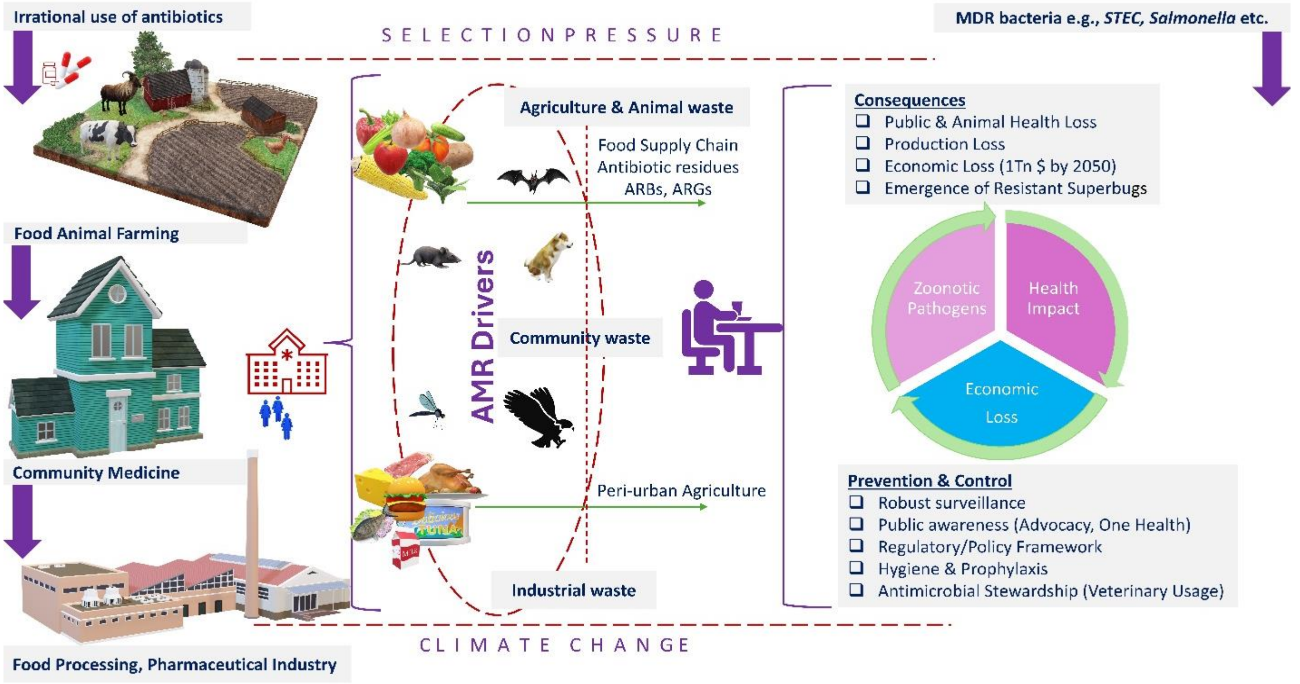

Fig. 1: Global animal-derived food chain AMR dynamics and its mitigation employing One Health approach.

This necessitates implementation of preventive action plan in FPAs, particularly in low- and middle-income countries (Van Boeckel *et al.,* 2017). The antimicrobials use as growth promoters and as prophylactics to mitigate disease outbreaks in livestock and aquaculture pose a challenge to curb AMR (Mulchandani *et al.,* 2023; Acosta *et al.,* 2025). Notably, economic analyses have aided policymakers in identifying the central drivers behind the alarming surge in antimicrobial use and evidence-based decision making (Baird *et al.,* 2025).

Over the last two decades, there has been a staggering increase in antimicrobial usage across European countries, Asia, and Africa. This dramatic upsurge in antimicrobial use can likely be attributed to the increasing global population and the growing demand for animal-derived products. Within this context, the emergence of AMR is more pronounced in the poultry industry compared to the livestock sector within low socio-economic settings. This discrepancy is attributed to the unsanitary and polluted conditions prevalent in animal environments. Such conditions play a pivotal role in the transmission and recurrence of infections, thus contributing significantly to the proliferation of AMR. The environmental reservoirs of AMR are rivers, canals, lakes, coastal waters, sewage pipelines and wastewater drains. The companion, pet animals, wildlife, predators, rodents, migratory birds and game birds are important but neglected reservoirs of AMR globally (Salam *et al.,* 2023).

The primary AMR pathogens have been identified by the World Health Organization (WHO) as *Enterobacteriaceae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*. Within the realm of *Enterobacteriaceae*, particular attention is directed towards *E. coli* due to its role as a prominent food-borne zoonotic pathogen, closely followed by *Salmonella* spp. and *Campylobacter* spp. (WOAH, 2024). The dissemination of these pathogens occurs through excretions such as urine and feces, contributing to their presence in the surrounding environment (Zhu *et al.,* 2013).

Notably, among the *Enterobacteriaceae* family, strains harboring the drug-resistance extended-spectrum beta-lactamase (ESBL) gene have exhibited rapid dissemination in the gastrointestinal tract of both humans and animals (Pires *et al.,* 2022). These antibiotic-resistant microorganisms, carrying genes conferring resistance, have now become intertwined with environmental pollutants, hospital waste discharge, and contaminated wastewater. A poignant example can be found in India, where effluents carry extended-spectrum cephalosporins and fluoroquinolones contributing to increased AMR (Diwan *et al.,* 2012).

Mechanisms of bacterial drug resistance include spontaneous mutations or by acquiring genes from other bacteria during reproduction, transduction (through bacteriophages), conjugation (cell-to-cell contact and genetic material exchange), and transformation (uptake of free DNA through cell lysis). Mobile genetic elements such as plasmids, integrases, and transposons play a role in the rapid spread of resistance through horizontal gene transfer (HGT) among different bacterial species. Recipient cells acquire both the resistant genes and the virulence factors of the donor cell (Hegstad *et al.,* 2010). The emergence of multi-drug-resistant microbes and the therapeutic failure of antimicrobials have caused widespread concern in society and underscored the urgent need for the development of new antimicrobial strategies to address new challenges in the community.

This review collated data of various facets that directly or indirectly contribute to the dissemination of AMR, antibiotic-resistant bacteria (ARB), or antibiotic resistance genes (ARGs) in animal food chain, ultimately impacting human health. This review provides insights into disease prediction models and policymakers to establish connections between antimicrobial usage in FPAs and the emergence of diverse infections in humans, driven by multidrug-resistant (MDR) pathogens and to take corrective measures to address AMR.

Drivers of AMR in animal-derived food chain: The animals shed and spread drug residues into the environment through contaminated wastewater and sludge. This contamination can then reach humans through direct exposure to waste, consumption of vegetation irrigated with such water, and even mix with clean water supply lines. Inappropriate animal waste disposal practices can further increase the prevalence of antibiotics and their residues (Elbehiry and Marzouk, 2025). Denmark firstly address this issue by implementing a complete ban on growth-enhancing drugs commonly used in animal husbandry to prevent the development of MDR pathogens (Muaz *et al.,* 2018). Although maximum antibiotic limits are not exceeded in animal-derived food but antibiotic residues can persist for a long time in the environment (Li *et al.,* 2017; Fatima *et al*., 2026). Data reported transmission of antibiotic resistance from food animals to humans, transmission of drug-resistant genes into the broader community and workplaces is indeed a potential threat to society (Kim *et al.,* 2019). However, in low- and middle-income countries (LMICs), limited steps have been taken to reduce AMR due to poor supervision, which remains a significant cause of resistant infections in those regions (Wall *et al.,* 2016). Investigations have shown a strong link between the use of various classes of antimicrobials and the frequency of antimicrobial-resistant commensal *E. coli* in pigs, poultry, and cattle (You and Silbergeld, 2014). The risk of AMR is exacerbated by the movement of people, food products, and the absence of environmental barriers in different communities.

The increasing global demand for animal protein has driven the expansion of intensive farming practices, resulting in high AMU and contributing to the emergence of MDR pathogens, persistence of drug resistance genes and drug residues in the environment. An estimated 73% of all antimicrobials sold globally are used exclusively in FPAs (Van Boeckel *et al.,* 2017; Matheou *et al.,* 2025) which is a significant contributor to the transmission of MDR pathogens to humans and their surroundings.

Reports spanning from 2001 to 2022 indicate a notable increase in resistance percentages attributed to excessive AMU, particularly drugs like streptomycin, sulphonamides, and tetracycline. This increase has been predominantly observed in pigs (51.8%), followed by chickens (25.9%), and the livestock sector, specifically broilers (11.1%) (Chowdhury *et al.,* 2022). Voluntary bans on the use of such drugs may reduce likelihood of AMR transmission in bacteria by up to 15%, and MDR transmission by 24% to 32% (Maron *et al.,* 2013).

The transmission of AMR by antibiotic-resistant bacteria in FPAs can occur through direct contact with humans, primarily via consumption of raw foods or inadequately cooked items. Indirect transmission occurs through contaminated wastewater, which is often used for irrigation in peri-urban areas and mixed with clean water supplies. Furthermore, AMR can spread in the environment through animal waste. In this context, resistant bacteria carrying ARGs can be found in wastewater treatment plants, where they accumulate in sludge and act as reservoirs for human and animal transmission (Nguyen *et al.,* 2021). The interplay between humans, animals, and the environment establishes a multidirectional connection that dictates actions across all health sectors against AMR, a concept referred to as the One Health approach (Zhang *et al.,* 2024). The One Health global joint action plan 2022-2026 developed a roadmap to curb AMR and pandemics by AMR stewardship programs and policy implementation engaging veterinary, medical and ecosystem sectors.

Foodborne MDR pathogens of animal origin: The impact of foodborne resistant pathogens on public health varies and is complex, contingent on factors such as excessive antimicrobial usage in farming, slaughter practices, storage and distribution systems, access to clean water, hygiene practices, and cooking methods. While there is ongoing debate about the precise impact of these resistant foodborne pathogens on health, there is consensus that regardless of the reasons for antimicrobial usage (as growth promoters or disease prevention), the resistant pathogens can transfer through animal processing units. Notable MDR Gram-positive microbes include *Staphylococcus aureus, Listeria monocytogenes, Clostridium botulinum, and Bacillus cereus. Listeria monocytogenes* is a facultative foodborne MDR bacterium often isolated from dairy products (Ali and Alsayeqh, 2022). Unhygienic and ready-to-eat foods are the main sources of infection. *L. monocytogenes* has demonstrated resistance against antibiotics like kanamycin, streptomycin, and cephalosporins in cheese (Gebretsadik *et al.,* 2011). Gram-negative organisms comprise *Salmonella* spp., *Shigella* spp., and *Escherichia coli O157:H7*. It has been further revealed that the rapid increase in infections can largely be attributed to methicillin-resistant *Staphylococcus aureus*, cephalosporin, and fluoroquinolone-resistant *E. coli*, fluoroquinolone-resistant *Campylobacter* species, and streptomycin, gentamicin, and tetracycline-resistant *Salmonella* species (Yaseen *et al.,* 2025). In some cases, strains of *Staphylococcus aureus* have been associated with food poisoning and act as superbugs, displaying resistance against methicillin, commonly known as Methicillin-Resistant *Staphylococcus aureus* (MRSA).

According to the CDC, *Salmonella enterica* is one of the most important MDR zoonotic pathogens involved in multiple food-related outbreaks, as it can contaminate food supply chains at any stage of processing. In a study conducted in the USA, multiple *Salmonella* strains (up to 20) were identified in both animals and humans, suggesting zoonotic transmission and resistance to streptomycin, ampicillin, and tetracycline (Puzari *et al.,* 2018). *Shigella* is another significant MDR foodborne pathogen that causes high death rates of up to 600,000 annually worldwide (Puzari *et al.,* 2018).

AMR in FPAs-human-environment nexus: One of the key factors contributing to the escalation of AMR is the inadequate use of antimicrobials in animal production and lack of awareness. Antimicrobial growth promoters (AGPs) like Sulfasuxidine, Streptothricin, and Streptomycin were firstly used in chicken and pig feed as reported by Moore, Stokstad and Jukes in the mid-1950s. Food, water, and manure are primary sources through which resistant bacteria can be transmitted to humans (Hedman *et al.,* 2020). Various strains of enterococci, *E. coli*, and *Salmonella*, which are common foodborne pathogens, have demonstrated similar associations in both human and animal populations. Reports of AMR in FPAs date back to the 1950s when streptomycin was administered to turkeys, leading to observed resistance.

In the United States and Europe, over two million infections and 25,000 deaths annually are attributed to antibiotic-resistant pathogens. These resistant bacteria can easily be transmitted to individuals working in farmhouses, slaughterhouses, veterinary settings, and those in close contact with these environments due to their daily exposure to infected animals (Balta *et al.,* 2024). The presence of ESBL producing *E. coli* strains was also observed in Algeria (Barour *et al.,* 2019). Patients infected with *E. coli*, as well as animals and raw meat, were found to harbor isolates of the mcr-1 gene in *E. coli* strains during the period of 2011-2014 (Liu *et al.,* 2016). Genetic links between human ciprofloxacin-resistant *E. coli* strains and poultry-resistant *E. coli* strains have also been established. An investigation in Canada found that discontinuing the use of ceftiofur injection, which was used for the growth of eggs and chickens, resulted in a reduction of resistant Salmonella isolates in both humans and poultry strains. A study examining the use of nourseothricin in pig food for approximately two years revealed that resistant plasmids containing nourseothricin resistance genes were not only present in pigs but also in the gut flora of farm workers, their families, water sources, manure, and food. These plasmids were also responsible for causing 1% of urinary tract infections in humans (Bich *et al.,* 2019).

The last option of antibiotics, such as colistin, has demonstrated resistant plasmids in *Klebsiella*, *E. coli*, and *Salmonella* strains both in humans and farm animals across regions including Asia, Africa, Europe, and North America (Vieira *et al.,* 2011; Ahmad *et al.,* 2021). Studies have established a strong correlation between amoxicillin-resistant *E. coli* in food animals and humans. An outbreak of extensively drug-resistant (XDR) *Salmonella* strains in Pakistan exhibited 100% resistance to fluoroquinolones in 2016 (Qamar *et al.,* 2018) and 93.7% of isolates from bloodstream infections were resistant to third-generation cephalosporins.

Global AMU in FPAs: The exponential growth of the global population and increasing demand for animal protein worldwide prompted 70% use of antibiotics in animal production systems and 30% in clinical human use (Naylor *et al.,* 2020). A substantial portion of animals, up to 73%, is raised for food purposes, and a diverse array of antimicrobials are employed in these settings to mitigate microbial loads (Van Boeckel *et al.,* 2019). Data have shown that the immoderate use of drugs in animal farming may constitute a primary source of AMR in human and environment (Webb *et al.,* 2016). For instance, excessive use of fluoroquinolones in FPAs correlates with resistance mechanisms observed in indicator organisms such as *E. coli*, *Salmonella* spp., and *Campylobacter jejuni* in both animals and humans. Similarly, the usage of tetracycline has shown analogous resistance pattern in *E. coli*, *Salmonella* spp., and *C. jejuni* (EFSA 2017). This scenario becomes even more perilous if identical or modified versions of these antimicrobials are prescribed for human clinical use. A noteworthy trend is the substantial decline in commensal *E. coli* isolated from livestock and poultry sectors. Gram-negative microbes, due to their complex mixture of peptidoglycans and lipopolysaccharides (LPS), exhibit enhanced resistance to certain antibiotics, such as penicillin G. This resistance arises from the inability of these drugs to traverse the outer cell wall layer (Klein *et al.,* 2024).

Data on usage of antimicrobials in food animals reported from 42 countries revealed global consumption of antimicrobials in FPAs estimated at 99,502 tons in 2020, with potential increase up to 107,472 tons by the year 2030. Asia remained a main hotspot of AMR with a global AMU up to 67% (Mulchandani *et al.,* 2023). However, another study demonstrated that global antibiotic usage could reach ~143,481 tons by 2040, representing a 29.5% increase from the 2019 baseline of ~110,777 tons (Acosta *et al.,* 2025). The AMU exhibits considerable diversity among countries, ranging from a minimum of 8 mg/population correction unit (PCU) in Norway to a maximum of 318 mg/PCU in China. China, being a major player in veterinary antimicrobial distribution, plays a crucial role in the context of AMR management. Simultaneously, China remains pivotal as the last resort for certain drugs intended to combat human infections. Contrasting this, European practices still encompass the use of these antimicrobials within animal husbandry.

Reports indicate that a significant portion, approximately 93.75%, of antimicrobials is consumed by chicken, cattle, and pigs among all food animals (Tiseo *et al.,* 2020; Mulchandani *et al.,* 2023). The consumption of antimicrobials was previously recorded at 93,309 tons in 2017 and is projected to rise to 104,079 tons by 2030, representing an increase of 11.5% (Tiseo *et al.,* 2020). Within the livestock sector, there is a predicted 45% surge in antimicrobial consumption in pigs, with an average previous antimicrobial usage of 193 mg/PCU.

Turning to the dairy sector, there is a slight global increase of 22% in antimicrobial consumption among cattle. Previously, the antimicrobial consumption stood at 42 mg/PCU, which is the lowest amount per animal weight compared to other animal-derived food groups. Within the poultry industry, among chicken, antimicrobial usage was 68 mg/PCU, contributing to a 33% global increase on average (Tiseo *et al.,* 2020; Hosain *et al.,* 2021; Mulchandani *et al.,* 2023).

Among the continents, Asia emerges as the largest consumer of antimicrobials since 2017, with a consumption of 57,167 tons projected to reach 63,062 tons by 2030, reflecting a 10.3% anticipated rise. In Asia, the projected antimicrobial usage in 2030 accounts for a > 55% increase globally from the 2017 levels. Over the last few decades, Africa has consumed a comparatively smaller number of antimicrobials (4606 tons) in comparison to other continents. A predicted increase of 37% is anticipated, resulting in a 6.1% global rise in antimicrobial consumption by 2030. Conversely, reduced antimicrobial sales are expected in Oceania, North America, and Europe (3.1%, 4.3%, and 6.7% respectively) (Mulchandani *et al.,* 2023).

In animal production systems, China and Brazil have consistently ranked top in AMU, contributing to a 45% increase in global consumption. This trend is projected to persist until 2030, with a predicted 43% consumption rate (Van Boeckel *et al.,* 2015; Mulchandani *et al.,* 2023). The antimicrobial stewardship program encompasses a range of parameters, including disease control strategies, antibiotic resistance patterns, and practical guidelines for the judicious use of individual drugs. Table-1 demonstrated a comprehensive overview of antimicrobial usage in FPAs, MDR pathogens, and relevant ARGs by continent.

Table-1: Spatial distribution of antimicrobial usage, multi-drug-resistant pathogens, genes and sequence types (STs) in food producing animals

Region	Country	FPA origin	Pathogen	AMU%	Antibiotics	No. of farms	Associated Factors	STs	ARGs	Reference
Asia	Japan	Cattle swine	*S.* Typhimurium *Sal. enterica*	86%	Ampicillin, Sulfonamides, Macrolides, Tetracycline, Polymyxin, Chloramphenicol, Quinolones, Gentamycin	214	higher external security, isolated farms, less post weaning death rate will lower AMU	ST19 ST213	*bla*$_{TEM}$, strA, strB,Sul2,tet(B)	(Isomura *et al.,* 2018)
	Thailand	swine	*Salmonella spp.*	75%	Ampicillin, Sulfonamides, Macrolides, Tetracycline, Polymyxin, Chloramphenicol, Quinolones,	114	small size pig farms, less resistance fluoroquinolones	ST34	sul3 sul3, tet(A), aph (3')-Ia, foR, lnu(F), dfrA14, aac(3)-Iia	(Pires *et al.,* 2022)
	Bangladesh	poultry		broiler =52% layer= 37%	Macrolides, Tetracycline, Polymyxin, Chloramphenicol, Quinolones, Penicillin	768	chicken morbidity, farm location	-	-	(Imam *et al.,* 2021)
	Vietnam	pig	*E. coli*	72%	Ampicillin, Sulfonamides, Macrolides, Tetracycline, Polymyxin, Chloramphenicol, Quinolones,	116	less veterinary facility, easy access to antimicrobials, less safety parameters opted at farm level	-	-	(Truong *et al.,* 2021)
Africa	Kenya	Sheep Cattle	MRSA	94%	Tetracycline Macrolides, Oxacillin, Aminoglycosides, beta-lactams	603	-	ST338	mecA, (tetK, tetM, blaZ, (msrA/ermA), s (blaZ),	(Omwenga *et al.,* 2021)
	Sudan	Dairy cattle	*E. coli* *K. pneumoniae*	93%	Tetracycline Gentamycin, Ciprofloxacin, Ampicillin, Imipenem	25 village	-	ST1485 ST219	*bla*$_{SHV-F}$ *bla*$_{SHV-R}$ tetK, tetM	(Badri *et al.,* 2017)
	Nigeria	poultry	*Salmonella spp.*	68%	Tetracycline Gentamycin, Ciprofloxacin, Sulfonamide, Oxacillin, Macrolides	41	Irrational AMU	ST11	sul3, tet(A), tet(B)	(Jibril *et al.,* 2021)
	Malawi	Livestock manure	*E. coli* *K. pneumoniae*	52%	Cefotaxime, Sulfamethoxazole–trimethoprim, Gentamycin	4	Untreated livestock manure	-	*bla*ctx-m-$_{14}$ and *bla*ctx-m-$_{79}$	(Abraham *et al.,* 2025)
GCC	Saudi Arabia	FPAs	*E. coli,* *Salmonella,* *S. aureus,* *Campylobacter*	70%	Amikacin Ampicillin Chloramphenicol Ciprofloxacin Gentamycin Kanamycin trimethoprim	Different sources	Irrational AMU	-	*bla*$_{CTX-M}$, *mcr-1*, and *tetM*	(Elbehiry and Marzouk, 2025)
US	United states	Mink	Non. typhoidal Salmonella	26.60% 12.50%	Ampicillin, Streptomycin, Tetracycline, Sulfisoxazole	1	-	ST183	*bla*$_{TEM}$ sul2 tetA	(Agga *et al.,* 2022)
South America	Brazil	pig	*E. coli*		Beta-lactams, Tetracycline, Sulfonamides	30	-	ST10	*bla*$_{SHV}$ *bla*$_{OXA}$ *bla*$_{CTX-M}$ sul3, aadA cmlA	(Blanco-Lizarazo and Sierra-Cadavid 2023)
	Mexico	poultry	*Salmonella enterica*	75%	Tetracycline, Macrolides, Quinolones, Sulfonamides	43	Vaccination status Farmers clothing Workers personal hygiene	ST15	hilA, orgA, sifA, ssaQ sseL	(Ornelas-Eusebio *et al.,* 2020)
European union	Denmark Spain France	turkey	*E. coli*	60 - 70%	Tetracycline, Macrolides, Quinolones, Sulfonamides, Fluoroquinolones, beta lactams	60	More visitors Turkey moves outside farm Diff age groups mix	ST156 ST23	ermB, tetW sul2 aph3	(Horie *et al.,* 2021)
	Netherland	Dairy sheep goat	STEC *E. coli*	65%	Tetracycline, Macrolides, Quinolones, Sulfonamides,	182	-	ST131 ST38 ST1193	Stx genes TetA, fosA7 StrA, StrB SulA, *bla*$_{TEM}$	(Van Hoek *et al.,* 2023)

					Fluoroquinolones, beta lactams					
	Sweden	Young calves	*E. coli*	26 to 60%	Tetracycline, Macrolides, Quinolones, Sulfonamides, Fluoroquinolones, beta lactams, ceftazidime	30	Low internal and external biosecurity	ST69 ST648	Mcr-1-5 ESBL genes	(Backhans *et al.,* 2016)
	Germany	Turkey poultry	*E. coli*	71%	Ampicillin, Colistin, Tetracycline, Gentamycin, Aminopenicillin	Turkey =185 chicken =344	Weak security outside farm, Respiratory diseases	-	-	(Mesa-Varona *et al.,* 2020)
	Italy	pig	ETEC *E. coli*	83%	Ampicillin, Colistin, Tetracycline, Gentamycin, Aminopenicillin, Lincosamide	826	Excessive prophylactic use of antimicrobials	ST10 ST361 ST641 ST48	*E. coli* adhesion gens (F4, F5, F6, F8) Toxin genes (LT, STaP, STb)	(Bassi *et al.,* 2023)
	Finland	pig	*E. coli*	59.60%	Ampicillin, Colistin, Tetracycline, Gentamycin, Aminopenicillin	406	Poor farm management Musculoskeletal disorders	-	-	(Stygar *et al.,* 2020)
	Spain	swine	*E. coli, Enterococcus* spp.	60%	Penicillin, Aminoglycosides, Sulfonamides, Lincosamide, Phenolics	37 15	Organic farms have low AMU	ST183 ST59 ST23 ST11626 ST69 ST2930	tetL, tetM cfr, optrA $bla_{\text{CTX-M-14}}$ ST405	(Mencía-Ares *et al.,* 2021)
Australia	New Zealand	Dairy cattle	ESBL *E. coli*	65%	Penicillin, Aminoglycosides, Sulfonamides, Lacosamide, Phenolics, Penicillin	19	-	ST69 ST2930	$bla_{\text{CTX-M-14}}$ ST405	(Collis *et al.,* 2019)

Economic impact of AMR: Globally, AMR stands as a paramount health concern due to its economic and health impact on delayed treatment and the dissemination of infectious diseases. The prevalence of AMR varies rapidly across nations, with the United States, for instance, grappling with an alarming annual cost of up to $55 billion, encompassing expenses within the healthcare sector and inadequate production costs (Utt and Wells, 2016).

Moreover, the World Bank's 2017 data indicated a decline in annual global GDP by 1.1% to 3.8% in low-impact to high-impact scenarios by 2050. The World Economic Forum, 2024 data estimated $100 trillion (cumulative global loss) due to AMR by 2050 in worst-case scenarios. This substantial economic loss is attributed to the impact of AMR with additional annual cost of $1 trillion in healthcare by 2050, it may lead to 28 million people into poverty. Prolonged exposure to AMR among the workforce could lead to a significant reduction in global trade forecasting an anticipated 11% decrease by 2050. The livestock sector mirrors a similar pattern of resistance concerning AMR, where non-judicious use of antimicrobials for growth promotion and disease prevention led to persistence of AMR and trade halts due to drug residues. The exacerbated AMR effect contributes to food insecurity with annual decline of 2.6% to 7.5% in global livestock production by 2050.

Preventive Measures and Global AMR Policy Insights: AMR has now become an integral part of the global trade landscape, impacting on international organizations and trade agreements. Collaborative efforts involving organizations like the FAO-WHO-WOAH-UNEP and initiatives of Codex Alimentarius Commission provided guidelines for rational use of antimicrobials in the context of AMR. Establishing robust surveillance and monitoring systems is crucial for early detection and mitigation of AMR. Inappropriate usage of antibiotics as animal feed additives has been addressed by various countries by implementing restrictions or bans on its use as growth promoters. The UK Government, for instance, placed the first ban on tetracycline in the mid-1970s, leading to a reduction in tetracycline-resistant strains. Other European countries like Norway, Denmark, and Sweden took similar steps, discontinuing the use of antimicrobials such as bacitracin, virginiamycin, tylosin, and spiramycin, which were also used in human medicines. In 2006, most European countries banned the use of antimicrobial growth promoters (AGPs) altogether (Grave *et al.,* 2006).

Following the ban on AGPs, the therapeutic use of antibiotics increased, and negative effects on factors like mortality, weight gain, and food products were not observed (Aarestrup *et al.,* 2010). Some countries experienced an increase in the incidence of conditions like colitis in pigs and necrotizing enteritis in chickens shortly after the AGPs ban. Research indicated that antibiotic use in the swine industry increased after the ban, while therapy intensity remained stable. These observations highlight the complex dynamics that can arise when addressing AMR in animal agriculture and the need for careful consideration of the consequences of regulatory changes.

Implementing a complete ban on antibiotic usage in animal production can have significant implications for animal health, production, and food prices. However, careful management of feed and maintaining good hygienic conditions can help mitigate the adverse effects of such bans in animal production system (Van Boeckel *et al.,* 2015). The WHO advises member countries to develop National Action Plans to address AMR in food production, including the use of antibiotics as growth promoters and reduction of therapeutically important antibiotics in animal feed.

The United Nations (UN) and FAO have acted through an AMR action plan, focusing on investigating and monitoring the optimal use of antimicrobials in animal agriculture. The UK government, for instance, established the Fleming Fund to address AMR through cross-disciplinary collaboration (Al-Khalaifah *et al.,* 2025). Despite these efforts, tackling AMR remains a global challenge, and progress could not achieve desired levels (Mestrovic *et al.,* 2022). In developing countries like Pakistan, combating the prevalence of AMR requires concerted efforts and the implementation of effective strategies. Despite efforts to implement antimicrobial stewardship programs in Pakistan, studies have shown that inappropriate antibiotic use and low awareness among physicians remain significant challenges. In Pakistan, antibiotic consumption was alarmingly high, reaching up to 65% between 2000 and 2015 (Klein *et al.,* 2018). A global study indicated that antibiotics were being sold without prescription in Pakistan (Morgan *et al.,* 2011). In countries like Pakistan, antibiotic supply is regulated by conventional laws, and antibiotics should only be dispensed with a prescription written by a physician. The global picture reveals that only 42 countries have developed systems to report the use of antimicrobials in FPAs (Rushton *et al.,* 2014). Developing countries have reported inappropriate antimicrobial use due to complex policies and limited implementation, among other factors. The AMR global action plan, policy and governance index have been improved; however, disparities in AMR stewardship exist owing to low economic status of the countries, availability of clean water, sanitation and awareness (Patel *et al.,* 2026).

Stewardship programs can be initiated in developing countries through alternatives to antibiotics, biosecurity measures and promoting better hygienic standards in livestock production system following Global Antimicrobial Resistance and Use System (GLASS) and HACCP guidelines. This requires a comprehensive understanding of antimicrobial use for FPAs (Baird *et al.,* 2025). Public education and awareness campaigns can significantly contribute to the reduction of antimicrobial misuse and overuse. A collaborative and robust surveillance system is imperative in the pursuit of enhancing animal health, agricultural practices, and the quality of food products, research into alternative and organic approaches is indispensable (Balkhy *et al.,* 2018; Pinheiro *et al.,* 2020). Although antimicrobial growth promoters (AGPs) historically boosted livestock productivity, it contributed to global AMR. Novel alternatives to antibiotics or AGPs, including probiotics, herbal medicine, bacteriophages, and immune-stimulating agents, are recommended in animal production systems (Ibeagha-Awemu *et al.,* 2025). Use of nutritional and biochemical additives such as organic acids, fungal metabolites and enzymes is also promising to tackle AMR. The application of antimicrobial polymers, nanoparticles, and liposomes for antibiotic delivery has been explored in several studies (Gao *et al.,* 2014). Additionally, the CRISPR-Cas system, known as the clustered regularly interspaced short palindromic repeats-CRISPR-associated system, presents a contemporary approach to combat antimicrobial-resistant strains. The programmable Cas nuclease of CRISPR-Cas, when directed against bacterial genomic sequences, holds promise in decreasing AMR (Gholizadeh *et al.,* 2020). By offering an array of tools, bioinformatics has significantly contributed to drug development and combat against AMR. For instance, homology modeling enables the creation of 3D structures of macromolecules, facilitating a comprehensive understanding of their intricacies.

Conclusion and way forward: AMR has emerged as an alarming global priority to ensure human, animal and environmental health closely linked with animal-agri food systems. The irrational utilization of antimicrobials in healthcare, animal-derived food production, and animal husbandry forms an interconnected web that facilitates the transmission of drug resistance. Residues of antimicrobials, MDR pathogens and genes of drug resistance persist in animals, environment and byproducts, which are subsequently transferred to humans. Considering these challenges, exploring alternative and combined antimicrobial therapies emerges as a promising approach to mitigate drug resistance. The One Health Joint Plan of Action (2022-2026) promotes a paradigm shift of AMR control from isolated sector efforts to a coordinated One Health approach, integrating surveillance, stewardship, prevention, and environmental action. In summary, addressing AMR in animal-derived food items and its potential transmission to the general populace necessitates a coordinated strategy that encompasses regulatory interventions, genomic surveillance, data sharing, innovative research, and public awareness initiatives. Global AMR advocacy, governance, financing, regional collaboration and pragmatic framework implementation could control silent pandemic and attainment of UN-SDGs.

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