



GLOBAL SYSTEMATIC REVIEW OF ANTIMICROBIAL RESISTANCE (AMR): TAXONOMIC PATTERNS, CURRENT METHODOLOGIES, AND FUTURE DIRECTIONS FOR WILDLIFE AND LIVESTOCK SURVEILLANCE

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ABSTRACT

Antimicrobial Resistance (AMR) is the ability of microorganisms to survive exposure to drugs intended to eliminate them. Regarded as one of the global threats in the 21st century, AMR undermines the effectiveness of antimicrobial treatments while posing major risks to ecosystems, food security, and the global economy. Although AMR has been widely studied in animals, research remains heavily focused on livestock and a limited number of charismatic wildlife species, leaving many understudied taxa. Using a systematic search of the Scopus database, the prevalence, patterns, and transmission roles of AMR were examined across taxonomic groups of livestock and wildlife. The findings reveal that 62% of the AMR studies focus on livestock while wildlife research primarily focuses on mammals and birds, with fish, amphibians, reptiles, and invertebrates being comparatively understudied. This review also identifies key trends and critical knowledge gaps across all animal taxa. Although phenotypic methods remain the standardised approach for AST, emerging genotypic AST techniques show potential to elucidate the origins, diversity, and evolutionary history of AMR. Further research is needed to clarify AMR's impacts on biodiversity, improve surveillance of understudied groups, and prioritise wildlife–livestock interfaces.

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Introduction

Antimicrobials are substances that can kill or inhibit the growth of microorganisms. Although initially developed for treating infections, their use was subsequently expanded to disease

treatment, prevention, and as growth promoters in food animals, agriculture, and aquaculture (Serwecińska, 2020), leading to the emergence of Antimicrobial Resistance (AMR). AMR

refers to the ability of microorganisms, including bacteria, viruses, fungi, and parasites, to thrive despite exposure to antimicrobials designed to stop their growth or kill them (Akwongo *et al.*, 2025). AMR occurs when bacteria become less susceptible to the antimicrobial through overexpression or duplication of certain genes, chromosomal mutations, or the acquisition of resistance genes from other bacteria via Horizontal Gene Transfer (HGT) (Doyle *et al.*, 2025). Antibiotic resistance genes (ARGs) are the culprits and are currently recognised as emerging pollutants (Sanderson *et al.*, 2016).

ARGs are ancient and naturally occurring substances that were discovered in bacteria long before the clinical introduction of antibiotics (D'Costa *et al.*, 2011; Bhullar *et al.*, 2012; Larsen *et al.*, 2022). While AMR can naturally occur in bacteria as a defence mechanism against environmental antimicrobials, the indiscriminate use of antimicrobials is considered the main driver of AMR emergence (Holmes *et al.*, 2016). AMR emerged under selective pressure exerted by antimicrobial use outside of human medicine, specifically in veterinary medicine, food-animal production, and agriculture (Schwarz *et al.*, 2001; Economou & Gousia, 2015).

Metal contamination also contributes as a co-selective agent, driving the enrichment of both metal resistance genes and ARGs (Poole, 2017; Zhao *et al.*, 2019). Bacteria with metal-resistance genes are more likely to harbour ARGs than those without such genes (Peng *et al.*, 2021; Irfan *et al.*, 2022). Microplastics (MPs) contamination also contributes to AMR (Cholewińska *et al.*, 2025) by facilitating biofilm formation, which promotes HGT (Gross *et al.*, 2025; Liu *et al.*, 2025). Mixed pollutants, including disinfectants, metals, and antibiotics can also adhere to MPs, creating favourable conditions for co-selection (Balta *et al.*, 2025).

AMR is considered one of the greatest threats in the 21st century, hindering the efficacy of common antimicrobials and affecting global healthcare and economy (CDC, 2024). In Europe, an estimated 35,000 human deaths were attributed to AMR annually (ECDC, 2022).

Globally, AMR infections were attributed to and associated with 929,000 and 3.57 million deaths in 2019, respectively (Murray *et al.*, 2022). By 2050, AMR-associated infections are expected to cause 10 million deaths annually, surpassing cancer (O'Neill, 2016). From an economic aspect, AMR is estimated to cost 100 trillion USD globally by 2050 (Doyle *et al.*, 2025). In Europe, AMR results in additional healthcare expenditure of around €1.1 billion annually, driven by higher costs of last-resort antibiotics and prolonged disease duration or hospital stays (OECD, 2019).

The main routes of AMR dissemination to humans are through body contact, indirect contact transmission, and aerosols (Livermore, 2000), with the gut microbiome acting as a transporter of ARGs (Bengtsson-Palme *et al.*, 2015). Although AMR is considered one of the greatest threats to global health, most research has focused on clinical and agricultural settings (Davies & Davies, 2010). Over the past decade, the environment has gained recognition in AMR dynamics. Anthropogenic sites, including sewage systems, wastewater treatment plants, livestock farms, and agricultural land are critical areas for AMR transmission (Pruden *et al.*, 2012; McEachran *et al.*, 2015; Pal *et al.*, 2016). Furthermore, ARG transmission can occur between food animals and people through direct contact or in proximity. Wildlife living near humans, including companion animals, are known to harbour ARGs and may contribute to their spread (Bonnedahl *et al.*, 2009; Stedt *et al.*, 2015).

Despite advances in AMR research, significant knowledge gaps persist across wildlife and livestock. In livestock, while the profile of AMR has been well elucidated, the factors influencing its prevalence remain poorly understood (Graham *et al.*, 2019). In wildlife, despite increasing interest, AMR research lacks depth regarding transmission dynamics, drivers of acquisition, and the duration of AMR carriage and shedding in the environment (Doyle *et al.*, 2025). Wildlife, including mammals, birds, reptiles, fish, amphibians, and invertebrates

is a critical indicator of environmental AMR spread with zoonotic spillover risks (Vezeau & Kahn, 2024), yet studies predominantly focus on mammals and birds (Vittecoq et al., 2016; Doyle et al., 2025). Addressing AMR dynamics across all major taxonomic groups in livestock and wildlife is critical, as a detailed understanding of AMR and species-specific ecological factors would ensure comprehensive surveillance and effective mitigation strategies.

The AMR crisis transcends species boundaries; however, the interconnectedness of AMR transmission among wildlife, domesticated animals, and humans remains poorly understood. Existing studies often compartmentalise these domains, overlooking the complex exchange of AMR that occurs at shared animal interfaces. It is critical to consider all elements (Arnold et al., 2016), as policies for one sector can affect another (Rahman & Hollis, 2023). The One Health (OH) approach is essential as it involves interdisciplinary efforts to address AMR dynamics by acknowledging the interconnectedness among the health of humans, domestic animals, wildlife, and ecosystems (McEwen & Collignon, 2018;

Ahmad et al., 2023). Therefore, the primary aim of this study is as follows: (A) To review the key patterns and determinants of AMR across these animal groups following their taxonomy level; (B) elucidate the roles of these animal groups in the transmission of AMR; and (C) to assess current methodologies employed to monitor AMR in these animals.

Materials and Methods

Literature Search and Data Gathering

Bibliographic research was conducted to identify previous studies on antimicrobial resistance (AMR). Peer-reviewed articles were retrieved from the Scopus database using a set of relevant keywords. A list of 20 keywords (Table 1) was used for the initial search, followed by further filtering using “Antimicrobial Resistance” as the main keyword. Information such as the authors’ names, affiliations, publication years, and covered aspects was used to create infographics that visualised trends, identified research gaps, and highlighted areas for future study. The cut-off point for publication mining from Scopus was on 1st of July 2025.

Table 1: List of keywords used for publication mining

No.	Search Topics	No.	Search Topics
1	“Antimicrobial Resistance” + “Livestock”	11	“Antimicrobial Resistance” + “Freshwater”
2	“Antimicrobial Resistance” + “Agriculture”	12	“Antimicrobial Resistance” + “Aquatic”
3	“Antimicrobial Resistance” + “Aquaculture”	13	“Antimicrobial Resistance” + “Invertebrate”
4	“Antimicrobial Resistance” + “Wildlife”	14	“Antimicrobial Resistance” + “Insect”
5	“Antimicrobial Resistance” + “Ecology”	15	“Antimicrobial Resistance” + “Vertebrate”
6	“Antimicrobial Resistance” + “Biodiversity”	16	“Antimicrobial Resistance” + “Fish”
7	“Antimicrobial Resistance” + “Conservation”	17	“Antimicrobial Resistance” + “Amphibian”
8	“Antimicrobial Resistance” + “Fauna”	18	“Antimicrobial Resistance” + “Reptile”
9	“Antimicrobial Resistance” + “Terrestrial”	19	“Antimicrobial Resistance” + “Avian”
10	“Antimicrobial Resistance” + “Marine”	20	“Antimicrobial Resistance” + “Mammal”

Criteria Selection and Process

The criteria for study inclusion were refined to include articles focusing on the prevalence of AMR in animals (including research and reports but excluding review papers). The initial search returned 6,684 articles using 20 keywords. Only peer-reviewed research articles published in English were included. A few articles were also excluded if they were inaccessible or did not align with this review’s aim. Database search records were then imported for screening and de-duplication, during which full-text articles were retrieved and screened before a comprehensive Excel list of acceptable articles was developed. A complete Excel list was utilised to ease the extraction of information for each article. Data were extracted and categorised by animal

group, as shown in Table 2. All the gathered information was collated and summarised, the data were presented in tables or graphs.

Study Selection and Data Extraction

This review adhered to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines (Moher *et al.*, 2009). The PRISMA flow diagram was utilised to illustrate the review process, encompassing four key stages: Identification, screening, eligibility assessment, and final inclusion. A three-stage screening strategy was employed, beginning with a review of titles, keywords and abstracts, followed by an in-depth examination of full-text articles as shown in Figure 1.

Table 2: List of animal categorisation criteria

Category	Definition
Captive animal	Non-domesticated animals that are housed in managed or controlled environments such as zoological parks, sanctuaries, or research facilities.
Companion animal	Animals that are kept by humans primarily for companionship, recreation, or emotional support. This category includes traditional pets (e.g., canines, felines), exotic species (e.g., reptiles), and equines.
Food animal	Food products derived from animals (e.g., meat, poultry, fish) that are obtained from commercial sources like markets or supermarkets, where the origin of the animal is not specified in the study. This category is distinct from other classifications in this review, as it focuses on post-slaughter products rather than live animals and is used when the animal’s source (e.g., farm-raised or wild-caught) is not explicitly stated.
Livestock	Animals that are raised in agricultural settings for commercial purposes. This category encompasses poultry (e.g., broilers, layers), swine, ruminants (e.g., cattle, goats, sheep), and aquaculture systems (e.g., shrimp and fish farms) and includes studies conducted across various farming systems, including conventional and organic.
Pest	Animals that are a nuisance or detrimental to human health, agriculture, or the environment. Examples include rodents found in urban habitats and insects (e.g., flies) associated with agricultural operations.
Wildlife	Non-domesticated animals living in natural habitats. This category encompasses a broad range of species from diverse ecosystems and includes those that may be hunted for consumption as game meat.

Source: Adapted from Palmer (2012) and Brasileiro *et al.* (2023)

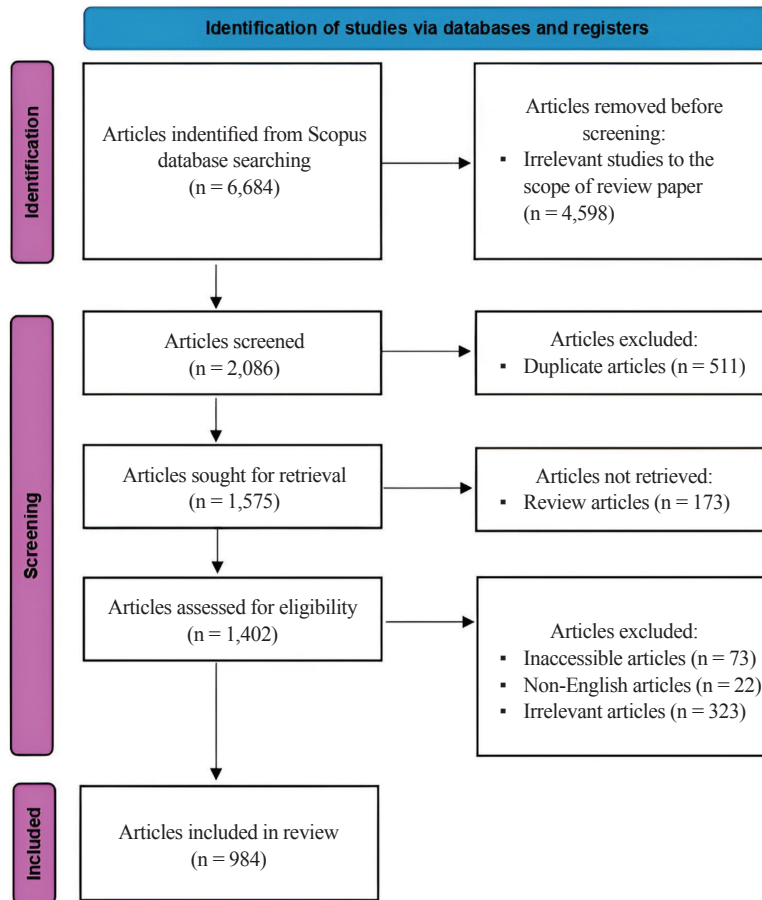


Figure 1: The PRISMA flow diagram illustrates the systematic process of study selection and data extraction

Results and Discussion

Overview of Extracted Articles

From the literature, using 20 search strings, a total of 6,684 related research articles were identified in the Scopus database (Table 3). Following the identification phase, 4,598 articles were excluded as irrelevant based on the study's inclusion criteria. In the screening phase, 2086 articles were assessed for relevance, with 511 articles removed due to duplication. This reduced the dataset to 1,575 articles; review articles were then excluded, leaving 1,402 articles for screening. After retrieval, 73 inaccessible articles, 22 non-English articles, and 323 irrelevant articles were excluded, leaving 984 suitable for inclusion in the review.

The selected peer-reviewed articles were then classified by country, year, animal category, taxonomic group, and methodology used in AMR studies. From publications across six animal groups, we further categorised livestock and wildlife into taxonomic groups; only these two groups will be discussed in the subsequent subtopics, in line with the original objectives.

A global rise in publications on AMR surveillance in animals is observed from 1995 to 2024 (Figure 2). This indicates a growing scientific interest in this topic over the past decades. From 2014 to 2015, a rapid increase in

Table 3: List of search strings used and number of research articles in each bibliographic search

No.	Keywords	Number of Publications (Scopus)	
		Total of Research Articles Available	Total of Extracted Papers
1	“Antimicrobial Resistance” + “Livestock”	1,048	422
2	“Antimicrobial Resistance” + “Agriculture”	731	147
3	“Antimicrobial Resistance” + “Aquaculture”	609	185
4	“Antimicrobial Resistance” + “Wildlife”	233	179
5	“Antimicrobial Resistance” + “Ecology”	232	27
6	“Antimicrobial Resistance” + “Biodiversity”	198	28
7	“Antimicrobial Resistance” + “Conservation”	139	26
8	“Antimicrobial Resistance” + “Fauna”	8	1
9	“Antimicrobial Resistance” + “Terrestrial”	19	4
10	“Antimicrobial Resistance” + “Marine”	422	87
11	“Antimicrobial Resistance” + “Freshwater”	118	88
12	“Antimicrobial Resistance” + “Aquatic”	555	92
13	“Antimicrobial Resistance” + “Invertebrate”	99	23
14	“Antimicrobial Resistance” + “Insect”	325	15
15	“Antimicrobial Resistance” + “Vertebrate”	38	2
16	“Antimicrobial Resistance” + “Fish”	696	262
17	“Antimicrobial Resistance” + “Amphibian”	127	0
18	“Antimicrobial Resistance” + “Reptile	45	22
19	“Antimicrobial Resistance” + “Avian”	163	48
20	“Antimicrobial Resistance” + “Mammal”	879	185

publication frequency was observed, concurrent with the publication of the “Global Action Plan on Antimicrobial Resistance” guidelines by the World Health Organisation (WHO) in 2015. However, despite the rising trend of AMR studies in animals over the past decade, these studies have been conducted in only 93 of 195 countries worldwide, with most concentrated in several countries, with China leading, followed by the United States (Figure 3).

Publications on AMR research in animals exhibit a clear bias toward livestock (Figure 4), as livestock are often perceived as the primary reservoirs for AMR due to the extensive use of

antibiotics (Economou & Gousia, 2015). Wildlife has previously been reported as a neglected group in AMR studies (Vittecoq *et al.*, 2016). An increasing interest in this group since 2019 is evident (Figure 5). However, the remaining animal categories, food animals, companion animals, captive animals, and pests, remained stagnant. While being underrepresented and stagnant in research, food animals, companion animals (Saengsitthisak *et al.*, 2020; Marques *et al.*, 2021; Unger *et al.*, 2022; Sebola *et al.*, 2023), captive animals (Ahmed *et al.*, 2007; Wang *et al.*, 2013; Kim *et al.*, 2024), and pests (Ge *et al.*, 2019; Kakooza *et al.*, 2025) harbour AMR of medical importance.

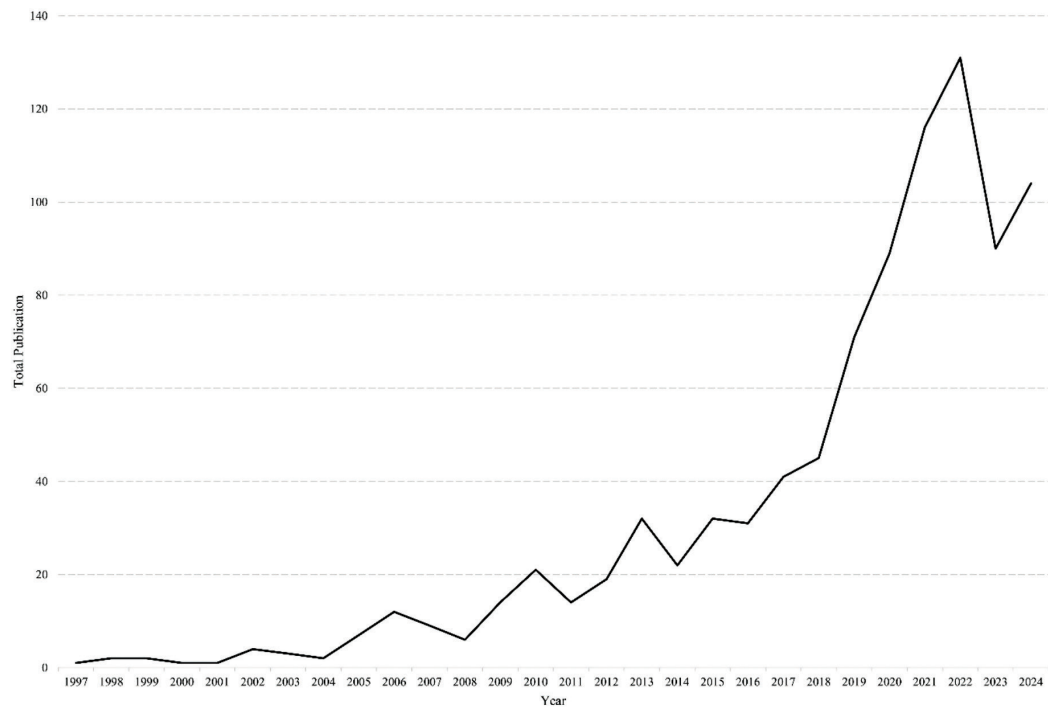


Figure 2: Trends in publication of AMR research in animals from 1997 to 2024

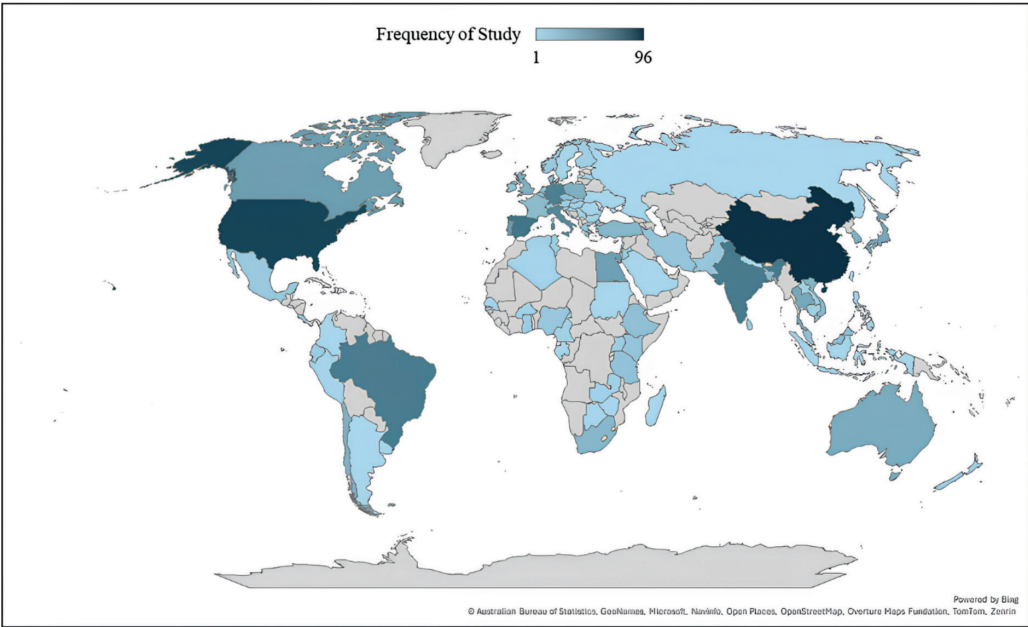


Figure 3: Geographic distribution of published research on AMR in animals

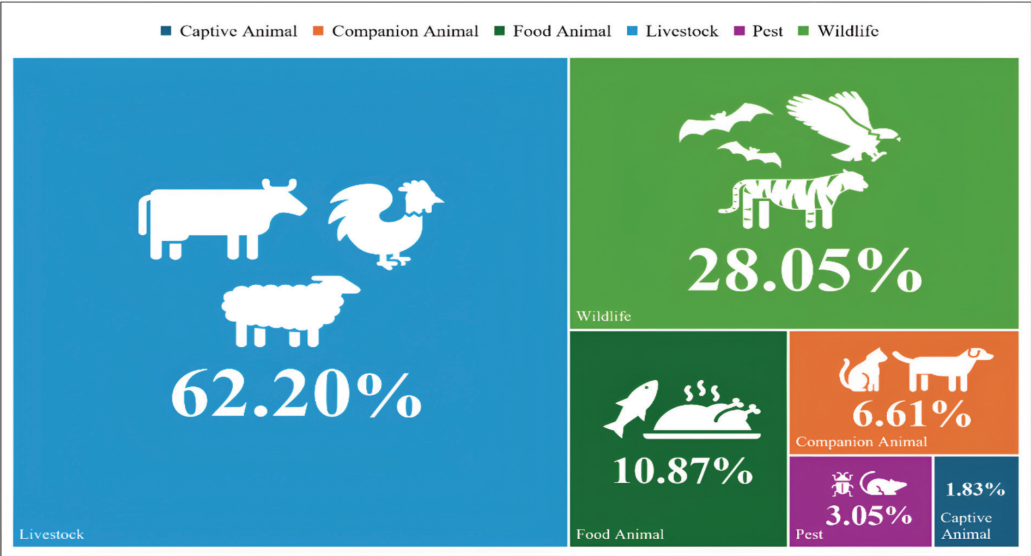


Figure 4: Distribution of AMR research publications by animal categories

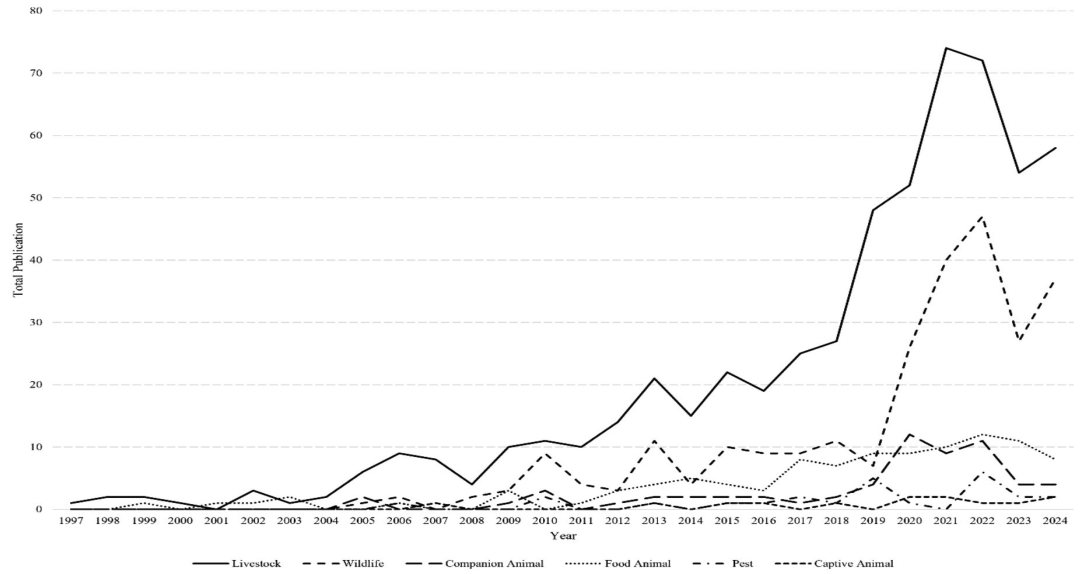


Figure 5: Publication trends in AMR research by animal categories from 1997 to 2024

In both livestock and wildlife, the largest animal groups studied for AMR are mammals, birds, and fish (Figure 6). Within livestock, research has primarily focused on mammalian species such as swine, cattle, and sheep, rather than on poultry. This is unsurprising, as the global biomass of livestock is dominated by pigs

and cattle, which exceeds domesticated poultry, primarily chickens (Bar-On *et al.*, 2018). Fish production should be prioritised, as aquaculture is one of the fastest-growing food sectors globally (Garlock *et al.*, 2020), with current practices heavily dependent on antimicrobials (Liu *et al.*, 2017).

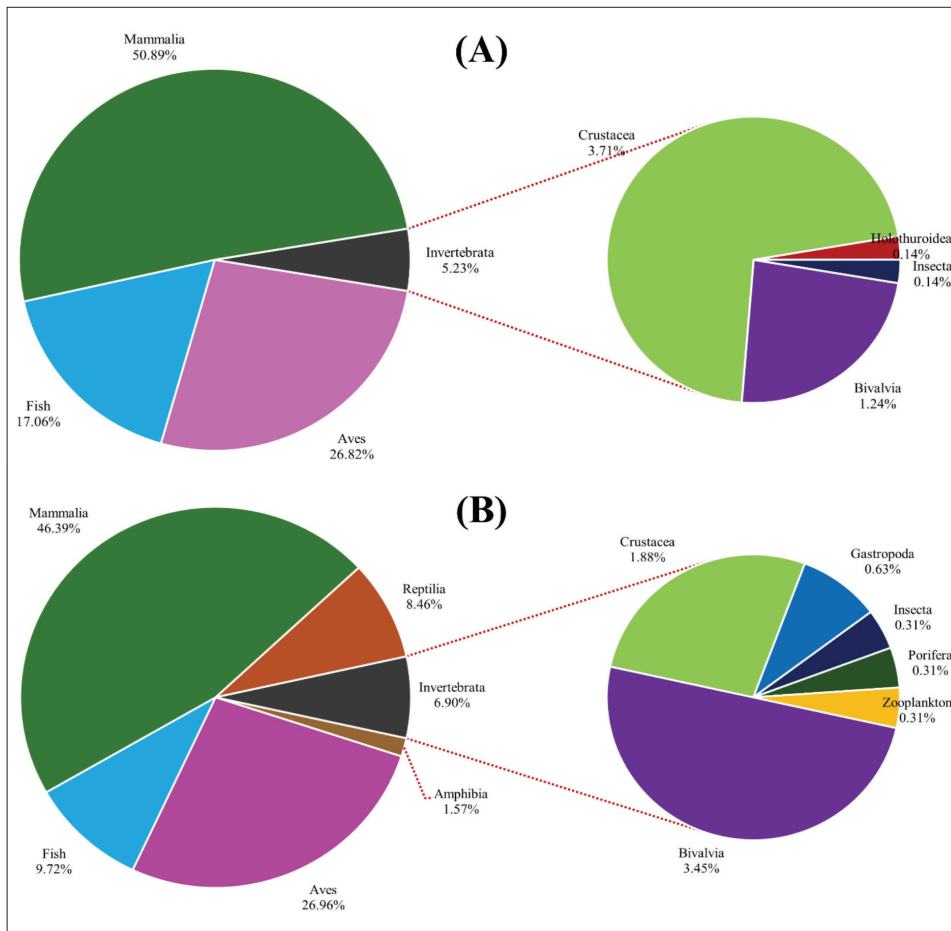


Figure 6: Taxonomic distribution of published research on AMR in (A) livestock and (B) wildlife

In wildlife AMR, studies have been conducted on major mammalian groups, including rodents (Furness *et al.*, 2017), bats (McDougall *et al.*, 2019), shrews (Furness *et al.*, 2017), primates (Tanga *et al.*, 2024), even-toed ungulates (Darwich *et al.*, 2021; Mbehang Nguema *et al.*, 2021), odd-toed ungulates (Rojas-Jiménez *et al.*, 2019), carnivores (Osińska *et al.*, 2020), lagomorphs (Silva *et al.*, 2010), marine mammals (Prichula *et al.*, 2016), and marsupials (McDougall *et al.*, 2023). Studies have been conducted in urban (Darwich *et al.*, 2021), semi-wild (Mushahidur Rahman *et al.*, 2025), and wild populations (Mbehang Nguema *et al.*, 2021). Wild fish and reptiles remain comparatively understudied, with both

groups representing less than 10% of research. Increased attention toward these groups is crucial, as wild fish are consumed as food animals (Díaz-Formoso *et al.*, 2023) and reptiles are increasingly kept as pets (Zajac *et al.*, 2021). Amphibians are the most understudied group despite being highly sensitive to environmental changes and represent the most threatened vertebrate taxon (IUCN, 2026).

In both wildlife and livestock, invertebrate studies primarily focus on taxa relevant to direct food production. Among wildlife, bivalves are the most studied group while in livestock, research focuses on crustaceans, largely driven by studies on the shrimp aquaculture industry, which represents one of the most heavily traded

aquaculture commodities worldwide (Miao & Wang, 2020). Insects are neglected despite the rapid growth of edible insect farming (Han *et al.*, 2017) and their long-standing role as a food source in several regions and cultures (Raheem *et al.*, 2019).

Overall, AMR surveillance studies on animals, including both livestock and wildlife, mainly focus on zoonoses and public health risks. As AMR in livestock and wildlife is mainly attributed to the indiscriminate use of antimicrobials (Holmes *et al.*, 2016), it is expected that AMR will have profound ecological and biodiversity impacts. Previously, the presence of antibiotics in the environment may reduce microbial diversity and alter the microbial community structure (Grenni *et al.*, 2018). Consequently, loss of microbial diversity could facilitate the spread of AMR in the environment (Chen *et al.*, 2019). While the impacts of antimicrobial use on ecosystems are being better elucidated, the causal link between AMR and wildlife and biodiversity loss remains poorly understood (Mitchell, 2023; UNEP, 2023).

Patterns and Determinants of AMR in Animal Populations

AMR in Livestock

The livestock sector is the major user of antimicrobials for growth stimulants, prophylaxis and disease treatment, animal health maintenance, and productivity improvement (Musa *et al.*, 2021; Amancha *et al.*, 2023; Dančová *et al.*, 2024; Kerek *et al.*, 2024).

AMR in Swine

The swine industry accounts for the highest global antimicrobial use (AMU) among livestock, surpassing both cattle and poultry (Van Boeckel *et al.*, 2015). Accordingly, swine-derived isolates often exhibit higher levels of AMR, including a greater prevalence of MDR and ARGs, than those from other livestock (Lettini *et al.*, 2016; AbuOun *et al.*, 2021; Fu *et al.*, 2024; Kiula & Makene, 2025). Although

AMU is strongly associated with AMR in swine, MDR remains elevated in swine-derived isolates, even in settings with lower AMU than in other livestock sectors (AbuOun *et al.*, 2021). Environmental drivers, including antibiotics, heavy metals and nutrients, likely act together to support the long-term persistence of ARGs in swine production systems (Tu *et al.*, 2023). However, lower AMR and MDR prevalence have been reported in swine-associated isolates compared to those from cattle (Chung *et al.*, 2025) and poultry (Mtemisika *et al.*, 2022; Chea *et al.*, 2025).

Most AMR comparative studies have not included direct comparisons of AMU across livestock species. Surveillance methodologies also differ in terms of sample sources and number, the bacterial species of interest, and the antimicrobial susceptibility testing (AST) approaches, which can bias prevalence estimates. The contrasts in AMR prevalence across different species may reflect not only true differences in AMU but also differences in surveillance coverage and reporting standards.

The choice of surveillance sample type also affects the observed AMR profiles. Higher levels of antibiotic resistant bacteria (ARB) and ARGs have been reported in environmental samples, including slaughterhouse effluents, farm dust, and air, compared to faecal samples (Gao *et al.*, 2023; Niharika *et al.*, 2024). Swine nasal samples also show a higher prevalence of AMR than faecal or feed samples (Narvaez-Bravo *et al.*, 2016) while airborne dust often contains the highest AMR levels compared with swine carcasses and end products (Hein *et al.*, 2024). Farm dust acts as a major ARG reservoir, largely originating from faeces and other sources such as skin, mucus, feed, and the environment via aerosolisation (Luiken *et al.*, 2022). Given the frequent zoonotic transmission of AMR from swine to farmers (Oppliger *et al.*, 2012), incorporating diverse sample types is essential for AMR surveillance as it not only yields distinct AMR patterns but also reflects different transmission risks.

AMR prevalence in swine also varies geographically. In China, MDR levels in swine-associated isolates can exceed 99% (Li *et al.*, 2025), whereas isolates from New Zealand remain largely susceptible to key antimicrobials (Harrow *et al.*, 2004; Rivas *et al.*, 2020). AMR in livestock was also more prevalent in China than in European and other Asian countries (Liu *et al.*, 2013). High AMR levels in China can be attributed to its position as the largest consumer of antimicrobials in livestock production globally (Van Boeckel *et al.*, 2015), driven by rising demand for animal protein and the expansion of intensive farming systems.

Swine production systems further influence AMR patterns. Intensive farming is associated with higher ARG abundance and increased AMR prevalence compared to extensive systems (Pirolo *et al.*, 2019; Mencía-Ares *et al.*, 2020). Swine from large-scale farms and slaughterhouses also exhibit higher AMR levels than those from small-scale and free-range farms (Yan *et al.*, 2014). Organic and low-AMU farming systems are often proposed to reduce AMR. While some reported lower ARGs and AMR prevalence in organic farms (Keelara *et al.*, 2013; Bassitta *et al.*, 2022), others find no differences in overall ARG classes between production systems (Lee *et al.*, 2025). This indicates that reducing AMU alone may not immediately decrease AMR. Other factors, including environmental stress, seasonality, biosecurity, and farm management practices also contribute to AMR dynamics in swine farming (Moro *et al.*, 1998; Farzan *et al.*, 2010; Luiken *et al.*, 2022).

AMR in Ruminant

AMR in ruminants is largely attributed to AMU. Antibiotics are commonly administered to livestock; however, this contributes to long-term risks to food security (Kaur *et al.*, 2024). Antibiotics, including tetracycline, ampicillin, and sulfonamides are often applied at sub-therapeutic levels in ruminant production systems, creating selective pressure that favours the survival and proliferation of ARB (Manyi-Loh *et al.*, 2018). This is further exacerbated by

the persistence of antibiotic residues in animal products even after treatment has stopped. These residues enter the food chain, acting as a reservoir for resistance that can be transmitted to humans (Ghimpețeanu *et al.*, 2022; Aminzare *et al.*, 2024; Bacanlı, 2024).

In ruminants, the prevalence of AMR is more widespread than previously thought (Xu *et al.*, 2022). Key bacteria include *E. coli*, *Salmonella* spp., and *Campylobacter* spp., which serve as major carriers of ARGs (Zhao *et al.*, 2001; Zare *et al.*, 2014; Barlow *et al.*, 2015; Lee *et al.*, 2023; Veloo *et al.*, 2025). These bacteria frequently exhibit MDR, thus, limiting treatment options for animals and humans (Haulisah *et al.*, 2021; Nazir *et al.*, 2025). Recently, isolates from cattle have developed resistance to clinically important antibiotics (García-Díez *et al.*, 2024; Barrientos-Villegas *et al.*, 2025; Oh *et al.*, 2025). This not only affects the animal's health but also poses a significant public health threat through zoonotic transmission risks from direct animal contact, consumption of contaminated animal products, or environmental contamination (Ma *et al.*, 2021). Inadequate waste management on farms facilitates the spread of ARB into groundwater, rivers, and surrounding ecosystems (Endale *et al.*, 2023).

Heavy metals also contribute to the development of AMR in ruminants. Resistance to heavy metals often co-occurs with AMR through co-selection mechanisms (Engin *et al.*, 2023). High concentrations of copper, zinc, and mercury in feed additives, fertilisers, and irrigation systems create an environment that promotes the persistence and spread of resistant strains (Yazdankhah *et al.*, 2018; Samreen *et al.*, 2021). This highlights that AMR in ruminants is driven not only by AMU, but also by the complex interplay between antibiotics, metals, and environmental contaminants.

AMR in Poultry

Poultry farming is one of the fastest-growing livestock industries worldwide and an important source of affordable protein. However, the intensive use of antimicrobials has made poultry

farming a contributor to the global AMR crisis. Large-scale production systems and routine AMU are common in low- and middle-income countries with limited veterinary oversight and regulatory control (Hedman *et al.*, 2020; Hosain *et al.*, 2021). High levels of resistance have been reported from poultry-associated isolates, including *Salmonella*, *E. coli*, *Campylobacter*, and *Enterococcus*.

Across Africa and Asia regions, MDR isolates are widespread, with frequent resistance to fluoroquinolones, tetracyclines, sulfonamides, and β -lactams (Panyako *et al.*, 2022). Avian pathogenic *E. coli* (APEC) often carries multiple ARGs, while isolates from poultry farms show resistance rates exceeding 70% to common antimicrobials. Despite this, research has focused more on mammalian livestock, even though AMU in poultry ranks just below swine globally (Van Boeckel *et al.*, 2015). This is concerning, given the rapid growth of poultry production and the heavy reliance on antimicrobials. The consequences extend beyond farms, as ARB and antimicrobial residues can spread through contaminated meat, eggs, manure, and farm dust, posing risks to human health and the wider environment (Hedman *et al.*, 2020; Hosain *et al.*, 2021).

AMR in Aquaculture

Aquaculture has increasingly been recognised as a significant reservoir of AMR. Multiple regional studies reported a high prevalence of ARB populations in farmed fish, shrimp, and prawns, as well as in their surrounding environments. ARBs have been isolated from aquaculture ponds, sediments, and aquatic animals (Shakerian *et al.*, 2018; Narayanan *et al.*, 2020; Yang *et al.*, 2021; Patel *et al.*, 2023; Ubeyratne *et al.*, 2023; Devadas *et al.*, 2025). These isolates exhibit MDR, especially to tetracyclines, sulfonamides, β -lactams, quinolones, and aminoglycosides (Lim *et al.*, 2013; Liu *et al.*, 2017; Nadella *et al.*, 2021). Intensive use of antibiotics in aquaculture creates strong selective pressure, promoting the persistence of ARB populations (Liu *et al.*, 2017; Zhou *et al.*, 2023).

Aquaculture environments also harbour diverse ARGs and MGE, which promote HGT (He *et al.*, 2015; 2019; Lin *et al.*, 2016). Isolates carrying MGEs have been found in shrimp ponds in China (He *et al.*, 2015; 2019) while the highly resistant carbapenemase-encoding gene *bla*_{NDM-5} has been detected in fish isolates (Dwivedi *et al.*, 2023). Environmental factors also contribute to the spread of AMR. Heavy metals, including copper and zinc in pond sediments can co-select ARGs even in the absence of antimicrobials (Ajewole *et al.*, 2021). Faecal contamination in aquaculture ponds also contributes to elevated ARG levels, highlighting the impact of anthropogenic activities on AMR (Thongsamer *et al.*, 2021).

Regional evidence shows patterns of AMR emergence and dissemination in the aquaculture industry. In China, bacterial resistance is strongly linked to intensive farming and MGE (He *et al.*, 2015; 2019; Liu *et al.*, 2017; Narayanan *et al.*, 2020). Similar trends are observed in India and Sri Lanka, where MDR bacteria have been isolated from tilapia, shrimp, and poultry-linked aquaculture, suggesting that cross-sectoral AMU contributes to AMR spread (Ubeyratne *et al.*, 2023; Zhou *et al.*, 2023; Nadella *et al.*, 2025). In Southeast Asia, resistant zoonotic ARB were identified in Malaysian shrimp farms (Devadas *et al.*, 2025) while faecal pollution was linked to increased AMR prevalence in Thailand (Thongsamer *et al.*, 2021). Metagenomic studies in Bangladesh further reveal extensive ARG diversity in fishponds (Bell *et al.*, 2023). Similar patterns are reported outside Asia. In Nigeria, isolates from aquaculture systems carried both antibiotic- and heavy-metal-resistance genes (Ajewole *et al.*, 2021). In South America, resistant *Streptococcus* has caused disease outbreaks in catfish farms (Tavares *et al.*, 2018).

Aquatic invertebrates such as bivalves and farmed shrimp/prawns are also important reservoirs of ARGs. Multiple ARB have been identified in both farmed and retail produce (Fukuda *et al.*, 2023). Bivalves accumulate bacteria through filter feeding (Strehse & Maser, 2020) while AMR levels in shrimp

ponds often increase throughout the production cycle, following antibiotic treatments (Natrah *et al.*, 2025). These pose a critical food safety risk as bivalves are frequently consumed raw or undercooked while farm workers face occupational risks.

Effluents from farm aquaculture can also disseminate ARGs into coastal ecosystems (Ngajilo & Jeebhay, 2019). The detection of ARGs in shrimp and bivalves, including cases linked to seafood trade, highlights the potential for global AMR spread via food supply chains (Elbehiry *et al.*, 2025).

AMR in Wildlife

In wildlife, particularly among vertebrates, AMR research has predominantly focused on mammals, followed by birds, fish, reptiles, and amphibians. This likely reflects the recognised role of vertebrates as hosts or reservoirs of zoonotic diseases, where approximately 60% of the known infectious diseases affecting humans are of animal origin (Shaheen, 2022). Within the context of AMR, wildlife is widely regarded as a sentinel group, with members of the *Enterobacteriaceae* family frequently detected across wildlife species (Dolejska, 2020).

AMR in Wild Mammal

Mammals are of particular concern as AMR hosts because of their frequent ecological overlap with humans. Mammals can forage in environments contaminated with livestock waste, sewage, aquaculture runoff, or landfill waste. For example, *Macaca fascicularis* has become highly adapted to human environments, often scavenging near waste disposal sites (Entezami *et al.*, 2024), increasing its zoonotic risk. Rodents and bats are also critical surveillance targets due to their abundance, close association with humans, and roles as agricultural pests (Ravindran *et al.*, 2022). Evidence of zoonotic pathogens in macaques and bats further highlights their importance (Ain-Najwa *et al.*, 2020). Although wildlife is not directly exposed to antimicrobials, their commensal microbiota can act as reservoirs of

ARGs, which may be transferred horizontally to pathogens. Therefore, wildlife can harbour AMR bacteria or acquire ARGs from anthropogenic activities.

Mammalian AMR studies are dominated by carnivores, followed by ungulates, primates, and rodents. Carnivores and ungulates are of particular concern due to their role as reservoirs of zoonotic diseases. Carnivores are exposed to a diverse range of prey and environments, increasing their likelihood of harbouring and transmitting pathogens. As apex predators, they accumulate infectious agents from prey, and repeated exposure through hunting and feeding can facilitate co-infection and the emergence of novel genetic variants through recombination (Leendertz *et al.*, 2008). Carnivores are recognised hosts for several zoonotic diseases, including canine distemper, toxoplasmosis, rabies, and echinococcosis (Malmberg *et al.*, 2021; Macpherson *et al.*, 2022; Pal & Tolawak, 2023).

In contrast, ungulates often act as asymptomatic carriers of bacteria such as *E. coli*, *Salmonella*, and *Campylobacter*, which can persist in their gastrointestinal tracts without clinical disease (Navarro-Gonzalez *et al.*, 2016). Despite the absence of clinical signs, these animals continue to interact with other animals and humans while silently shedding pathogens through faeces or secretions. This leads to contamination of soil, water, feed, and animal products, facilitating transmission to livestock and humans (Pal *et al.*, 2016). This silent carriage promotes bacterial adaptation and gene diversification under environmental pressures, contributing to the development of AMR.

AMR in Wild Bird

Birds inhabit a wide range of habitats, including wetlands, agricultural and urban areas, and forests, making them valuable for monitoring AMR across diverse ecosystems. The presence of ARB has been reported in multiple bird species, including barnacle geese (*Branta leucopsis*) (Hatha *et al.*, 2013), gulls (Bonnedahl & Järhult, 2014), brant geese (*Branta bernicla*),

glaucous gulls (*Larus hyperboreus*) (Sjölund *et al.*, 2008), and western sandpipers (*Calidris mauri*). The high number of avian AMR studies is also driven by methodological advantages. Birds can be sampled relatively easily and non-invasively through faecal and cloacal sampling. Fresh faeces can be collected directly from habitats such as pastures, nesting sites, or roosting areas.

Most avian AMR studies have focused on scavengers and migratory species. Scavengers, like terrestrial predators consume diverse prey and therefore serve as important hosts for a wide range of pathogens. Migratory birds are of particular concern as important AMR vectors, as they can disseminate resistant bacteria across continents through long-distance movements (Zhao *et al.*, 2020). A study on Arctic terns (*Sterna paradisaea*) revealed increased bacterial resistance after migration (Akhil Prakash *et al.*, 2022). These birds acquire ARB from the local environment and spread them into new regions primarily via faecal excretion. They may also ingest ARB through food sources, including insects, fish, or waste contaminated with ARGs genes (Dolejska, 2020).

AMR in Wild Reptile

Reptiles are recognised reservoirs of diverse pathogens, several of which pose public health concerns (Mendoza-Roldan *et al.*, 2020). Their growing role in the pet trade and aquaculture increases the risk of human exposure, making them relevant in AMR research. Pet reptiles can transmit parasites and bacteria through direct contact or faecal contamination. Notably, reptiles are asymptomatic carriers of *Salmonella*, which they shed in faeces, often exhibits MDR. Prevalence varies across taxa, with higher rates reported in snakes (56.0%), followed by lizards (36.9%), tortoises (34.2%), turtles (18.6%), and crocodilians (9%) in descending order (Pees *et al.*, 2023). Several pet species, including chameleons (Willis *et al.*, 2002), geckos, anoles, snakes (Whitten *et al.*, 2015; Krishnasamy *et al.*, 2018), and iguanas (Cellucci *et al.*, 2010) have been linked to human infection.

Invasive and exotic reptile species further contribute to AMR dissemination by facilitating spillover into native ecosystems. The invasive California kingsnake (*Lampropeltis californiae*) was identified as a reservoir of zoonotic *Salmonella*, capable of spreading multiple ARB into the environment, posing a public health concern (Santana-Hernández *et al.*, 2023). Beyond pets and invasive species populations, reptiles have long been consumed as a protein source in tropical countries and are regarded as delicacies in parts of Europe and North America (Janssen, 2021). The risk of infection from reptile-derived foodborne pathogens depends heavily on handling and cooking practices, where cross-contamination throughout the food production and distribution chain further increases these risks. In Asia, reptiles are also used in traditional practices such as applying snake meat to wounds, which can facilitate the transmission of pathogens (Edila *et al.*, 2024). The presence of ARB in reptile products poses an additional risk, especially in regions with poor food safety controls and weak veterinary drug regulations.

AMR in Wild Amphibian

Currently, knowledge of AMR in amphibians remains limited, restricting our understanding of AMR drivers and dissemination risks in this group. In Brazil, bacteria resistant to widely used clinical and veterinary antibiotics have been isolated from the critically endangered *Melanophryniscus admirabilis* (Admirable Redbelly Toad) (Ienes-Lima *et al.*, 2023). The presence of these ARB indicates possible anthropogenic contamination in the toad's habitat.

Additionally, antibiotic- and heavy-metal-resistant isolates have been reported in amphibians (Hacioglu & Tosunoglu, 2014; La Tela *et al.*, 2021). These raise concerns that amphibians may act as reservoirs of AMR, transferring their antibiotic- and heavy-metal-resistance genes into aquatic environments. While studies on other animal groups have shown the intrinsic occurrence of AMR in

wildlife, no study has yet been conducted in amphibians to determine the true origin of AMR. Existing studies relied primarily on phenotypic assessments and lacked genotypic analyses, which are crucial to determine the evolutionary origins and dissemination pathways of AMR.

AMR in Wild Fish

Fish are among the most traded food commodities globally and a major source of nutrients. Global fish consumption has increased steadily, with an average annual growth of 5.9% (Díaz-Formoso *et al.*, 2023). Despite this, bacteria with resistance to clinically important antibiotics were isolated from wild fish intended for human consumption, suggesting their role as AMR vectors (Díaz-Formoso *et al.*, 2023). Wild fish are also reservoirs of ARB, harbouring plasmids (Miranda *et al.*, 2024), and clinically important ARGs (Håkonsholm *et al.*, 2020). Notably, fish from well-preserved ecosystems harbour ARGs commonly associated with HGE and MDR (Boyras *et al.*, 2025).

Anthropogenic activities contribute significantly to the dissemination of AMR in marine environments. Bacterial isolates from fish in areas under anthropogenic pressure exhibited higher levels of AMR compared to those from regions with less direct human impact (Brauge *et al.*, 2024). Fish exposed to antibiotic-influenced environments also showed elevated ARG expression (Sibel Doğan & Şükrü Önal, 2023). Additionally, turbidity and inorganic suspended matter also affect the prevalence of ARB (Brauge *et al.*, 2024). Ecological habits of fishes were previously thought to influence AMR prevalence, with demersal fishes expected to harbour higher levels of AMR due to greater contact with contaminated sediment than pelagic fishes (Miranda *et al.*, 2024). However, minimal differences in AMR profiles between pelagic and demersal fish have been reported, likely due to widespread exposure to untreated urban effluents in aquatic environments (Miranda *et al.*, 2024).

Wild fish may play a critical role in the global dissemination of AMR through the international seafood trade. In Jordan, 86% of *Vibrio* isolates from several imported fish species were MDR (Obaidat *et al.*, 2017), highlighting the potential for transboundary spread of resistant pathogens through the food supply chain. However, despite the presence of AMR in wild fish, their suitability as bioindicators of AMR pollution remains debated (Tskhay *et al.*, 2025). Wild fish may not be effective sentinels for assessing AMR in freshwater ecosystems, as their resistomes are less responsive to colonisation from environmental AMR (Tskhay *et al.*, 2025). Since fish microbiomes appear less susceptible to colonisation by external AMR, reliance on fish alone may underestimate the true extent of AMR contamination in aquatic ecosystems.

AMR in Wild Invertebrates

As important food sources, bivalves and crustaceans are the focal taxa in AMR studies of invertebrates. Bacterial isolates from this group have shown resistance to clinically important antimicrobials (Harakeh *et al.*, 2006; van Hamelsveld *et al.*, 2023). In wild oysters and clams, AMR is associated with heavy metal tolerance (Jo *et al.*, 2020). Isolates from freshwater mussels in areas with high anthropogenic pressure also exhibit higher resistance to antibiotics, compared to those originating from areas with lower anthropogenic pressure (Saavedra *et al.*, 2022; Martins *et al.*, 2024). This indicates that AMR in wild bivalves is attributable to anthropogenic pollution.

In crustaceans, exposure to antimicrobials is associated with elevated resistance in *Vibrio* isolates (DeLorenzo *et al.*, 2016). However, the presence of AMR in wild shrimp is not solely attributable to AMU. High prevalence of ARB was isolated from wild shrimp, likely due to combined exposure to sewage discharge, agricultural runoff, and additional environmental pressures such as climate change and plastic pollution (Tate *et al.*, 2022). AMR has also been

observed in other invertebrates, including crabs and zooplankton. Anthropogenic pressure, along with water temperature, pH, dissolved oxygen, and turbidity, correlated with the abundance of ARGs in both zooplankton and phytoplankton (Bourdonnais *et al.*, 2024). Freshwater sponges are also found to facilitate HGT of AMR (Cartwright *et al.*, 2020).

Driver and Transmission Pathway of AMR and ARG across Animal Groups

This review shows that the drivers and transmission pathways of AMR and ARGs vary across animal groups (Table 4). In livestock, key pathways include animal crowding (Manson *et al.*, 2019), zoonotic transmission to humans, environmental contamination (Tan *et al.*, 2023; Pandey *et al.*, 2024), and dissemination through

the food chain (Cheng *et al.*, 2019; Tan *et al.*, 2023).

The evolution of MDR bacteria may result from the exposure of environmental matrices, including soil and water to antimicrobials (Pokharel *et al.*, 2020). Agriculture is among the major anthropogenic drivers of environmental AMR (Rothrock *et al.*, 2016). AMR transmission within the food chain is multidirectional, involving transfer between food animals, the environment, and humans via consumption or direct contact (Cheng *et al.*, 2019).

Although wildlife was previously considered a recipient of AMR, it is now recognised as a reservoir and vector (Manson *et al.*, 2019). The presence of ARB in wildlife without prior exposure to antimicrobials indicates widespread ecosystem contamination

Table 4: Drivers and transmission pathways of AMR and ARGs across animal groups

Animal Category	Animal Group	Key AMR Drivers	AMR Dissemination
Livestock	Swine	Production practices; antimicrobial usage (AMU); farm management practices; environmental conditions	Airborne farm dust; manure; farm wastewater
	Ruminants	AMU; heavy metal contamination; production practices	Manure
	Poultry	AMU; production practices	Manure; farm environment/runoff
	Aquaculture	AMU, faecal contamination; heavy metal contamination; farm management practices	Wastewater/effluent
Wildlife	Mammals	Intrinsic AMR occurrence; close contact or shared resources with livestock; feeding behaviour	Game meat consumption; pet ownership/handling
	Avian	Anthropogenic pollution; shared environment with livestock	Pet ownership/handling
	Reptile	Anthropogenic pollution	Pet ownership/handling; trade; consumption
	Amphibians	Limited data	Limited data
	Fish	Shared environment with aquaculture; wastewater contamination; anthropogenic pollution	Consumption as food
	Invertebrates	AMU, anthropogenic and environmental pollution; metal pollution	Consumption as food

(Konputtar *et al.*, 2023). Shared ARGs between wildlife and livestock indicate possible interspecies AMR transmission; however, the higher ARG diversity observed in wildlife compared to livestock suggests multiple or unidentified sources of AMR (Konputtar *et al.*, 2023). Similarly, free-living wild birds have been reported to harbour clinically relevant ARGs, albeit at lower prevalence than in livestock (da Silva *et al.*, 2024). While proximity to livestock likely facilitates AMR acquisition in wildlife (Sulzner *et al.*, 2014), the transmission pathways are not always clear. While evidence suggests wildlife could introduce AMR to livestock, the lack of similarity in molecular subtypes and AMR patterns between the two groups suggests that interspecies transmission was uncommon (Viswanathan *et al.*, 2017).

Methodological Approaches of AMR Surveillance in Livestock and Wildlife

This review identified that phenotypic-based methods are the most widely used approach for AMR surveillance, followed by genotypic

methods and mass spectrometry (Figure 7). Traditionally, AMR surveillance has relied on AST, which employs phenotypic, culture-dependent techniques to assess AMR profiles. However, genotypic approaches are increasingly applied, as AMR is fundamentally encoded by ARGs, which can be detected and characterised using Polymerase Chain Reaction (PCR) and gene sequencing technologies (Gajic *et al.*, 2022).

The advantages and limitations of common AMR surveillance methods are summarised in Table 5. Phenotypic methods are restricted to cultivable microbes (Gajic *et al.*, 2022) and together with mass spectrometry, cannot fully elucidate the mechanisms of AMR emergence, dissemination, and acquisition in complex livestock and wildlife microbial communities (Rojas-Jiménez *et al.*, 2019; Gonzalez *et al.*, 2022).

Genotypic methods, especially Whole-genome Sequencing-based AST (WGS-AST) overcome this limitation by enabling analysis of both cultivable and uncultivable bacteria

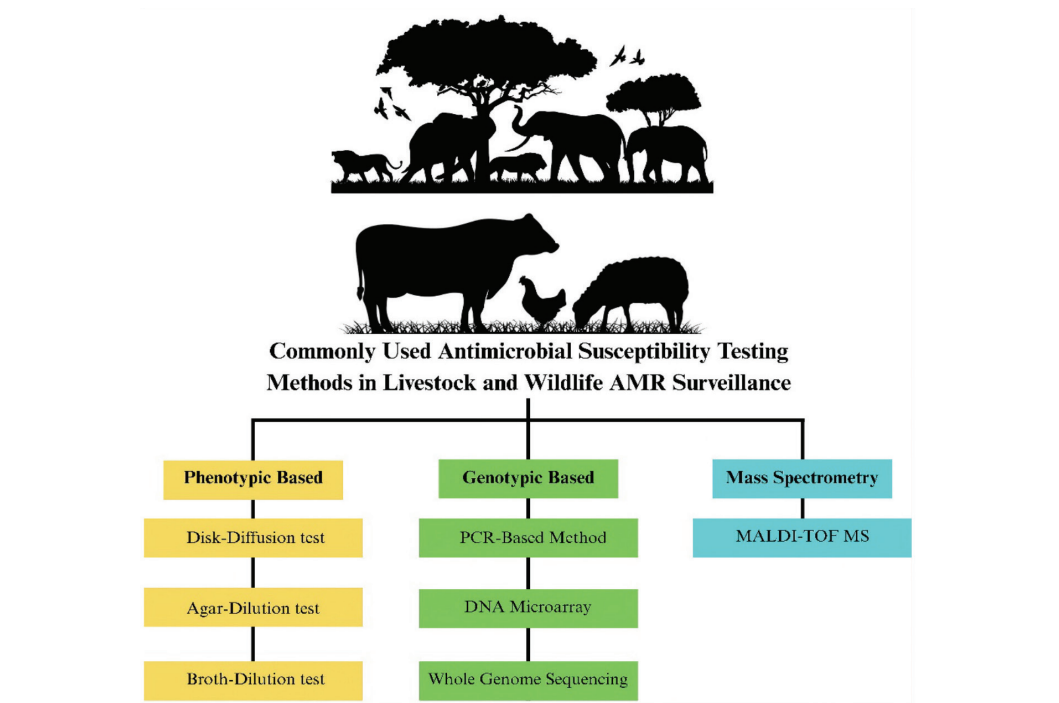


Figure 7: Commonly used AST methods in livestock and wildlife AMR surveillance

(Gajic *et al.*, 2022). Additionally, WGS-AST provides insight into the genetic basis of resistance mechanisms, evolutionary patterns, and pathogen population dynamics in animal settings (Avberšek *et al.*, 2021; Abdalla *et al.*, 2025; Sebastian *et al.*, 2025).

Despite their advantages, genotypic methods are highly technical and expensive, they pose challenges for accurate ARG detection, with a risk of false positives. Since these methods rely on ARG detection, they may overestimate or underestimate resistance, as the

Table 5: Key advantages and limitations of selected AST methods widely used in AMR surveillance in livestock and wildlife settings

Category	Method	Advantages	Limitations
Phenotypic	Disk-Diffusion	• Simple and easy to perform • Low cost and reproducible • Applicable to a wide range of bacteria and antibiotics • Highly standardised • Reliability improved with automated software	• Unable to determine the MIC • Cannot distinguish between bactericidal and bacteriostatic effects • Requires a long incubation period
	Agar-Dilution	• Simple with well-established parameters • Cost-effective (allows simultaneous testing of multiple strains)	• Labour-intensive and time-consuming without automation
	Broth-Dilution	• Gold standard for phenotypic AST • Can determine both MIC and MBC • Development of automated MIC and MBC determination • Microdilution is highly efficient, accurate, and cost-effective	• Microdilution has long turnaround times, requires significant space and reagents, and is labour-intensive
Mass Spectrometry	MALDI-TOF	• Rapid turnaround time • Requires very low sample volume	• Expensive instrument • High maintenance costs
Genotypic	PCR-based methods	• Samples do not need to be sterile • Can be used on samples containing mixtures of bacteria	• Highly technical and require a good laboratory facility • Higher cost compared to phenotypic methods • Risk of false positive and negative results
	DNA microarray	• Produces broad-spectrum, multi-gene characteristics	• High cost and time-consuming • Requires highly skilled personnel • Potential for non-specific binding of DNA probes
	WGS	• Offers rapid pathogen identification and typing • Can detect all known ARGs	• High cost and requires skilled personnel • Lacks definite standardisation supporting its routine application for AST in most bacterial species

MIC: The lowest concentration of an antimicrobial that inhibits the bacterial growth
MBC: The lowest concentration of an antimicrobial that results in the bacterial death
Source: Al Amin *et al.*, (2022); Gajic *et al.*, (2022); Salam *et al.*, (2023a)

presence of ARGs does not always correlate with resistance expression. While some studies show strong correlations between phenotypic and genotypic resistance (Avberšek *et al.*, 2021; Athira *et al.*, 2024), discrepancies are frequently observed (Kerluku *et al.*, 2023; Dančová *et al.*, 2024; Sebastian *et al.*, 2025). Abdalla *et al.* (2025) noted that such discrepancies are often isolate-dependent. This emphasises the need for standardised WGS-AST guidelines, comprehensive resistance ARGs databases, and advanced bioinformatics tools to ensure reliable genotype–phenotype resistance correlations in AMR surveillance (Abdalla *et al.*, 2025).

While WGS-AST allows for in-depth (Sousa *et al.*, 2020) and understudied AMR characterisation (Sebastian *et al.*, 2025), it cannot distinguish viable and non-viable bacteria or pathogenic and commensal bacteria (Al Amin *et al.*, 2022). Genotypic methods are also incapable of providing quantitative AMR data such as MIC values. Consequently, WGS-based analysis does not currently eliminate the need for phenotypic AMR data (Al Amin *et al.*, 2022). Therefore, genotypic findings should be validated alongside appropriate phenotypic tests, supported by the extensive use of molecular markers, and paired with robust bioinformatics tools (Gajic *et al.*, 2022). For broad surveillance in animal settings, the use of reverse transcription qPCR (RT-qPCR) is recommended, which measures gene transcripts (RNA levels) or gene expression rather than the presence of genes (Shifman *et al.*, 2019). Overall, while molecular-based AST is an efficient AMR screening tool (Gajic *et al.*, 2022), quantitative phenotypic methods remain the most accepted and accessible technique for low- and medium-output laboratories (Salam *et al.*, 2023a).

Future Directions of AMR Studies in Animal Settings

Future research on AMR in animal settings should address its impacts across different animal species. Current literature predominantly emphasises the risk of AMR to public health, often neglecting its direct effects on wildlife

health and biodiversity (Bengtsson & Greko, 2014; Mitchell, 2023). In livestock settings, AMR mitigation strategies are largely centred on reducing AMU, with limited exploration of alternative approaches. This remains a significant limitation, as antimicrobials remain essential for maintaining animal welfare and sustaining the food production system (Bengtsson & Greko, 2014).

Geographical disparities in AMR research further limit the understanding of the global burden of AMR. Most studies are concentrated in developed regions, including China, North America, and Europe, whereas low-income or lower-middle-income countries remain underrepresented. Later regions may experience a high AMR burden due to a weak antimicrobial regulatory system and the circulation of poor-quality antibiotics (Salam *et al.*, 2023b). Addressing these gaps is crucial to evaluate better the impact of AMR on human health, ecosystem stability, food chain systems, and biodiversity.

In 2015, the WHO published the Global Action Plan on Antimicrobial Resistance (GAP-AMR), which provides a global framework and encourages countries to develop and implement National Action Plans (NAPs). While many countries have adopted NAPs, their scope, implementation, and reporting standards are different (Willemsen *et al.*, 2022). High-income countries generally have greater progress while low- and middle-income countries lagged behind (Willemsen *et al.*, 2022). Additionally, although AMR in animal settings shows transboundary and transcontinental spread (Obaidat *et al.*, 2017), NAPs often lack collaborative efforts. For effective global AMR mitigation efforts, it is critical to strengthen international collaboration through data sharing and collaborative AMR surveillance.

Conclusions

This review highlights current knowledge of AMR in wildlife and livestock, emphasising AMR patterns and transmission dynamics across these animal groups. This is the first quantitative assessment of research bias toward livestock,

revealing underrepresentation of animal groups despite their ecological significance in the AMR crisis. Additionally, this review systematically analyses AMR research by taxonomic groups across both wildlife and livestock, uncovering diverse driver-transmission dynamics across different animal taxa.

There is an urgent need for methodical research, particularly in underrepresented countries and animal groups, including wildlife, especially invertebrates and amphibians, captives, pests, and companions, given the data gaps in low-income regions and the ecological roles of these species. Integrated surveillance approaches are essential, combining genotypic and phenotypic methods and incorporating diverse sample types across human, animal, and environmental sectors.

Future recommendations include enhancing surveillance for less-studied animals to elucidate AMR transmission dynamics, research on the effects of AMR on biodiversity and ecosystems, and prioritising wildlife-livestock interfaces within national frameworks to mitigate AMR's ecological footprint and inform sustainable health policies.

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Author Contributions Statement

SHA and MABAL designed the outlines and drafted the manuscript. SHA, NHA, TN, NHS, NO, HH, NAFAF, and FFR wrote the initial draft of the manuscript. MABAL reviewed the

scientific content in the manuscript, providing critical editing and evaluation. MSSO, MSM, PDS, and KVK have provided suggestions and feedback to improve the quality of the manuscript. All authors read and approved the final version of the manuscript.

Conflict of Interest Statement

The authors declare no conflicts of interest.

Ethical Conduct

All information presented in this article does not require ethical approval or informed consent, as no human or animal subjects were involved.

Declaration of AI-usage

AI tools were used in this work solely for grammatical improvements and clarity. All content was carefully reviewed and edited by the authors to ensure scientific and factual integrity. The authors bear full responsibility for the content of this manuscript.

Data Availability Statement

Supplemental data for this article will be provided upon request.

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