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REVIEW ARTICLE

Wildlife as reservoirs and vectors of antimicrobial resistance: Ecological drivers, movement dynamics, and One Health implications for spillover to humans

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ABSTRACT

Antimicrobial resistance (AMR) is a major global health concern affecting humans, animals, and the environment. Although surveillance has traditionally focused on healthcare settings and livestock, wildlife is increasingly recognized as a potential reservoir, carrier, and indicator of antimicrobial-resistant bacteria and resistance genes. This review examines the ecological factors, movement patterns, and transmission pathways influencing AMR in wildlife, with particular emphasis on potential spillover to humans and domestic animals. Wildlife can acquire resistant microorganisms through contaminated water, soil, food, agricultural runoff, wastewater, and interactions with humans and livestock. Habitat fragmentation, urbanization, agricultural expansion, feeding behavior, and predator–prey relationships further influence exposure and opportunities for bacterial transmission. Local movements and long-distance migration may contribute to the geographical dissemination of resistant bacteria and resistance genes between ecosystems. Evidence from different wildlife populations has identified extended-spectrum β-lactamase-producing *Escherichia coli* in migratory birds, methicillin-resistant *Staphylococcus aureus* in wild mammals, and fluoroquinolone-resistant bacteria in primates inhabiting areas with frequent human contact. Marine and aquatic wildlife may also contribute to AMR circulation through exposure to wastewater, pharmaceutical residues, and other environmental contaminants. Horizontal gene transfer involving plasmids, integrons, and transposons further contribute to the persistence and dissemination of resistance genes within microbial communities. Humans may be exposed through direct contact, wildlife handling, hunting, and indirect exposure to contaminated water, soil, and food. However, detecting resistant bacteria in wildlife does not necessarily establish the direction or occurrence of transmission to humans. Key challenges include limited wildlife surveillance, inconsistent sampling methods, insufficient ecological data, and difficulty identifying transmission sources. Integrating wildlife monitoring with genomic analysis, environmental surveillance, and animal movement studies could improve understanding of AMR distribution and transmission risks. A coordinated One Health approach involving human health, veterinary, environmental, and wildlife sectors is essential to better characterize potential transmission pathways, strengthen surveillance, and develop effective strategies to reduce AMR spread across interconnected ecosystems.

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Keywords: antimicrobial resistance, environmental contamination, horizontal gene transfer, migratory birds, One Health, resistance genes, wildlife reservoirs, zoonotic spillover.

INTRODUCTION

Antimicrobial resistance (AMR) is one of the most significant global health threats of the 21st century, affecting human health, animal health, food security, and environmental sustainability [1]. From a One Health perspective, AMR is a complex biological and ecological phenomenon arising from interactions among humans, animals, microorganisms, and their shared environments [2]. Traditionally, AMR surveillance and control strategies have focused primarily on healthcare facilities, livestock production, and companion animals, where antimicrobial use contributes to the selection and dissemination of resistant microorganisms [3]. However, increasing evidence indicates that wildlife also contributes to AMR dynamics, although its ecological and epidemiological roles remain comparatively understudied [4]. Wildlife may serve as reservoirs, carriers, or environmental indicators of resistant bacteria and AMR genes because wild animals move across different habitats, encounter contaminated environmental resources, and harbor diverse microbial communities capable of acquiring and maintaining resistance determinants [5].

The ecological characteristics and exposure pathways of wildlife differ considerably from those of domestic animals [6]. Livestock and companion animals may be exposed to antimicrobials through therapeutic or preventive treatments and, in some production systems, through their use for growth promotion, creating selective pressures that favor resistant bacterial populations [7]. Consequently, antimicrobial-resistant commensal and pathogenic bacteria have been widely documented in domestic animals [8–10]. In contrast, many free-ranging wildlife populations have limited direct exposure to antimicrobial treatments. The detection of resistant bacteria in these populations may therefore reflect environmental contamination, natural resistance mechanisms, or microbial exchange through interactions with other animals and contaminated habitats [11]. Wildlife can therefore provide valuable information on the environmental distribution of AMR, including resistance patterns that conventional surveillance programs focused on humans and domestic animals may miss [12]. Understanding the contribution of wildlife to AMR circulation is therefore important for evaluating potential ecological reservoirs, potential transmission pathways, and connections among natural, agricultural, and urban ecosystems [13].

Despite growing recognition of wildlife in AMR epidemiology, substantial knowledge gaps remain regarding the ecological mechanisms responsible for the acquisition, persistence, and dissemination of resistant bacteria and resistance genes in free-ranging animal populations [14]. Existing AMR research has predominantly examined humans, livestock, aquaculture, and environments directly affected by antimicrobial use, whereas wildlife has received comparatively limited attention [15–17]. Investigations involving wild animals face several methodological challenges, including difficulty obtaining representative samples, substantial variation in species ecology and behavior, differences in microbiological detection methods, and a lack of standardized surveillance protocols [18]. Furthermore, many available investigations are geographically restricted or focus on individual wildlife species, limiting comparisons across habitats, ecological communities, and geographical regions [19–21].

Another limitation is the limited integration of microbiological findings with ecological information, including habitat characteristics, feeding behavior, predator–prey relationships, population movements, and patterns of contact with humans and domestic animals. Consequently, it remains difficult to distinguish the relative contributions of environmental contamination, wildlife movement, and interspecies microbial exchange to AMR dissemination. Although researchers have detected resistant bacteria and resistance genes in diverse wildlife populations, their presence alone does not establish transmission pathways or demonstrate spillover to humans. Increasing urbanization, agricultural expansion, habitat fragmentation, and changes in wildlife movement patterns may further intensify interactions among wildlife, livestock, humans, and contaminated environments [22]. These developments highlight the need for an integrated assessment that connects wildlife ecology and movement dynamics with microbiological evidence while distinguishing documented AMR carriage from potential transmission pathways and confirmed spillover events.

This review aims to critically examine the role of wildlife as potential reservoirs, carriers, and environmental indicators of AMR, emphasizing the ecological factors and movement dynamics that influence the acquisition, persistence, and dissemination of resistant bacteria and resistance genes across ecosystems. Specifically, it explores the fundamental mechanisms of bacterial resistance and horizontal gene transfer, major environmental sources of antimicrobial-resistant microorganisms, and the influence of habitat characteristics, landscape

modification, feeding behavior, predator–prey interactions, and contact among wildlife, domestic animals, and humans. The review also evaluates how local movements, regional dispersal, and long-distance migration may facilitate the geographical redistribution of resistant microorganisms and genetic determinants, including their circulation between natural and human-modified environments.

This review also examines evidence on direct and indirect AMR transmission pathways between wildlife and humans, with particular attention to the distinction between potential exposure, microbial exchange, and demonstrated spillover. It discusses the implications of wildlife-associated AMR for public health, livestock production, biodiversity conservation, and environmental health. Finally, the review identifies major limitations in existing surveillance and research approaches and highlights opportunities for integrating wildlife ecology, genomic investigations, animal movement data, and environmental monitoring into coordinated One Health strategies. By integrating ecological and microbiological perspectives, this review aims to support a more comprehensive understanding of wildlife-associated AMR and inform future surveillance, research priorities, and risk-mitigation efforts.

REVIEW METHODOLOGY

Review design

This study was designed as a narrative literature review to examine the role of wildlife in the acquisition, maintenance, and dissemination of AMR across natural and human-modified ecosystems. The review focused on the relationships among wildlife ecology, animal movement patterns, environmental contamination, and potential transmission pathways involving humans and domestic animals. Particular attention was given to evidence concerning antimicrobial-resistant bacteria, resistance genes, ecological reservoirs, horizontal gene transfer, and the implications of wildlife-associated AMR within the One Health framework.

Literature search strategy

Relevant scientific literature was identified through searches of PubMed, Scopus, Web of Science, and Google Scholar. The initial literature search covered publications published between 2007 and 2025 and was last conducted in November 2025, before manuscript submission. Additional relevant publications and policy developments published in 2026 were incorporated during manuscript revision to ensure that the review reflects recent developments in antimicrobial resistance and the One Health framework. Search terms included combinations of "antimicrobial resistance," "antibiotic resistance," "wildlife," "wild animals," "resistance genes," "environmental contamination," "wildlife migration," "migratory birds," "horizontal gene transfer," "zoonotic transmission," "spillover," and "One Health." Boolean operators (AND and OR) were used, where supported, to combine terms and identify studies addressing the ecological distribution and potential transmission of AMR. Reference lists of relevant publications were also examined to identify additional studies.

Literature selection

Publications were considered relevant when they addressed at least one of the following topics: antimicrobial-resistant bacteria or resistance genes detected in wildlife; ecological and environmental factors influencing AMR distribution; wildlife movement and migration associated with the geographical spread of resistant microorganisms; interactions among wildlife, domestic animals, humans, and contaminated environments; or potential AMR transmission pathways and their implications for public health and conservation. Original research articles, relevant review articles, and reports from recognized international organizations were considered. Publications without a clear relationship to wildlife-associated AMR or the objectives of this review were excluded from the main discussion. No formal methodological quality assessment or risk-of-bias evaluation was conducted because this study was designed as a narrative review.

Data extraction and narrative synthesis

Information from the selected publications was organized according to wildlife species or groups, geographical settings, bacterial organisms, resistance characteristics, environmental exposure pathways, ecological interactions, and movement patterns. The literature was synthesized thematically to examine mechanisms of AMR acquisition and persistence, the role of wildlife ecology and mobility in resistance dissemination, and potential transmission pathways to humans and domestic animals. Findings were interpreted in relation to their ecological and epidemiological context, with particular attention to distinguishing the detection of resistant microorganisms from evidence of actual transmission. The synthesis also considered implications for

wildlife conservation, livestock health, environmental monitoring, and integrated One Health surveillance.

Limitations of the review approach

As a narrative review, this study was intended to provide a broad interpretation of existing evidence rather than a quantitative estimate of AMR prevalence or transmission risk. Differences in wildlife species, geographical coverage, sampling strategies, microbiological methods, and study designs may limit direct comparisons among published findings. Furthermore, the detection of similar resistance characteristics in wildlife, humans, and domestic animals does not independently establish transmission direction or causality. These limitations were considered when interpreting the available literature and identifying priorities for future research.

BASIC CONCEPTS OF AMR IN THE CONTEXT OF WILDLIFE

AMR in wildlife is a complex biological and ecological phenomenon influenced by interactions between microbial resistance mechanisms, environmental conditions, and the behavior of free-ranging animal populations [23]. Wildlife may acquire, maintain, and disseminate resistant microorganisms and resistance genes through exposure to contaminated habitats, feeding activities, interspecies interactions, and movement across ecosystems. Understanding these processes is essential for evaluating how AMR circulates among wildlife, domestic animals, humans, and their shared environments.

Definition and basic mechanisms of AMR

AMR refers to the ability of microorganisms, including bacteria, to survive or multiply in the presence of antimicrobial agents that would normally inhibit their growth or eliminate them [24]. In bacteria, resistance may result from inherent cellular characteristics, genetic mutations, or the acquisition of resistance determinants, potentially reducing treatment effectiveness and contributing to therapeutic failure [25]. Bacterial resistance is generally classified into two major categories: intrinsic and acquired resistance.

Intrinsic resistance is a naturally occurring characteristic of certain bacterial species that does not depend on previous exposure to antimicrobial agents [26]. It may arise from structural or physiological properties, including reduced cell membrane permeability, the absence or modification of antimicrobial targets, and the activity of naturally occurring efflux pumps [27]. For example, the outer membrane of Gram-negative bacteria acts as a permeability barrier that limits the entry of certain antimicrobial agents. Intrinsic resistance is generally associated with stable species-specific characteristics that can be transmitted vertically across bacterial generations [28].

In contrast, acquired resistance develops when previously susceptible bacteria undergo genetic mutations or acquire resistance determinants from other microorganisms [29]. Chromosomal mutations may alter antimicrobial targets, affect membrane permeability, or modify the expression of resistance-associated mechanisms. Alternatively, bacteria may acquire resistance genes through horizontal gene transfer (HGT), allowing genetic material to move between bacterial cells, including those belonging to different species [30]. These mechanisms contribute to the emergence and dissemination of resistant bacterial populations across human, animal, and environmental settings [31].

HGT is facilitated by several mobile genetic elements (MGEs), including plasmids, transposons, and integrons, which contribute to the acquisition, rearrangement, and dissemination of resistance determinants [32]. Bacteriophages may also mediate bacterial gene transfer through transduction. These mechanisms enable resistance genes to circulate among bacterial populations and contribute to the development of multidrug resistance [33]. Plasmids are particularly important because they may carry genes encoding β-lactamases, including extended-spectrum β-lactamases (ESBLs), and mobile colistin resistance determinants such as *mcr* genes [34]. Genetic exchange occurs primarily through conjugation, transformation, and transduction, allowing susceptible bacteria to acquire resistance determinants under suitable conditions [35].

Integrons also contribute to the organization and expression of AMR determinants by capturing and incorporating gene cassettes, many of which encode resistance to different antimicrobial classes [36]. Class 1 integrons have been identified in bacteria associated with livestock and wildlife environments, illustrating the potential for resistance determinants to occur across interconnected ecological settings [37]. In addition, transposons and insertion sequences facilitate the movement and rearrangement of genetic material within and between bacterial genetic structures, contributing to the diversity and dissemination of resistance-associated genes [38].

Importantly, AMR in wildlife cannot be attributed exclusively to human activities. Resistance determinants may occur naturally in environmental microbial communities, including those inhabiting ecosystems with limited

direct anthropogenic influence. Swift *et al.* [39] investigated antimicrobial-resistant *Escherichia coli* recovered from wildlife fecal samples and reported variation in resistance patterns and prevalence that was not consistently associated with sampling locations. These findings suggest that wildlife exposure to resistant bacteria may vary according to ecological conditions and species-specific characteristics rather than geographical proximity to human activities alone. However, detecting resistant microorganisms in wildlife does not, by itself, establish their source, persistence, or subsequent transmission to other hosts.

AMR entry routes into wildlife

The introduction of antimicrobial-resistant microorganisms and resistance determinants into wildlife populations involves interactions among environmental contamination, animal behavior, habitat characteristics, and human activities [40]. Although many free-ranging wildlife species have limited direct exposure to antimicrobial treatments, resistant bacteria have been detected in diverse animal groups, including migratory birds and wild mammals [41]. Three major exposure pathways are particularly relevant: environmental contamination, food-associated and trophic interactions, and contact with domestic animals and humans [42].

Environmental contamination represents an important route through which wildlife encounters resistant bacteria and resistance genes [43]. Wastewater and runoff originating from livestock production, healthcare facilities, pharmaceutical industries, and human settlements may introduce antimicrobial residues, resistant microorganisms, and MGEs into surrounding water bodies, soils, and sediments [44]. Aquatic environments receiving agricultural or domestic waste may contain clinically important resistant bacteria, including ESBL-producing *E. coli* and vancomycin-resistant enterococci [45]. Wildlife species that depend on these environments, including waterbirds, aquatic reptiles, and semiaquatic mammals, may encounter resistant microorganisms during feeding, drinking, or other habitat-associated activities [46]. Similarly, landfills and waste disposal sites provide opportunities for scavenging wildlife, including vultures, rodents, and other mammals, to encounter resistant bacteria associated with discarded food, animal remains, and domestic waste [47].

Food-associated exposure and trophic interactions represent additional pathways through which resistant microorganisms may circulate among wildlife populations [48]. Predators may encounter resistant bacteria through the consumption of infected or colonized prey, potentially facilitating microbial transfer across trophic levels [49]. Scavenging species, including vultures, foxes, and ferrets, may acquire resistant microorganisms when consuming animal carcasses or organic waste originating from agricultural and urban environments [50]. Herbivorous wildlife may also encounter resistant bacteria through contaminated vegetation, drinking water, or soil associated with feeding activities [51]. Similarly, aquatic invertebrates may harbor resistant microorganisms that can subsequently be ingested by predatory species [52]. These interactions illustrate how feeding relationships and ecological food webs can create opportunities for the movement of resistant microorganisms between species, although ingestion does not necessarily result in persistent colonization or onward transmission [53].

Interactions among wildlife, domestic animals, and humans constitute another important pathway for AMR exchange [54]. Habitat fragmentation, urban expansion, and agricultural development have increased opportunities for wildlife and domestic animals to occupy overlapping habitats and use shared environmental resources [55]. Livestock and companion animals may harbor resistant bacteria associated with antimicrobial exposure, creating potential sources of microbial exchange at wildlife–domestic animal interfaces [56]. Direct contact in shared grazing areas and indirect exposure through fecally contaminated soil, water, or feed may facilitate the transfer of resistant microorganisms between animal populations [57]. Urban-adapted wildlife, including rodents, pigeons, and bats, may also encounter resistant bacteria through contaminated food, wastewater, waste disposal sites, and environmental surfaces associated with human activities [58]. Furthermore, hunting, wildlife trade, animal handling, and intentional feeding may increase contact among humans, wildlife, and potentially contaminated materials, creating additional opportunities for microbial exchange through fecal–oral exposure and contaminated objects or surfaces [59].

Together, these pathways demonstrate that wildlife-associated AMR is influenced by multiple, interconnected ecological and anthropogenic processes. Environmental contamination, trophic interactions, and shared habitats may contribute to the acquisition and redistribution of resistant microorganisms, while wildlife movement can extend opportunities for exposure and microbial exchange across ecosystems. Figure 1 illustrates the principal environmental and anthropogenic pathways through which antimicrobial-resistant bacteria and resistance determinants may enter wildlife populations [43–59].

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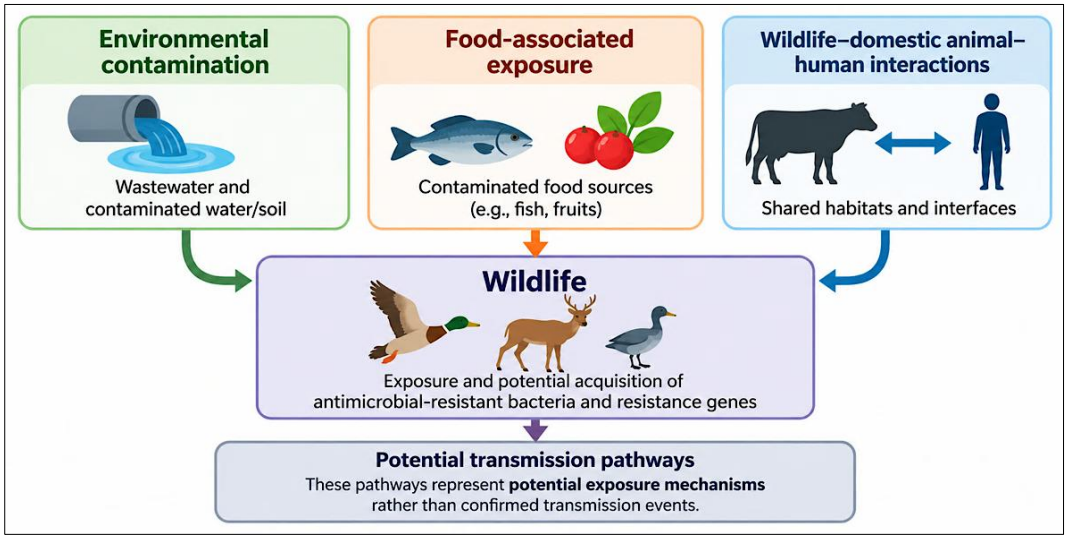


Figure 1: Potential pathways of antimicrobial resistance introduction into wildlife. The figure illustrates possible routes through which wildlife may acquire antimicrobial-resistant bacteria and resistance determinants from anthropogenic and environmental sources, including contaminated water, soil, food resources, wastewater, and interactions at wildlife–domestic animal–human interfaces [43–59]. These pathways represent potential exposure mechanisms rather than confirmed transmission events.

WILDLIFE ECOLOGY AND ITS ROLE IN AMR DYNAMICS

Wildlife ecology influences the acquisition, maintenance, and dissemination of AMR across natural and human-modified ecosystems [46]. Variations in habitat characteristics, species behavior, feeding patterns, and interactions across trophic levels create ecological networks through which resistant bacteria and resistance genes may circulate among animal populations and their environments [49]. Understanding these relationships is essential for identifying ecological factors associated with AMR distribution and evaluating the potential contribution of wildlife to resistance dissemination at local, regional, and global scales.

Ecological factors influencing AMR colonization

The colonization of wildlife by antimicrobial-resistant bacteria is influenced by environmental conditions, habitat characteristics, and species-specific behavior [60]. Although many free-ranging wildlife populations have limited direct exposure to antimicrobial treatments, researchers have detected resistant microorganisms in diverse species, suggesting that environmental exposure and ecological interactions may contribute to the acquisition and maintenance of resistance determinants [61]. Habitat characteristics, landscape fragmentation, and ecological pressures are among the major factors influencing opportunities for bacterial exposure, colonization, and dissemination within wildlife communities [2].

Habitat characteristics determine the physical, biological, and environmental conditions that influence wildlife exposure to antimicrobial-resistant microorganisms and antimicrobial residues [46]. Wildlife in relatively undisturbed forest ecosystems may experience lower exposure to human-associated sources of AMR, although contamination can occur through waterways that receive wastewater or agricultural runoff from surrounding areas [62]. In contrast, urban-adapted wildlife, including rodents, pigeons, bats, and foxes, may encounter resistant microorganisms through contact with domestic waste, contaminated surfaces, wastewater, and environments associated with healthcare and human settlements [47]. In agricultural landscapes, wildlife may interact with livestock, animal waste, contaminated soil, and shared water sources, creating opportunities for exposure to resistant bacteria and MGEs associated with animal production systems [63]. Consequently, differences in land use and environmental contamination may produce spatial variation in AMR exposure across natural, agricultural, and urban habitats [64].

Habitat fragmentation and landscape modification further influence wildlife exposure to resistant microorganisms by altering habitat availability, animal movement, and interactions among species [65]. Infrastructure development, agricultural expansion, and deforestation may displace wildlife or modify their movement patterns, increasing opportunities for contact with human settlements and livestock production areas [66]. Such changes can increase spatial overlap among wildlife, domestic animals, and humans, potentially facilitating microbial exchange through direct contact or shared environmental resources [67]. For example,

vultures and small carnivores may use landfills and other waste disposal sites as alternative food sources, increasing their exposure to resistance-associated bacteria from discarded organic materials [68]. Landscape modification may also alter soil properties, water quality, and microbial community composition, potentially influencing the environmental persistence and distribution of resistance determinants [69].

Ecological pressures, including interspecific competition, population density, and environmental stress, may also influence the circulation of resistant microorganisms within wildlife populations [70]. Competition for limited resources can increase contact among individuals and species, creating additional opportunities for microbial exchange [71]. High population densities, particularly in colonial wildlife such as bats and waterbirds, may facilitate bacterial transmission through fecal–oral exposure, contaminated environmental surfaces, and other relevant transmission routes [72]. Environmental disturbances, food scarcity, and climate-related stressors may also affect wildlife physiology and susceptibility to microbial colonization, although these effects depend on species-specific and environmental conditions [73]. Collectively, these ecological pressures may influence the exposure, persistence, and circulation of antimicrobial-resistant bacteria within wildlife communities. However, their contribution to resistance selection and long-term maintenance requires evaluation within the specific ecological and microbiological context [74].

Wildlife species as potential AMR reservoirs

Different wildlife groups may contribute to AMR dynamics according to their habitat preferences, feeding behavior, movement patterns, and interactions with human-modified environments [4]. Wild birds, mammals, reptiles, and amphibians have been investigated as potential carriers, reservoirs, or environmental indicators of antimicrobial-resistant microorganisms [6]. The detection of resistant bacteria in these animals suggests that AMR distribution extends beyond settings involving direct antimicrobial administration and may reflect environmental contamination and microbial exchange across ecological networks [75]. Nevertheless, the presence of resistant bacteria does not necessarily demonstrate that a wildlife species maintains or transmits these microorganisms over time. Table 1 summarizes the major wildlife groups associated with AMR occurrence and their potential ecological roles [41, 76–82].

Table 1: Wildlife groups associated with the carriage and potential dissemination of antimicrobial-resistant bacteria and resistance determinants [41, 76–82].

Wildlife group	Example species	Resistant bacteria/ resistance determinants	Potential AMR acquisition pathways	Ecological significance	Reference
Wild birds (migratory birds and waterfowl)	Wild ducks, geese, gulls, and shorebirds	*Escherichia coli*, *Salmonella* spp., and *Campylobacter* spp.; ESBL-associated genes, including *bla*$_{CTX-M}$, and carbapenemase-associated resistance determinants	Exposure to water contaminated by domestic, hospital, or livestock waste; contact with contaminated sediments during foraging	Potential long-distance dissemination of resistant bacteria; indicators of environmental contamination; possible introduction of resistance determinants into wetlands and agricultural ecosystems	[41, 76–78]
Wild mammals – Rodentia	Wild rats and mice	*Escherichia coli*, *Enterococcus* spp., MRSA, and MDR *Salmonella* spp.	Exposure to human and livestock waste; frequent contact among individuals in densely populated habitats	Potential maintenance and local dissemination of resistant bacteria in urban and agricultural environments; possible exposure of other hosts through fecal contamination	[74, 80]
Wild mammals – nonhuman primates	Macaques and baboons	Ciprofloxacin-resistant *Escherichia coli* and other resistant bacteria associated with human activities	Indirect contact with tourists; consumption of discarded food; exposure to contaminated surfaces and waste	Indicators of human-associated environmental contamination; potential microbial exchange at human–wildlife interfaces	[74, 83]
Wild mammals – carnivores	Foxes, raccoons, and civets	Resistant *Salmonella* spp., MRSA, and other antimicrobial-resistant bacteria	Predation and scavenging; consumption of contaminated carcasses; exposure to urban and agricultural waste	Potential movement of resistant bacteria across trophic levels and between human-modified and natural ecosystems	[74, 80]
Reptiles and amphibians	Freshwater turtles, snakes, and frogs	Resistant *Salmonella* spp. and other opportunistic bacteria carrying resistance determinants	Exposure to contaminated water, soil, and sediments; contact with microorganisms in aquatic and terrestrial habitats	Potential indicators of environmental AMR contamination; possible carriage and redistribution of resistant microorganisms within local food webs	[74, 86, 87]

AMR = antimicrobial resistance; ESBL = extended-spectrum β-lactamase; MDR = multidrug-resistant; MRSA = methicillin-resistant *Staphylococcus aureus*; CTX-M = cefotaximase-Munich-type β-lactamase family. The presence of resistant bacteria or resistance determinants does not necessarily establish persistent reservoir status or confirmed transmission to other hosts.

Wild birds, particularly migratory birds and waterfowl, are among the most extensively investigated wildlife groups in AMR research [41]. Their capacity for long-distance movement creates opportunities for the geographical redistribution of resistant microorganisms across ecological regions and national boundaries [76].

However, the detection of resistant bacteria in migratory birds does not independently demonstrate transmission along migration routes. Many water-associated bird species use wetlands, lakes, estuaries, and other aquatic habitats that may receive wastewater, agricultural runoff, or contamination from human settlements and livestock production [77]. Exposure to these environments may facilitate the acquisition of resistant bacteria, including *Escherichia coli*, *Salmonella* spp., and *Campylobacter* spp., some of which may carry genes encoding ESBLs or carbapenemases [78]. Waterfowl, including wild ducks and geese, and other water-associated birds, such as gulls, may also serve as environmental indicators because their feeding and habitat use patterns bring them into frequent contact with potentially contaminated water and sediments [79].

Wild mammals represent another important group in wildlife-associated AMR research, encompassing rodents, nonhuman primates, and carnivores with distinct ecological characteristics and exposure pathways [80]. Rodents, including wild rats and mice, frequently inhabit urban, peri-urban, and agricultural environments, where they may encounter resistant microorganisms through contact with domestic waste, livestock facilities, contaminated food, and wastewater [81]. Their population densities and frequent interactions within shared habitats may create opportunities for bacterial circulation among individuals [82]. Nonhuman primates inhabiting tourist destinations or areas adjacent to human settlements may encounter resistant bacteria through food provision, contaminated surfaces, human waste, and other forms of direct or indirect human-associated exposure [83]. Carnivorous mammals, including foxes, raccoons, and mustelids, may acquire resistant microorganisms through predation, scavenging, or contact with contaminated environments, particularly when feeding near agricultural facilities or waste disposal sites [51]. These ecological characteristics make wild mammals relevant to investigations of AMR distribution and potential microbial exchange among wildlife, livestock, and human-associated environments [84].

Reptiles and amphibians are also being investigated as potential carriers and environmental indicators of antimicrobial-resistant bacteria, although the available evidence remains comparatively limited [49]. Freshwater turtles, snakes, and amphibians frequently interact with aquatic and terrestrial environments where resistant microorganisms may occur in water, soil, or sediments [85]. Reptiles may harbor opportunistic bacteria, including *Salmonella* spp., within their intestinal microbiota, and these microorganisms may possess resistance determinants acquired through mutation or HGT [86]. Their close association with environmental substrates and, in some settings, agricultural landscapes may create opportunities for exposure to resistant bacteria. Consequently, reptiles and amphibians may contribute to the circulation of resistant microorganisms within ecological food webs, although their capacity to maintain and transmit specific resistance determinants requires further investigation [87].

Ecological interactions across species

Ecological interactions among wildlife species influence the movement of microorganisms and resistance determinants within natural ecosystems [88]. Predation, scavenging, trophic relationships, and overlapping ecological niches create opportunities for bacterial exposure and exchange among animals occupying different ecological roles [89]. These interactions may also connect wildlife populations with domestic animals and human-associated environments, making them relevant to understanding potential AMR transmission pathways in veterinary public health [90].

Predation represents an important ecological interaction through which microorganisms may be transferred between prey and predators [91]. During consumption, predators encounter microorganisms present in the tissues, gastrointestinal contents, and external surfaces of their prey [92]. When prey animals harbor antimicrobial-resistant bacteria, ingestion may expose predators to these microorganisms, which may subsequently survive passage through the gastrointestinal tract or, under suitable conditions, colonize the intestinal microbiota [93]. Birds of prey, reptiles, and carnivorous mammals have been investigated in relation to the carriage of zoonotic microorganisms and resistance determinants acquired through ecological interactions [23]. Therefore, predation may contribute to the movement of resistant bacteria across trophic levels, although the extent of persistent colonization and subsequent transmission depends on the microorganisms, host species, and environmental conditions involved [94].

Food-web interactions may extend opportunities for microbial exchange beyond individual predator–prey relationships [95]. Organisms occupying lower trophic levels, including aquatic invertebrates and small vertebrates, may carry resistant microorganisms that become available to predators through feeding activities [96]. Repeated interactions across trophic levels can create interconnected pathways for microbial exposure

within ecological communities [97]. These processes may be particularly relevant in agricultural landscapes, where wildlife encounters resistant microorganisms associated with livestock waste and contaminated environmental resources [98]. For example, rodents exposed to contaminated agricultural environments may subsequently be consumed by birds of prey, creating a potential pathway for the transfer of resistant bacteria between trophic levels [52]. However, such ecological pathways should be distinguished from demonstrated transmission events unless supported by microbiological or molecular evidence.

Overlapping ecological niches between wildlife and domestic animals may further increase opportunities for interspecies microbial exchange [71]. These interactions occur when different animal populations share habitats, feeding areas, water sources, or other environmental resources [99]. In extensive livestock production systems, wild and domestic birds may use common feeding grounds and water sources, creating opportunities for direct contact and indirect exposure to microorganisms through contaminated environmental materials [100]. Similar interactions may involve wild mammals, including civets, wild boars, and feral cats, that enter livestock production areas in search of food or shelter [101]. Such ecological overlap may facilitate the circulation of resistant microorganisms among wildlife, domestic animals, and their shared environments, highlighting the importance of considering interspecies interactions when investigating AMR distribution and potential transmission pathways [102].

WILDLIFE MOVEMENT AND THE SPREAD OF AMR

Wildlife movement, ranging from local dispersal to long-distance migration, influences the geographical distribution and potential dissemination of AMR across ecosystems [62]. Animal mobility creates opportunities for contact with different microbial communities, exposure to contaminated environments, and the redistribution of resistant bacteria and resistance genes. Consequently, wildlife may provide ecological connections among natural habitats, agricultural landscapes, urban environments, and geographically distant regions, contributing to the complexity of AMR circulation [80].

Local and regional movements

Local and regional wildlife movements influence patterns of exposure to antimicrobial-resistant microorganisms and their potential circulation within and between ecosystems [11]. Species with relatively restricted home ranges, including rodents, civets, reptiles, and other small mammals, frequently interact with the same habitats and environmental resources over extended periods [103]. These repeated interactions may make certain wildlife populations useful indicators of local environmental contamination and antimicrobial selection pressures, particularly in agricultural and densely populated urban areas [104]. Prolonged exposure to contaminated soil, water, food, and waste may facilitate the acquisition and persistence of resistant bacteria within local wildlife populations, creating opportunities for repeated microbial exchange through direct contact or shared environmental resources [105].

In contrast, highly mobile wildlife species, particularly migratory birds, may transport resistant microorganisms between geographically separated populations and ecosystems [77]. Seasonal migration creates opportunities for the redistribution of resistant bacterial strains across regional and international boundaries, potentially increasing the complexity of AMR transmission networks [22]. Wetlands, ponds, estuaries, and migratory stopover sites located near human settlements or agricultural activities may serve as important locations for exposure to resistant microorganisms and microbial exchange among animal species [106]. Consequently, migratory wildlife may contribute to the geographical movement of resistant bacteria, although the extent of successful colonization and onward transmission requires further investigation [107].

Urban-adapted wildlife, including sparrows, crows, bats, raccoons, and feral cats, may function as ecological links between natural ecosystems and human-modified environments [108]. Their ability to exploit urban habitats increases opportunities for contact with domestic waste, contaminated surface water, markets, livestock facilities, and waste disposal sites [109]. Through movement between these environments, urban wildlife may acquire resistant microorganisms from human-associated sources and potentially introduce them into surrounding natural habitats. Conversely, wildlife entering urban environments may carry microorganisms acquired elsewhere, creating opportunities for microbial exchange among wildlife, domestic animals, and humans [110]. However, the direction and frequency of such exchanges cannot be established solely from the detection of resistant bacteria in these populations.

Bats, belonging to the order Chiroptera, represent another wildlife group of interest because of their

mobility, diverse feeding behavior, and frequent use of habitats that may overlap with human activities [111]. Habitat modification, urban expansion, and agricultural development may increase their exposure to environmental sources of resistant microorganisms [112]. Bacterial taxa reported in association with bats include members of the family Staphylococcaceae, *Clostridioides difficile*, *Bacillus* spp., and *Chlamydia*-like organisms [113]. Some bacteria associated with bats may possess resistance determinants or mechanisms that support persistence under environmental conditions, including biofilm formation and HGT [114]. Nevertheless, detecting these microorganisms does not necessarily mean bats are persistent AMR reservoirs or that they transmit resistant pathogens to humans. Their epidemiological significance should therefore be evaluated using species-specific microbiological, ecological, and molecular evidence.

Long-distance migration

Long-distance migration is an important ecological process that may contribute to the geographical redistribution of antimicrobial-resistant microorganisms [115]. Migratory birds, including waterfowl, shorebirds, and certain raptors, can travel thousands of kilometers across national boundaries and ecological regions [116]. These movements create opportunities for resistant bacteria carried by migratory species to reach geographically separated environments [77]. During migration, birds encounter diverse habitats, including wetlands, agricultural fields, rice paddies, human settlements, and landfills, each characterized by different microbial communities and potential sources of antimicrobial contamination [41].

Exposure to contaminated habitats along migration routes may facilitate the acquisition of resistant microorganisms from domestic wastewater, livestock waste, and other human-associated environmental sources [117]. Birds colonized by resistant bacteria may retain these microorganisms within their gastrointestinal microbiota during movement between habitats [118]. The shedding of bacteria through feces at feeding, resting, and stopover locations may subsequently introduce resistant microorganisms into local environments, creating opportunities for exposure among other wildlife species and domestic animals [119]. However, the persistence of bacterial colonization throughout migration and the extent of subsequent transmission depend on host characteristics, bacterial survival, and environmental conditions. Therefore, the detection of similar resistant bacteria or resistance genes at geographically distant locations should not, by itself, be interpreted as evidence of migration-mediated transmission.

Migration routes influence the geographical distribution of potential exposure sites and opportunities for microbial exchange [120]. Major migratory pathways, including the East Asian–Australasian Flyway, Central Asian Flyway, and African–Eurasian Flyway, connect numerous wetlands and other habitats used by migratory bird populations [121]. Along these routes, estuaries, lakes, ponds, and seasonal stopover sites may support large aggregations of birds from different species and geographical origins [122]. Such concentrations can increase opportunities for environmental contamination and microbial exchange, particularly where resistant bacteria and MGEs are already present. Resistance determinants of concern include genes encoding ESBLs and carbapenemases, as well as mobile colistin resistance genes such as *mcr* [123].

Beyond the transport of resistant bacteria, migratory wildlife may contribute to the redistribution of resistance determinants across ecological regions [124]. Migratory birds can harbor microbial communities containing resistance-associated genetic elements that may interact with environmental microorganisms or the microbiota of other animals [76]. At contaminated stopover sites, newly encountered bacteria may interact with existing intestinal microbial communities, potentially creating conditions for HGT [125]. Nevertheless, HGT during migration and the subsequent establishment of transferred resistance determinants require direct molecular evidence. Therefore, long-distance migration should be regarded as a potential pathway for AMR dissemination rather than definitive evidence of cross-border transmission.

AMR in marine and aquatic wildlife

Marine and aquatic ecosystems are increasingly recognized as important environmental compartments in AMR circulation because they receive contaminants originating from terrestrial and aquatic human activities [126, 127]. Wastewater discharge, agricultural runoff, aquaculture operations, and other pollution sources may introduce antimicrobial residues, resistant bacteria, and resistance determinants into freshwater, coastal, and marine environments. These inputs may influence microbial community composition and create conditions that favor the persistence or selection of resistant microorganisms. Pharmaceutical residues and heavy metals entering coastal waters may also contribute to environmental selection pressures associated with resistance development and maintenance [128].

Wastewater contamination and microplastic accumulation may further influence the distribution and persistence of resistant microorganisms in aquatic environments [129, 130]. Microplastic surfaces provide substrates for microbial attachment and biofilm development, forming distinct microbial communities commonly referred to as the plastisphere. These biofilms may bring different bacterial populations into close proximity, potentially creating opportunities for genetic exchange, including HGT. However, the extent to which microplastic-associated biofilms increase resistance gene transfer under natural environmental conditions requires further investigation.

Marine wildlife, including cetaceans, pinnipeds, sharks, seabirds, and deep-sea fish, may encounter resistant microorganisms through contaminated water, prey consumption, and interactions with aquatic microbial communities [131, 132]. Some of these species may serve as environmental sentinels because their microbiota can reflect exposure to resistant bacteria circulating within marine ecosystems. Detecting multidrug-resistant (MDR) microorganisms in aquatic wildlife also raises concerns about potential exposure pathways through seafood, shared water resources, and direct contact with marine animals. Nevertheless, identifying resistant microorganisms in marine wildlife does not, by itself, demonstrate transmission to humans or establish these animals as persistent reservoirs. These considerations highlight the importance of integrating marine and freshwater ecosystems into One Health surveillance strategies to improve understanding of environmental AMR distribution and potential transmission pathways.

The role of mobility in HGT

Wildlife mobility may influence opportunities for HGT by connecting microbial communities from different habitats and environmental settings [133]. HGT enables bacteria to acquire genetic material from other microorganisms, contributing to the dissemination of resistance determinants within and between bacterial populations [134]. As wildlife moves among natural, agricultural, and urban environments, animals may transport resistant bacteria within their gastrointestinal microbiota or on external body surfaces. These movements can introduce microorganisms into new ecological settings, potentially increasing opportunities for interactions among bacterial communities with different resistance characteristics [135].

Movement across forests, wetlands, agricultural landscapes, urban environments, and landfills may create ecological contact points where microorganisms from different sources encounter one another [136]. Under suitable conditions, bacteria may exchange resistance-associated genetic material through mechanisms involving plasmids, transposons, integrons, and other genetic elements [137]. Nutrient-rich and contaminated environments, including wetland sediments and organic waste disposal sites, may support dense microbial communities and biofilm formation, potentially creating favorable conditions for genetic exchange [138]. Antimicrobial residues originating from healthcare facilities, livestock production, or other sources may additionally exert selective pressures that favor bacteria carrying particular resistance determinants [139]. However, antimicrobial selection and HGT are distinct processes and should not be interpreted as equivalent mechanisms.

Wildlife movement may also introduce microorganisms into habitats containing different bacterial communities, increasing opportunities for microbial interactions [49]. Animals with diverse feeding behaviors or frequent contact with human-modified environments may encounter environmental, commensal, and pathogenic bacteria from multiple sources [140]. Where suitable biological conditions exist, resistance determinants may be exchanged through conjugation, transformation, or transduction [141]. Resistant bacteria carried by wildlife may subsequently be released into surrounding environments through fecal shedding or contact with contaminated surfaces, potentially contributing to the redistribution of microorganisms and resistance-associated genetic material [142].

At broader geographical scales, wildlife movement may connect microbial communities from distant ecological regions [143]. For example, bacteria carrying resistance-associated plasmids acquired in contaminated environments may potentially be transported to other locations through animal movement [144]. However, the geographical transport of resistant bacteria should be distinguished from confirmed HGT events, which require evidence of genetic exchange between microorganisms. Wildlife mobility may therefore influence both the spatial distribution of resistant microorganisms and opportunities for resistance gene exchange, linking ecological movement patterns with microbial evolutionary processes [38]. As illustrated in Figure 2, local movements of rodents and urban-adapted wildlife within fragmented landscapes, together with long-distance bird migration routes, represent potential ecological pathways connecting antimicrobial-resistant bacterial populations across different ecosystems [76, 84–90].

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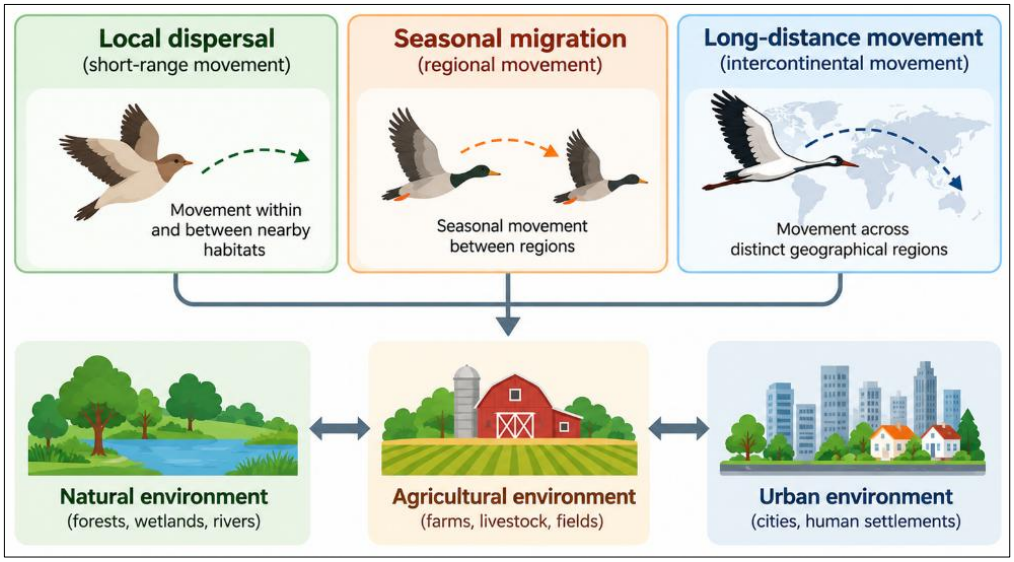


Figure 2: Wildlife movement pathways potentially contributing to antimicrobial resistance dissemination. The figure illustrates how local dispersal, seasonal migration, and long-distance movement may connect geographically separated habitats and create opportunities for the redistribution of resistant bacteria and resistance determinants. Movement between natural, agricultural, and urban environments may facilitate microbial exposure and environmental contamination [76, 84–90]. Animal movement alone does not establish bacterial transmission or successful colonization.

POTENTIAL SPILLOVER OF AMR FROM WILDLIFE TO HUMANS

The potential transmission of antimicrobial-resistant microorganisms from wildlife to humans is an emerging concern because habitat overlap and direct and indirect interactions between wildlife and human populations are increasing [62]. Ecological, biological, and environmental pathways may facilitate the movement of resistant bacteria and resistance determinants across the wildlife–human interface [110]. However, the detection of antimicrobial-resistant bacteria in wildlife does not necessarily establish transmission to humans. Understanding the mechanisms and conditions of potential spillover is therefore essential to distinguish environmental exposure, bacterial colonization, and confirmed transmission events.

Direct spillover pathways

Direct spillover of antimicrobial-resistant microorganisms from wildlife to humans may occur through physical contact with infected or colonized animals without an intermediate environmental exposure pathway [145]. Such interactions are particularly relevant in settings where humans frequently encounter wildlife through occupational activities, hunting, animal handling, tourism, or human–wildlife conflict [2]. Direct contact may expose humans to resistant pathogenic or commensal bacteria through bites, scratches, mucosal contact, or contamination of damaged skin with animal secretions or tissues [146].

Wildlife bites and scratches represent potential routes of bacterial transmission because they may introduce microorganisms into human tissues [147]. Wild primates, rodents, and carnivorous mammals may harbor bacteria of clinical relevance, including methicillin-resistant *Staphylococcus aureus* (MRSA), *Pasteurella multocida*, *Capnocytophaga* spp., and multidrug-resistant *Escherichia coli* [148]. When these organisms are present in the oral microbiota or on contaminated body surfaces, bites and scratches may introduce them into wounds, potentially causing infections that are harder to treat when AMR is present [149]. Human–wildlife interactions associated with habitat disturbance, settlement expansion, and competition for resources may increase opportunities for such exposure [150]. Nevertheless, the occurrence of resistant bacterial infections following wildlife injuries should be evaluated using organism-specific evidence rather than inferred from wildlife carriage alone.

Hunting, carcass handling, and processing wild animal meat provide additional opportunities for direct exposure to resistant microorganisms [151]. These activities are important in communities where wild animals are harvested for food, subsistence, or traditional practices [152]. During carcass processing, individuals may encounter bacteria associated with animal tissues, gastrointestinal contents, blood, or contaminated external surfaces [153]. Exposure to resistant *Salmonella* spp., *Campylobacter* spp., and members of the order Enterobacterales may occur when contaminated intestinal contents or other biological materials come into contact with hands, mucous membranes, or damaged skin [154]. Inadequate hygiene, contaminated processing

equipment, and the absence of appropriate protective measures may further increase opportunities for bacterial transfer during meat handling [155].

Wildlife capture, transportation, trade, and sale may also create conditions that facilitate microbial exposure at the human–wildlife interface [156]. These activities frequently involve repeated animal handling, confinement, and contact among animals originating from different habitats [157]. Individuals involved in wildlife capture, transportation, trading, and consumption may encounter resistant microorganisms through contact with animal feces, urine, secretions, or contaminated handling surfaces [72]. Wildlife markets and holding facilities may create additional opportunities for microbial exchange when multiple animal species are maintained in close proximity under conditions that facilitate environmental contamination [158]. However, increased exposure opportunities should not be interpreted as evidence of confirmed transmission or amplification of resistance determinants without supporting microbiological investigations.

Indirect spillover pathways

Indirect spillover may occur when humans encounter resistant microorganisms originating from wildlife through contaminated environmental media, including water, soil, food, and frequently contacted surfaces [40]. These pathways are difficult to characterize because they involve interactions among wildlife behavior, microbial survival, environmental transport, and human exposure patterns [159]. Environmental compartments contaminated by wildlife excreta may temporarily harbor resistant bacteria and resistance determinants, potentially creating opportunities for their subsequent introduction into human-associated settings [160]. Nevertheless, the contribution of wildlife to environmental AMR contamination must be distinguished from contamination originating directly from human activities, livestock production, or wastewater discharge.

Water contamination represents an important potential pathway of indirect exposure [161]. Waterbirds, semiaquatic mammals, and other wildlife species inhabiting aquatic environments may introduce resistant microorganisms into rivers, lakes, wetlands, and artificial water bodies through fecal shedding [162]. Resistant bacteria, including extended-spectrum β-lactamase-producing *E. coli*, vancomycin-resistant enterococci, and multidrug-resistant *Salmonella* spp., may persist in aquatic environments depending on temperature, nutrient availability, organic matter, and other environmental conditions [163]. Human activities involving untreated water, irrigation, recreation, or domestic water use may create opportunities for exposure to these microorganisms [164]. However, identifying resistant bacteria in water used by wildlife does not establish wildlife as the original contamination source, particularly where multiple environmental inputs are present.

Soil contamination represents another potential pathway for the environmental dissemination of resistant microorganisms [165]. Wildlife moving through agricultural landscapes, urban parks, and waste disposal sites may introduce bacteria into surrounding soils through fecal deposition and other activities [166]. Contaminated soil may subsequently contribute to microbial exposure in agricultural production systems, particularly where vegetables and other crops are consumed raw [167]. Resistant bacteria may reach plant surfaces through soil contact, contaminated irrigation water, or interactions with microbial communities associated with plant roots [45]. Consumption of inadequately washed or contaminated fresh produce may expose humans to resistant microorganisms, although the contribution of wildlife-derived contamination must be established through appropriate source attribution [168].

Spatial overlap between wildlife and human activities may further increase opportunities for indirect exposure in urban and peri-urban environments [169]. Urban birds, rodents, raccoons, and small carnivores frequently use parks, recreational areas, landfills, and other shared spaces where their feces may introduce microorganisms onto environmental surfaces [170]. Contact with contaminated playground equipment, picnic areas, recreational surfaces, or surrounding soil may create opportunities for human exposure [12]. Children, sanitation workers, and people participating in outdoor activities may encounter these environmental sources, but their actual infection risk depends on exposure frequency, microbial concentrations, hygiene practices, and individual susceptibility [22].

Figure 3 illustrates potential direct and indirect pathways linking wildlife-associated antimicrobial-resistant bacteria to human exposure [55–59, 99–102, 108–110]. Direct pathways include animal handling, bites, scratches, hunting, and wildlife trade, whereas indirect pathways involve contaminated water, soil, food, and shared environmental surfaces. These pathways represent potential opportunities for microbial transmission and should not be interpreted as confirmed spillover events without supporting epidemiological and molecular evidence.

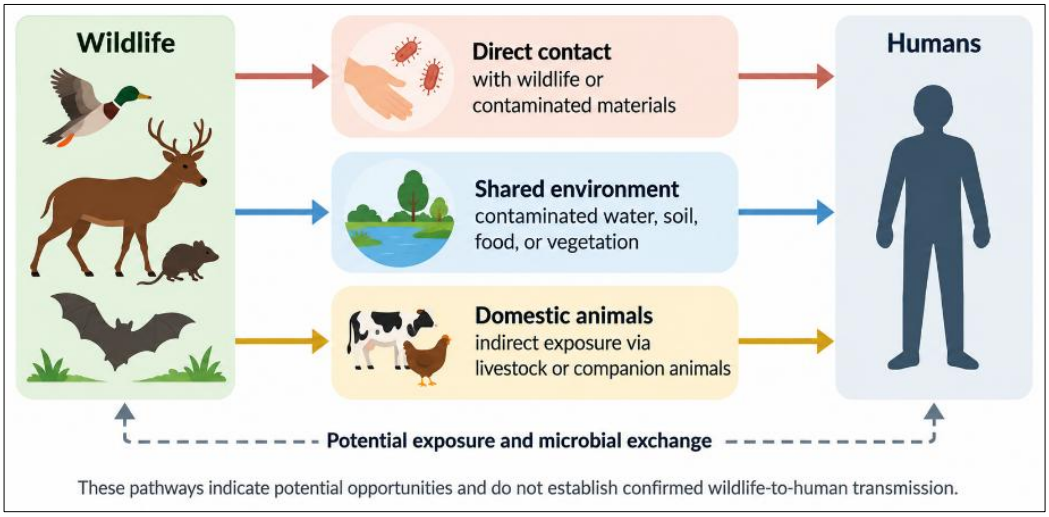


Figure 3: Potential pathways of antimicrobial resistance transmission from wildlife to humans. The figure illustrates possible direct and indirect routes of human exposure to wildlife-associated resistant microorganisms, including contact with wildlife or contaminated materials, shared environmental resources, and interactions involving domestic animals [55–59, 99–102, 108–110]. These pathways indicate potential opportunities for microbial exchange and should not be interpreted as confirmed wildlife-to-human transmission without supporting epidemiological and molecular evidence.

Global case studies

Studies from different geographical regions have documented antimicrobial-resistant bacteria in wildlife populations, providing evidence of their occurrence across diverse habitats and ecological settings [49]. Investigations involving migratory birds have identified extended-spectrum β-lactamase-producing *E. coli*, highlighting the potential contribution of highly mobile wildlife to the geographical redistribution of resistant microorganisms [171]. Waterfowl, shorebirds, and other migratory species may harbor bacteria carrying resistance determinants, including genes belonging to the *bla*CTX-M family, which are also reported in bacteria associated with healthcare facilities, livestock, and human-modified environments [78]. When migratory birds use wetlands, agricultural fields, and urban habitats, fecal shedding may introduce resistant microorganisms into local environments, creating opportunities for microbial interactions and potential resistance gene exchange [172]. However, similarities in resistance determinants across locations do not, by themselves, establish migration-mediated transmission or the direction of bacterial movement. Table 2 summarizes the global studies describing wildlife-associated AMR and their ecological or epidemiological implications [118–132, 167–172].

Wildlife populations inhabiting urban and peri-urban environments have also been investigated for the carriage of multidrug-resistant bacteria [173]. Urban mammals, including rodents, foxes, raccoons, and ferrets, may harbor clinically relevant resistant microorganisms, including MRSA and resistant strains of *Salmonella enterica* [11]. These species frequently encounter domestic sewage, municipal waste, agricultural runoff, and environmental contamination associated with healthcare and livestock production activities [174]. Such exposure may contribute to the acquisition of resistant bacteria, while movement between urban and natural habitats creates opportunities for their redistribution [164]. Identifying MRSA isolates in wildlife with genetic characteristics resembling those of human-associated strains suggests possible microbial exchange across the human–wildlife interface [175]. Nevertheless, molecular similarity alone does not establish transmission direction, and stronger epidemiological evidence is required to determine whether wildlife acts as a source, recipient, or intermediate carrier.

Investigations involving nonhuman primates in tropical tourism areas have identified AMR in populations that frequently interact with visitors and human settlements [176]. Macaques, baboons, and other primates habituated to human presence may encounter resistant microorganisms through food provisioning, contaminated waste, and shared environmental resources [177]. Detecting bacteria resistant to ciprofloxacin and other antimicrobial agents may reflect exposure to human-associated microbial contamination, although alternative environmental sources cannot be ruled out [178]. Because some primate populations move between tourist destinations, forest habitats, and residential areas, they may create ecological connections among environments with different levels of anthropogenic influence. These interactions raise concerns regarding potential microbial exchange with humans and domestic animals, but confirmed spillover or spillback requires evidence demonstrating the direction and circumstances of transmission [179].

Table 2: Representative ecological settings and reported patterns of AMR in wildlife [118–132, 167–172].

Case study category	Wildlife group	Reported resistance characteristics	Key findings	Potential implications
Migratory birds and potential international dissemination	Waterfowl, shorebirds, and other long-distance migratory birds	ESBL-producing *Escherichia coli*, including isolates carrying bla_{CTX-M} genes	Resistant bacteria and resistance determinants have been detected in migratory birds occupying geographically separated habitats. Fecal shedding may contribute to environmental contamination at wetlands, agricultural areas, and migration stopover sites.	Potential geographical redistribution of resistant microorganisms; opportunities for environmental microbial exchange; need for coordinated surveillance along migration routes
Urban wildlife near human settlements	Rats, foxes, raccoons, and civets	MRSA and MDR *Salmonella enterica*	Resistant bacteria have been reported in wildlife inhabiting human-modified environments. Exposure to domestic waste, urban refuse, and contamination associated with healthcare or livestock activities may contribute to bacterial acquisition.	Potential microbial exchange at wildlife–human–livestock interfaces; environmental contamination; possible redistribution of resistant bacteria between urban and surrounding natural habitats
Nonhuman primates in tourist areas	Macaques and baboons	Ciprofloxacin-resistant bacteria, including *Escherichia coli*	Frequent contact with tourists, discarded food, and human-associated waste may increase opportunities for exposure to resistant microorganisms.	Potential interspecies exposure and microbial exchange; value of nonhuman primates as indicators of anthropogenic AMR contamination; need for surveillance at tourism-associated wildlife interfaces

AMR = Antimicrobial resistance; ESBL = Extended-spectrum β-lactamase; MDR = Multidrug-resistant; MRSA = Methicillin-resistant Staphylococcus aureus; CTX-M = Cefotaximase-Munich-type β-lactamase family. Reported resistance patterns indicate bacterial carriage or environmental exposure; direct transmission, transmission direction, and persistent reservoir status require additional epidemiological and molecular evidence.

IMPLICATIONS FOR PUBLIC HEALTH, CONSERVATION, AND THE LIVESTOCK SECTOR

The occurrence and potential dissemination of AMR in wildlife have important implications for public health, biodiversity conservation, and livestock production [180]. From a One Health perspective, the detection of resistant microorganisms in wildlife demonstrates that AMR extends beyond clinical and intensive livestock production settings and is also associated with natural and human-modified ecosystems [181]. Wildlife inhabiting areas near human settlements may harbor clinically relevant resistant bacteria, including extended-spectrum β-lactamase-producing *Escherichia coli*, multidrug-resistant *Salmonella* spp., and MRSA, creating opportunities for human exposure through direct contact and contaminated environmental resources [78]. Urban expansion, habitat degradation, and changes in wildlife behavior may further increase interactions among wildlife, humans, and domestic animals, potentially facilitating microbial exchange [182]. Although wildlife-associated resistant bacteria may contribute to infections that are difficult to treat, their actual contribution to human disease burden, healthcare costs, and treatment failure requires epidemiological evidence linking wildlife-associated microorganisms to human infections [183].

Implications for wildlife conservation

AMR represents an emerging concern for wildlife conservation because resistant microorganisms and antimicrobial contaminants may occur in habitats occupied by free-ranging and captive animal populations [163]. Exposure to antimicrobial residues and contaminated environments may influence wildlife-associated microbial communities, potentially affecting host–microbiota interactions and susceptibility to bacterial colonization [184]. Infections caused by antimicrobial-resistant pathogens may complicate the management of wildlife diseases, particularly in animals already affected by habitat degradation, nutritional stress, or other environmental pressures [185]. Resistance may also reduce the effectiveness of antimicrobial treatments used in wildlife rehabilitation, veterinary care, captive breeding, and other *ex situ* conservation programs [186]. These concerns may be particularly relevant for small or vulnerable populations in which infectious diseases can have substantial consequences. However, the extent to which AMR independently contributes to wildlife population declines or extinction risk remains insufficiently established [2]. Integrating AMR monitoring into wildlife health assessments and conservation management may therefore help identify emerging risks and support evidence-based interventions.

Implications for livestock production

Wildlife-associated AMR also has potential implications for livestock health, farm biosecurity, and the sustainability of animal production systems [187]. Migratory birds, rodents, small carnivores, and other wildlife species may encounter resistant microorganisms in agricultural environments and potentially redistribute them through movement, feeding activities, and fecal shedding [188]. Shared water sources, feed storage areas, grazing lands, and contaminated farm environments may create opportunities for microbial exchange between wildlife and livestock. The introduction of resistant bacterial pathogens into livestock populations could complicate disease management, reduce treatment effectiveness, and potentially affect animal productivity and production costs [189]. However, the presence of resistant bacteria in wildlife near farms does not, by itself, establish wildlife-to-livestock transmission, and the direction of microbial exchange may vary with environmental and management conditions.

Captive animal facilities, including zoos, wildlife rehabilitation centers, and animal shelters, may also present opportunities for AMR circulation because of close animal contact, shared environments, and veterinary antimicrobial use [190]. These settings require appropriate infection prevention measures, antimicrobial stewardship, environmental hygiene, and surveillance to minimize the acquisition and dissemination of resistant microorganisms. In livestock production systems, practical preventive measures include restricting wildlife access to feed and water supplies, improving waste management, maintaining farm hygiene, and reducing opportunities for contact between livestock and potentially contaminated environmental resources [191]. Integrating these measures with coordinated surveillance across wildlife, livestock, humans, and the environment can strengthen One Health approaches to AMR prevention and control.

CHALLENGES IN AMR SURVEILLANCE IN WILDLIFE

Changes in wildlife ecology and increasing interactions among natural, agricultural, and urban ecosystems have highlighted the importance of wildlife in AMR surveillance [17]. Wildlife populations may harbor antimicrobial-resistant bacteria and resistance determinants acquired through environmental exposure, feeding activities, and interactions with other animals [192]. Agricultural expansion, urbanization, and natural resource exploitation have increased opportunities for contact among wildlife, livestock, humans, and environments contaminated with antimicrobial residues or resistant microorganisms [193]. These interconnected exposure pathways complicate efforts to identify the sources, persistence, and transmission of resistance determinants. Furthermore, microbial exchange and HGT may occur within environmental and host-associated bacterial communities, making it difficult to distinguish resistance acquired locally from resistance introduced through animal movement or environmental contamination [63].

Limitations of existing surveillance approaches

A major challenge in wildlife AMR surveillance is the difficulty of distinguishing bacterial carriage from persistent colonization and confirmed transmission. Several studies have identified antimicrobial-resistant bacteria in wildlife with resistance profiles resembling those reported in humans and domestic animals [4, 5, 194]. Although these similarities suggest possible connections among microbial populations from different ecological settings, they do not independently establish transmission direction or identify the original sources of resistance. Antimicrobial use in healthcare and livestock production, together with environmental contamination through wastewater and agricultural waste, may contribute to the occurrence of similar resistance determinants across ecosystems [110]. Consequently, surveillance approaches based exclusively on resistance phenotypes may be insufficient for identifying transmission pathways.

Wildlife mobility presents additional challenges for surveillance design and interpretation. Migratory species, particularly birds, may transport resistant microorganisms across geographical regions and encounter different environmental sources of contamination during seasonal movements [195]. Such movements can create opportunities for microbial redistribution through contact with other animals or contamination of shared water, soil, and feeding environments [145]. However, determining whether resistant microorganisms were acquired before migration, during stopovers, or at the sampling location requires information on animal movement, environmental exposure, and bacterial genetic characteristics. Surveillance restricted to a single location or sampling period may therefore provide an incomplete understanding of the spatial and temporal dynamics of wildlife-associated AMR.

Ecological and microbiological complexity

The diversity of wildlife-associated microbial communities further complicates AMR surveillance. Wildlife species differ in their gastrointestinal microbiota, habitat preferences, feeding behavior, and exposure to environmental microorganisms. These differences may influence the acquisition and persistence of resistant bacteria and resistance determinants [196]. Some resistance determinants may persist within bacterial populations even when direct antimicrobial selection pressure is limited, although their maintenance depends on microbial characteristics, ecological conditions, and associated fitness costs. Consequently, wildlife resistance cannot automatically be attributed to recent antimicrobial exposure.

Environmental changes, including climate-related disturbances, habitat degradation, and increasing Anthropogenic pressure, may alter wildlife distributions and their exposure to contaminated environments [197]. Such changes can modify interactions among wildlife, domestic animals, humans, and environmental microbial communities, potentially influencing opportunities for bacterial colonization and resistance gene exchange. Within these communities, resistance may emerge or spread through chromosomal mutations and the acquisition of genetic material, including resistance-associated plasmids [88]. However, identifying these mechanisms requires microbiological and molecular investigations that can distinguish bacterial species, resistance phenotypes, and the underlying genetic determinants.

The presence of antimicrobial-resistant microorganisms in wildlife may also provide information about environmental contamination and ecological interactions [198]. Nevertheless, interpreting wildlife as environmental indicators requires consideration of species-specific exposure patterns, background resistance, sampling locations, and potential contamination sources. Without these considerations, surveillance findings may overestimate or underestimate the contribution of particular wildlife populations to environmental AMR circulation.

Need for integrated One Health surveillance

Addressing these challenges requires surveillance approaches that integrate wildlife ecology, microbiology, environmental monitoring, and information from human and domestic animal populations. The One Health framework provides a basis for examining AMR as an interconnected problem involving human, animal, and environmental health [199]. Surveillance strategies should therefore consider differences among wildlife species, habitat characteristics, environmental contamination, and opportunities for interspecies microbial exchange.

Improved surveillance requires representative sampling, consistent microbiological methods, appropriate characterization of resistance determinants, and the integration of ecological and geographical information [1]. Where feasible, repeated sampling and molecular characterization may help distinguish temporary bacterial carriage from persistent colonization and identify genetic relationships among resistant microorganisms detected in different hosts and environments. Combining microbiological findings with information on wildlife movement and habitat use may also improve understanding of potential exposure pathways.

Without coordinated surveillance, the contribution of wildlife to AMR circulation may remain poorly characterized, limiting the ability to identify emerging environmental and interspecies transmission risks [3]. Research integrating wildlife ecology with AMR monitoring is therefore essential for identifying knowledge gaps, improving interpretation of surveillance findings, and supporting sustainable One Health strategies for AMR prevention and control [200].

RECENT DEVELOPMENTS IN GLOBAL AMR SURVEILLANCE: AN INTEGRATED ONE HEALTH FRAMEWORK

Recent developments in global AMR surveillance reflect increasing recognition of the need to integrate information from human, animal, and environmental health sectors. The World Health Organization (WHO) Global Antimicrobial Resistance and Use Surveillance System (GLASS) provides a standardized framework for collecting and analyzing data on AMR and antimicrobial use. The *Global antibiotic resistance surveillance report 2025* analyzed more than 23 million bacteriologically confirmed infections, drawing on data reported by 104 countries in 2023 and 110 countries during 2016–2023. The report presented adjusted global and regional resistance estimates for 93 infection type–pathogen–antibiotic combinations involving bloodstream infections, urinary tract infections, gastrointestinal infections, and urogenital gonorrhea. Its findings indicated that approximately one in six laboratory-confirmed bacterial infections causing common infections worldwide in 2023 was resistant to antibiotic treatment [201].

These findings underscore the need to strengthen surveillance coverage, laboratory capacity, and the

comparability of resistance data across countries. However, GLASS primarily reports information from human health surveillance and should not be interpreted as an established global system for the routine monitoring of wildlife-associated AMR. Integrating environmental and wildlife surveillance with existing human and animal health systems remains an important priority for understanding the ecological distribution of resistance and identifying potential pathways of microbial exchange.

A major policy development occurred in May 2026, when the Seventy-ninth World Health Assembly adopted the updated Global Action Plan on Antimicrobial Resistance (GAP-AMR) for 2026–2036. Developed through collaboration among the Quadripartite organizations, the WHO, Food and Agriculture Organization of the United Nations (FAO), United Nations Environment Program (UNEP), and World Organization for Animal Health (WOAH), the updated plan provides a comprehensive One Health framework for coordinated international action against AMR. It emphasizes infection prevention, responsible antimicrobial use, strengthened surveillance, environmental protection, sustainable financing, and multisectoral accountability [202].

The updated framework recognizes the importance of environmental contamination and interactions among human, animal, plant, and environmental health systems. Implementing it may support greater integration of monitoring activities across wastewater, agricultural environments, soil, surface water, and wildlife-associated microorganisms. In this context, wildlife surveillance could complement existing AMR monitoring systems by providing information on environmental exposure, ecological connectivity, and the occurrence of resistant bacteria in free-ranging animal populations. Nevertheless, the use of wildlife as an early-warning indicator requires standardized sampling approaches, validated microbiological methods, and evidence linking surveillance findings to relevant exposure or transmission pathways.

Integrated surveillance approaches, including the WHO Tricycle protocol, offer practical opportunities to improve cross-sector comparisons. The Tricycle approach uses extended-spectrum β-lactamase producing *Escherichia coli* as an indicator organism for surveillance across human, food chain, and environmental settings. Its standardized methodology can support comparisons of resistance occurrence among interconnected sectors and may provide a foundation for additional ecological investigations involving wildlife. However, wildlife sampling is not automatically included in all applications of the protocol and would require appropriate adaptation and validation.

The updated GAP-AMR also reinforces international commitments to reducing the health burden of bacterial resistance, strengthening national surveillance systems, and minimizing environmental contamination by antimicrobial residues and resistant microorganisms. Achieving these objectives requires collaboration among public health authorities, veterinary services, environmental agencies, wildlife researchers, and policymakers. Integrating ecological information, bacterial genomic characterization, and environmental monitoring with existing surveillance systems may improve the identification of AMR distribution patterns and potential transmission pathways. Such coordination could strengthen the contribution of wildlife surveillance to One Health risk assessment while supporting evidence-based interventions across human, animal, and environmental sectors [202].

RESEARCH DIRECTIONS AND RECOMMENDATIONS

Advancing research on wildlife-associated AMR requires an integrated, interdisciplinary approach that incorporates ecological, microbiological, epidemiological, and environmental perspectives within the One Health framework [199]. A major priority is developing coordinated surveillance systems that integrate data from humans, domestic animals, wildlife, and environmental sources [2]. Such systems could improve the identification of AMR distribution patterns, characterize ecological interfaces associated with microbial exchange, and support investigations of potential transmission pathways among host populations [203]. Integrating wildlife into surveillance is particularly important for highly mobile species that may encounter resistant microorganisms across multiple habitats and geographical regions [74].

Integrated and longitudinal AMR surveillance

Longitudinal studies involving multiple wildlife species and habitats are needed to characterize temporal and spatial variation in AMR occurrence [204]. Repeated sampling across seasons, geographical locations, and environmental conditions could help determine how migration, habitat modification, environmental contamination, and human activities influence the acquisition and persistence of resistant microorganisms. Such investigations should incorporate information on wildlife population characteristics, habitat use, antimicrobial

exposure, and environmental contamination. Combining longitudinal microbiological data with ecological observations may help distinguish transient bacterial carriage from persistent colonization and evaluate whether particular wildlife populations function as environmental indicators, potential reservoirs, or intermediate hosts in AMR circulation [205].

Genomic and metagenomic investigations

Advances in genomic sequencing, metagenomics, and resistome analysis offer opportunities to better characterize wildlife-associated AMR [206]. Whole-genome sequencing can identify resistance determinants, characterize bacterial lineages, and investigate genetic relationships among isolates recovered from wildlife, domestic animals, humans, and environmental samples [207]. Metagenomic approaches can also characterize resistance-associated genes in complex microbial communities, including microorganisms that conventional culture-based methods may not readily detect. Integrating genomic and metagenomic findings with phenotypic antimicrobial susceptibility testing may improve the interpretation of resistance patterns and the identification of potentially transferable genetic determinants [208].

However, detecting similar resistance genes or closely related bacterial isolates across host populations does not, by itself, establish transmission direction. Genomic findings should therefore be interpreted alongside epidemiological, ecological, and temporal information to strengthen investigations of potential microbial exchange.

Integration of wildlife movement and ecological data

Combining microbiological surveillance with wildlife tracking technologies, including global positioning system (GPS) devices and telemetry, may improve understanding of the relationships between animal movement and AMR distribution [209]. Movement data can show habitat use, migration routes, seasonal dispersal, and how often animals visit environments potentially contaminated with resistant microorganisms. Integrating these observations with microbiological findings and geographical information may support spatial analyses of wildlife exposure and identify locations where wildlife, livestock, and humans use shared environmental resources [210].

Such approaches may help prioritize surveillance in migration corridors, wetlands, agricultural landscapes, and habitats adjacent to human settlements [211]. Nevertheless, locations identified through movement-based models should be regarded as potential exposure or microbial exchange sites unless supported by direct microbiological evidence. Integrating tracking data with repeated environmental and animal sampling may improve the identification of ecologically relevant surveillance locations and inform targeted risk-mitigation strategies.

International collaboration and surveillance standardization

International cooperation is essential for investigating wildlife-associated AMR because many species, particularly migratory birds, move across national boundaries and connect geographically distant ecosystems [212]. Collaborative surveillance initiatives should prioritize standardized sampling procedures, harmonized antimicrobial susceptibility testing, consistent resistance gene characterization, and comparable reporting practices. Shared genomic and ecological datasets may improve the identification of geographical patterns and facilitate investigations of resistant microorganisms detected in different countries [213].

Cross-border research partnerships could also support coordinated surveillance along migration routes and within shared ecological regions. Integrating wildlife monitoring with existing human, veterinary, and environmental surveillance programs may improve the interpretation of regional AMR patterns and strengthen the evidence available for coordinated prevention and control strategies [214]. Such collaboration should account for differences in laboratory capacity, surveillance resources, wildlife ecology, and national research priorities. Beyond environmental surveillance, integrated approaches to animal and public health may also benefit from preventive food safety management and complementary investigations of biologically active compounds. Studies on microbial cross-contamination, plant-derived antioxidants, bioactive constituents, and processing-related changes in biological properties provide additional perspectives on food safety and preventive health strategies [215–218].

Priorities for future research

Future investigations should prioritize identifying wildlife species and ecological settings where resistant microorganisms persist, characterizing environmental exposure pathways, and evaluating potential transmission among wildlife, domestic animals, and humans. Particular attention should be given to distinguishing naturally

occurring resistance from resistance-associated with anthropogenic contamination and determining whether resistant microorganisms detected in wildlife represent transient carriage or sustained colonization.

Research should also evaluate the effectiveness of integrated surveillance approaches and targeted environmental or farm biosecurity interventions. Combining longitudinal sampling, genomic characterization, wildlife movement data, and environmental monitoring may provide stronger evidence to understand the ecological distribution of AMR and identify when microbial exchange occurs. These priorities could support more reliable risk assessments and strengthen the contribution of wildlife research to coordinated One Health strategies.

CONCLUSION

This review highlights the importance of wildlife in the ecological distribution and potential dissemination of AMR across natural and human-modified ecosystems. Wildlife may acquire and carry antimicrobial-resistant bacteria and resistance determinants through exposure to contaminated water, soil, food resources, and interactions with domestic animals and humans. Habitat characteristics, landscape fragmentation, feeding behavior, predator–prey relationships, and animal movement influence opportunities for microbial exposure and exchange. Local dispersal and long-distance migration may contribute to the geographical redistribution of resistant microorganisms, while environmental microbial communities provide opportunities for HGT. However, detecting resistant bacteria or resistance genes in wildlife does not, by itself, establish persistent reservoir status, transmission direction, or confirmed spillover to humans.

Wildlife-associated AMR affects public health, livestock production, environmental management, and biodiversity conservation. Integrating wildlife into One Health surveillance could improve understanding of resistance distribution across ecological interfaces and help identify environments where microbial exchange may occur. Practical priorities include reducing antimicrobial contamination of shared environments, improving livestock biosecurity, strengthening wastewater and waste management, and monitoring wildlife populations exposed to human-associated pollution. Coordinated surveillance involving public health authorities, veterinary services, environmental agencies, and wildlife researchers may support more comprehensive risk assessments and targeted preventive measures.

A principal strength of this review is its integrated consideration of wildlife ecology, movement dynamics, microbial resistance mechanisms, and potential transmission pathways within a One Health framework. By examining terrestrial, aquatic, and marine environments alongside interactions among wildlife, livestock, and humans, the review provides a broad perspective on the ecological processes associated with AMR circulation. It also emphasizes the distinction between bacterial carriage, environmental exposure, persistent colonization, and confirmed transmission, which is essential for interpreting the epidemiological significance of wildlife-associated resistance.

The available evidence varies substantially across wildlife species, geographic regions, sampling strategies, microbiological methods, and resistance-detection approaches, limiting direct comparisons among studies. Many investigations are cross-sectional or geographically restricted, providing limited information on temporal changes, long-term bacterial persistence, and transmission direction. Furthermore, the detection of similar resistance phenotypes or genetic determinants in wildlife, domestic animals, and humans does not necessarily demonstrate direct microbial exchange. As a narrative review, the present synthesis does not provide pooled prevalence estimates or a quantitative assessment of wildlife-associated transmission risks. These limitations should be considered when interpreting the ecological and public health significance of the available findings.

Future research should prioritize standardized, longitudinal surveillance across wildlife species, habitats, and geographical regions. Integrating phenotypic antimicrobial susceptibility testing with whole-genome sequencing, metagenomic analysis, environmental monitoring, and wildlife movement data may improve the characterization of resistance determinants and potential transmission pathways. Particular attention should focus on identifying conditions that support persistent bacterial colonization, distinguishing natural resistance from anthropogenic contamination, and evaluating microbial exchange at wildlife–livestock–human interfaces. International collaboration, harmonized surveillance protocols, and coordinated data sharing will improve the comparability of findings and strengthen evidence-based One Health interventions.

Wildlife represents an important but incompletely characterized component of AMR ecology. Its contribution to resistance dissemination depends on interactions among microbial characteristics, environmental contamination, animal behavior, and ecological connectivity. Although wildlife may transport resistant microorganisms between habitats, its role as a source of human or livestock infections requires stronger

epidemiological and molecular evidence. Incorporating wildlife ecology into integrated One Health research and surveillance, while avoiding unsupported assumptions about transmission, is essential for improving understanding of AMR circulation and supporting sustainable strategies to protect human, animal, and environmental health.

DATA AVAILABILITY

No new datasets were generated or analyzed during this study. All information discussed in this narrative review was obtained from previously published literature cited in the manuscript.

GENERATIVE AI DECLARATION

Generative artificial intelligence (AI) tools were used during manuscript preparation to assist with language editing, improving the clarity and readability of the text, and developing schematic illustrations. All AI-assisted text and visual materials were critically reviewed, revised, and verified by the authors. The authors take full responsibility for the accuracy, integrity, and final content of the manuscript and figures. Generative AI was not used to generate research data, perform data analysis, or independently formulate scientific conclusions.

AUTHORS' CONTRIBUTIONS

MHE, ARK, HP, and WT: Developed the review methodology and drafted the manuscript. BPP, DAAK, RZA, and IBM: Reviewed and edited the manuscript. BB, ANS, WW, and DAP: Contributed to manuscript preparation and critical review. IPN and NBA: Edited the figures and references. All authors have read and approved the final version of the manuscript.

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COMPETING INTERESTS

The authors declare that they have no competing interests.

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