Review

The Wildlife–Livestock Interface as a Bidirectional Pathway for the Spread of ESBL-Producing *Escherichia coli*

Margarita González-Martín , María Teresa Tejedor-Junco * , Nerea C. Rosales-González , Juan Alberto Corbera

Posted Date: 29 May 2026

doi: 10.20944/preprints202605.2038.v1

Keywords: ESBL-producing *Escherichia coli*; antimicrobial resistance; wildlife–livestock interface; One Health; wildlife; livestock; environmental reservoirs; genomic surveillance; biosecurity

 doi:10.20944/preprints202605.2038.v1

Review

The Wildlife–Livestock Interface as a Bidirectional Pathway for the Spread of ESBL-Producing *Escherichia coli*

Margarita González-Martín [1,2], María Teresa Tejedor-Junco [1,2,*], Nerea C. Rosales-González [3] and Juan Alberto Corbera [1,4]

[1] Research Institute of Biomedical and Health Sciences. University of Las Palmas de Gran Canaria. Paseo Blas Cabrera Felipe "Físico" s/n. 35016 Las Palmas de Gran Canaria. Canary Islands. Spain

[2] Clinical Sciences Department. University of Las Palmas de Gran Canaria. Paseo Blas Cabrera Felipe "Físico" s/n. 35016 Las Palmas de Gran Canaria. Canary Islands. Spain

[3] Servicio de Medicina Interna, Hospital Universitario de Gran Canaria Dr Negrín, C. Plaza Barranco de la Ballena, s/n, 35010 Las Palmas de Gran Canaria, Las Palmas de Gran Canaria. Canary Islands. Spain

[4] Hospital Clínico Veterinario. Facultad de Veterinaria. University of Las Palmas de Gran Canaria. Campus Universitario de Arucas, s/n. 35413 Arucas, Las Palmas. Canary Islands. Spain

* Correspondence: mariateresa.tejedor@ulpgc.es

Simple Summary

Antibiotic resistance is a growing problem that affects people, domestic animals, wildlife and the environment. One important example is *Escherichia coli*, a common gut bacterium that can acquire mechanisms allowing it to survive treatment with important antibiotics. Livestock may carry these resistant bacteria, but wildlife can also become exposed through contaminated water, soil, manure, farms, waste and other human-influenced environments. This review summarizes current knowledge on resistant *Escherichia coli* at the wildlife–livestock interface, with special attention to how these bacteria may move between farm animals, wild animals and the environment. The available evidence shows that transmission is not always one-way from livestock to wildlife or from animals to humans; rather, it is a complex and bidirectional process involving animals, people, food production systems and environmental reservoirs. Wildlife can act as a sentinel of environmental contamination and, in some cases, may contribute to the spread or reintroduction of resistant bacteria into farms. Understanding these connections is important for society because it can help improve surveillance, farm biosecurity, responsible antibiotic use and coordinated control measures to protect animal, human and environmental health.

Abstract

Antimicrobial resistance is a major global health challenge that requires a One Health approach integrating humans, animals, wildlife, food systems and the environment. Among resistant bacteria, extended-spectrum β-lactamase-producing *Escherichia coli* is particularly relevant because it is widely distributed across hosts and ecosystems, may carry mobile resistance genes and is commonly used as an indicator for antimicrobial resistance surveillance. This narrative review examines the occurrence, characteristics and transmission dynamics of ESBL-producing *E. coli* at the wildlife–livestock interface, with emphasis on its public health relevance and strategies for mitigation and control. The reviewed evidence indicates that livestock, wildlife and environmental matrices can be interconnected reservoirs of resistant *E. coli* and resistance genes. Transmission should not be interpreted as a simple linear process from livestock to wildlife or humans, but rather as a bidirectional and ecological phenomenon shaped by antimicrobial use, farm management, biosecurity, wildlife ecology, environmental contamination and mobile genetic elements. Wildlife may function as a sentinel, reservoir or disperser of resistant bacteria, although detection alone does not demonstrate direct transmission. Integrated surveillance combining livestock, wildlife, food-

 doi:10.20944/preprints202605.2038.v1

chain and environmental sampling, supported by genomic analysis, is essential to clarify transmission pathways and guide effective control measures.

Keywords: ESBL-producing *Escherichia coli*; antimicrobial resistance; wildlife–livestock interface; One Health; wildlife; livestock; environmental reservoirs; genomic surveillance; biosecurity

1. Introduction

Antimicrobial resistance (AMR) is a global problem that must be combated with a comprehensive "One Health" approach [1–3]. Infections caused by multidrug-resistant (MDR) bacteria have become a global health challenge.

Bacteria can transfer resistance genes horizontally, including between different species. The set of genes that confer resistance to one or more antibiotic families ("resistome") can be transferred between pathogenic and non-pathogenic bacteria in humans and animals (both domestic and wild), as well as with environmental bacteria [4–6]. This evolution toward multidrug resistance is the result of complex bacterial events involving mutations and gene transfers between species via mobile elements [7]. The increasing prevalence of MDR or extensively drug-resistant (XDR) bacteria reinforces the need to develop surveillance studies to detect and control these strains [8].

As indicated in the "WHO - Global Action Plan on Antimicrobial Resistance" [9], this problem represents a drain on the global economy, with economic losses due to reduced productivity caused by diseases (in both humans and animals) and increased treatment costs. Although not explicitly mentioned, it is clear that the increase in antibiotic resistance affects the achievement of sustainable development goals (SDGs). The increase in animal infections caused by antibiotic-resistant bacteria makes it difficult to build sustainable food production systems and, therefore, hinders the SDGs on health, poverty, food security and economic growth [10].

Wildlife has been identified as a driver of the spread of genes conferring resistance to clinically important antimicrobials [11–13]. Although theoretically wild animals are not exposed to clinically relevant antibiotics, the detection of MDR strains in wildlife is increasing considerably, reinforcing the need for studies focused on this issue [14,15]. Furthermore, monitoring these bacteria in wild animals has become an important surveillance tool, as it could reflect antimicrobial resistance in strains isolated from humans [16].

In recent years, increasing attention has been paid to multidrug-resistant Enterobacterales, particularly ESBL-producing, plasmid-mediated AmpC β-lactamase-producing and carbapenemase-producing strains, across clinical, community, animal and environmental settings [17–20]. Within this group, ESBL-producing *E. coli* has been proposed as a relevant and practical indicator for AMR surveillance [21].

The aim of this narrative review is to analyze the information on the incidence, characteristics and transmission dynamics of ESBL-producing *E. coli* between livestock and wildlife. The public health relevance of this interface and strategies for mitigation and control are also discussed. We highlight the need to address this issue from a One Health perspective.

2. ESBL-Producing *E. coli*

Escherichia coli is the bacterial species most frequently described in antibiotic resistance studies in wildlife [13]. Most animal species, as well as humans, carry *E. coli* in their intestinal tract. Most *E. coli* strains are commensals that inhabit the intestinal tract of humans and animals. However, *E. coli* also remains one of the most frequent causes of several common bacterial infections in humans and animals. In humans, it is an important opportunistic pathogen associated with severe sepsis and urinary tract infections, among other hospital-acquired infections [22].

In animals, *E. coli* can also cause various infections, with respiratory infections being particularly relevant in birds [22]. Vidal et al. [23] observed that *E. coli* was the most common microorganism

 doi:10.20944/preprints202605.2038.v1

recovered from necropsies of raptors with clinical signs of septicemia or respiratory disorders, finding MDR in 71% of *E. coli* isolates.

In livestock, infections caused by pathogenic strains of *E. coli* cause significant economic losses, affect animal welfare, and have repercussions for public health due to the transmission of certain serotypes to humans. In livestock, diseases associated with pathogenic *E. coli* include diarrhea in piglets, calves and lambs, urinary tract infections and mastitis [24–27].

β-Lactamases are bacterial enzymes capable of hydrolyzing the β-lactam ring of β-lactam antibiotics to render these compounds inactive [28]. To facilitate understanding of their structural, functional, and clinical relevance, β-lactamases are classified using two main schemes: the Ambler molecular classification [29,30] and the Bush–Jacoby–Medeiros (BJM) functional classification [31]. The latter system is particularly valuable in clinical microbiology, as it aids in predicting antimicrobial susceptibility and guiding therapeutic decisions.

The most epidemiologically significant enzymes in this context are extended-spectrum β-lactamases (ESBLs), which have become widely disseminated worldwide. These enzymes can hydrolyze penicillins, extended-spectrum cephalosporins and aztreonam. They are included in Group 2 in the BJM classification. Although ESBLs share common biochemical properties with regard to the hydrolysis of broad-spectrum beta-lactam antibiotics and inhibition by clavulanate, the genes encoding these enzymes are diverse in nature and can be grouped into several families. Table 1 summarizes the ESBL families described in *E. coli.*

The genetic flexibility and adaptability of *E. coli* to constantly changing environments allow it to acquire a large number of antimicrobial resistance mechanisms. CTX-M type beta-lactamases are the most frequently isolated ESBLs in Enterobacteriaceae species from human and animal samples [22,32,33].

There are several reasons for using ESBL-producing *E. coli* as a relevant and simple indicator for AMR surveillance. Among these, it is worth highlighting the possible connection between antibiotic use in farm animals and clinical cases in humans, and the correlation between interventions focused on decreasing the exposure to antibiotics in humans and animals and the decrease in occurrence of ESBL-producing *E. coli* [21]. In addition to this, ESBL-producing bacteria are resistant to critically important antimicrobials including most beta-lactams so treatment with last-line antimicrobials may be required.

Table 1. ESBL families described in *E. coli.*

ESBL Family	Nomenclature / Origin	Main characteristics in *Escherichia coli*	Reference
TEM	Derived from TEM-1 and TEM-2 β-lactamases ("Temoniera"). Common variants include TEM-3, TEM-10, TEM-52.	Class A ESBLs generated by point mutations. Hydrolyze penicillins and third-generation cephalosporins. Usually inhibited by clavulanic acid. Historically among the first ESBLs detected in *E. coli.*	[34]
SHV	"Sulfhydryl Variable". Common variants: SHV-2, SHV-5, SHV-12.	Class A ESBLs with mutations expanding activity toward cefotaxime and ceftazidime. Frequently plasmid-mediated and widely disseminated among Enterobacterales.	[35]
CTX-M	"Cefotaximase-Munich". Includes CTX-M-1, CTX-M-2, CTX-M-8, CTX-M-9, and CTX-M-25 groups.	Currently the predominant ESBL family worldwide in *E. coli*. Strong hydrolytic activity against cefotaxime. Associated with conjugative plasmids and community/hospital dissemination. Derived from chromosomal genes of *Kluyvera* spp.	[34,36]

 doi:10.20944/preprints202605.2038.v1

OXA	"Oxacillinases". Includes OXA-1, OXA-10, OXA-48 variants.	Class D β-lactamases. Some variants exhibit ESBL phenotype. Hydrolyze oxacillin and some cephalosporins. Less susceptible to inhibition by clavulanic acid.	[34,37]
PER	"*Pseudomonas* Extended Resistance". Example: PER-2.	Less common ESBLs in *E. coli*. Hydrolyze broad-spectrum cephalosporins. More frequently identified in *Pseudomonas aeruginosa* and *Acinetobacter* spp.	[34,38]
VEB	"Vietnam Extended-spectrum β-lactamase". Example: VEB-1.	Plasmid-mediated ESBLs able to hydrolyze third-generation cephalosporins and aztreonam. Occasionally reported in *E. coli.*	[34,39]
GES	"Guiana Extended Spectrum". Examples: GES-1, GES-5.	Some variants behave as ESBLs, while others evolved into carbapenemases. Frequently associated with mobile genetic elements and multidrug resistance.	[34,40]
BES	"Brazilian Extended Spectrum".	Rare ESBL family described in Enterobacterales. Confers resistance to broad-spectrum cephalosporins.	[34]
TLA	"Tlahuicas". Example: TLA-1.	Rare ESBL initially described in Latin America. Associated with transferable plasmids in Enterobacterales.	[34,39]
SFO	Derived from *Serratia fonticola*. Example: SFO-1.	Plasmid-mediated class A cefotaximase. Hydrolyzes broad-spectrum cephalosporins and often coexists with other resistance genes.	[34,41]
CMT	Complex mutant derived from TEM-1	TEM variants that are resistant to inhibition by clavulanate and sulbactam and also exhibit an ESBL phenotype.	[42]
BEL	Belgium extended β-lactamase. BEL-1 in *E. coli*	Preferentially hydrolyzes ceftazidime and aztreonam compared with cefotaxime.	[43]

3. ESBL-Producing *E. coli* in Wildlife

Antibiotic resistance can be a good indicator of human influence on wildlife exposure to bacteria. Animals in the wild can acquire these bacteria from treated water, farms, landfills, and other anthropogenically impacted environments [44–49].

ESBL-producing *E. coli* isolates have been reported in wildlife, particularly in wild birds [33,50–59].

The carcasses of domestic animals available in the field are essential as food for scavenging birds. However, they are also their main source of exposure to veterinary drugs, which could compromise their survival. The presence of antibiotics in carcasses of domestic animals that can be ingested by necrophagous birds can contribute to selecting antibiotic-resistant bacteria in their digestive tract [58,60–62].

These bacteria have also been described in other groups of wild animals. Among wild mammals, ESBL-producing *E. coli* isolates have been described in large carnivores, such as captive lion and tiger [63] and in mesocarnivores, such as the Iberian wolf [64,65], Iberian lynx [65,66], coyotes [67], raccoons [68,69] or foxes [11,70,71].

Wild ungulates and other ruminants, such as red deer, roe deer and buffalo, have been described as carriers of ESBL-producing *E. coli* [72–79]. They are frequently raised on farms or share pastures with domestic ruminants, which facilitates the transmission of microorganisms. These bacteria have been described also in isolates from captive camels (*Camelus dromedarius*) in Canary Islands [80].

 doi:10.20944/preprints202605.2038.v1

Wild boar (*Sus scrofa*) is considered the model animal species to study antimicrobial resistance at the WLI in Europe [81], probably due to its high population and the possible implications of contact with domestic pigs [65,76,79,82–87].

ESBL-producing *E. coli* have been found also in non-human primates like baboons, chimpanzees, green monkeys and gorillas [88–90].

Rodents have also been investigated as carriers of ESBL-producing *E. coli* and as potential reservoirs for livestock [91–97]. Prevalences found ranged from 1.5% to 5% and the rodent species most frequently cited was *Rattus norvegicus*.

Other small mammals, such as hedgehogs [53], coatis [98] and badgers [71] have also been described as reservoirs.

The presence of ESBL-producing *E. coli* in fecal samples of bats [65,99–102] is especially relevant due to the longevity of these animals, their ecological adaptability and ability for long distance flight. In addition to this, "guano" (bats' fecal material) is commonly used in agriculture as biofertilizer, raising public health concerns.

Regarding semi-aquatic or aquatic species, ESBL-producing *E. coli* have been described in wild fish from the Atlantic Ocean [103] and the Mediterranean Sea [104]. Also, these bacteria have been found in minks, otters and turtles [105–107]. An isolate of CTX-M-15 producing *E. coli* was obtained from a captive dolphin in Portugal [108].

4. ESBL-Producing *E. coli* in Livestock

In this review, the term "livestock" is mainly used to refer to domesticated farm animals, although poultry may be considered separately in some epidemiological and production contexts. In most countries, this category usually includes cattle, sheep, goats, pigs, horses and donkeys. In some countries, animal species like llama, alpaca, camel, buffalo, reindeer or yak for example, could be included in this description.

Given their public health implications, the presence of ESBL-producing bacteria in farm animals has been analyzed in several studies. In a recent review, prevalence of ESBL-producing *E. coli* in healthy food-producing animals in different countries was compared. With some exceptions (UK and The Netherlands), they found that prevalence was higher in pigs than in cattle. Some countries, like Thailand (37%), China (44%), Portugal (49%), Germany (62%) and, especially, Lebanon (98%) presented very high prevalences in pigs [22].

Other later studies show similar results. Song et al. [109] found marked differences in the prevalence of ESBL-producing *E. coli* between pigs (69.5%) and cattle (7%) in South Korea. Similarly, Miltgen et al. [110] describe a prevalence of 18.6% in swine but 1.6% in cattle in livestock from Reunion Island. Balázs et al. [111] also found a high prevalence (72%) in pigs in Hungary. However, in Guadeloupe island, Gruel et al. [112] found a higher prevalence (14.7%) in beef cattle than in pigs (7.3%), and Chai et al. [113] did not find any among swine isolates in Malaysia. In a study done in Italy, similar prevalences (29.4% and 27%) were found for cattle and pigs [114].

Studies in other livestock species are less frequent. Among sheep, pandemic blaCTX-M-8-Producing ST224 *E. coli* has been described in Brazil [115]. Benavides et al. [91] found a prevalence of 7.5% in sheep from small-scale farms in Chile. They studied also goats (n=6) and horses (n=60), but no ESBL-producing *E. coli* was detected. High differences between ESBL-producing *E. coli* prevalences in healthy cattle (17%) and sheep (1%) were found in Algeria [116]. In Portugal 5.5% of sheep was found to be ESBL-producing *E. coli* carriers [117]. In both sheep and goats from different farms in Tanzania, prevalences of 2.3% were found [118]. In Iran, goats harboring ESBL-producing *E. coli* isolates have also been described [119].

In samples from diarrheic lambs (n=21), Shi et al. [120] obtained 28 *E. coli* isolates, of which 53.6% were ESBL producers.

About 21% of carriers were observed among farm horses in Israel [121]. In Turkey, ESBL-producing *E. coli* isolates were found with high frequency (53.5%) in samples from racehorses [122].

 doi:10.20944/preprints202605.2038.v1

5. The Wildlife–Livestock Interface

The wildlife–livestock interface has been defined as "the physical spaces where wildlife and livestock species overlap in range and may interact, creating opportunities for direct or indirect contact that could result in pathogen transmission in either direction" [123]. Although this definition refers specifically to pathogen transmission, it is also applicable to the exchange of multidrug-resistant bacteria and antimicrobial resistance determinants. As previously highlighted, there is a marked imbalance between the large amount of data available on the prevalence of ESBL-producing *E. coli* in wildlife and livestock and the limited evidence regarding the actual transmission of these bacteria at the wildlife–livestock interface [7,67].

Several factors should be considered when assessing the risk of exchange of multidrug-resistant bacteria at this interface. These include the livestock species involved, the farming system, the wildlife species present in the geographic area, the type and frequency of contact between hosts, possible transmission routes, and the degree of human influence on the environment [124,125]. The definition of "wildlife" is also relevant, since different interpretations may modify the risk factors considered. According to the proposal by Jori et al. [126], wildlife would not include species that depend on humans for food or reproduction, such as feral animals, animals kept in zoological gardens or rehabilitation centers, or individuals dependent on supplementary feeding stations. Nevertheless, many studies on antimicrobial resistance in wildlife include precisely these situations, particularly when assessing the effects of anthropogenic pressure on resistant bacteria circulation [11,63,67,127].

Antimicrobial resistance in wildlife can be considered an indicator of human influence on ecosystems. Wild animals may acquire resistant bacteria from treated wastewater, farms, landfills, contaminated water bodies, agricultural environments or other anthropogenically impacted habitats [44–49]. Most publications on wild birds have focused on migratory, waterfowl or other highly mobile species [35,46,49,69]; however, urban-associated birds have also been investigated because of their public health relevance and their frequent exposure to anthropogenic sources of antimicrobial resistance [12,38,39,150].

Transmission of multidrug-resistant bacteria between wildlife and livestock may occur through several routes. Indirect transmission, through shared water sources, feed, pasture, soil, manure, fomites or contaminated environments, is generally considered the most common pathway [25,58,128]. Direct interactions between wildlife and livestock may also occur in some systems, although they are usually less frequent and more dependent on local ecological and management conditions [129,130]. In scavenging birds, carcasses of domestic animals available in the field constitute an important food resource, but they may also represent a source of exposure to veterinary drugs. The presence of antimicrobial residues in livestock carcasses consumed by necrophagous birds may contribute to the selection of resistant bacteria in their digestive tract, with possible implications for wildlife conservation and environmental dissemination of resistance [58,60–62].

Most available information on multidrug-resistant bacteria in wildlife is still based on prevalence studies. However, the detection of resistant bacteria in wild animals does not necessarily demonstrate their ability to transmit these microorganisms to livestock, humans or other wildlife species. Important knowledge gaps remain regarding whether these bacteria survive long enough in wild hosts or in the environment, and whether they are present at sufficient infectious doses to cause colonization or infection in other hosts. Future research should therefore assess the capacity of wildlife to disseminate resistant bacteria of relevance to livestock or public health, while also identifying where and how wild animals acquire these bacteria. This is essential both for limiting the spread of antimicrobial resistance and for reducing potential adverse effects on threatened wildlife populations [131].

Several studies have investigated the potential exchange of resistant *E. coli* and resistance determinants at the wildlife–livestock interface, although direct evidence of transmission remains scarce. Liu et al. [67] studied the genetic relatedness of ESBL-producing *E. coli* in wildlife and cattle sharing habitat using shotgun metagenomic sequencing. Although ESBL-producing bacteria were

 doi:10.20944/preprints202605.2038.v1

detected in feral swine, no direct evidence of transfer to grazing cattle was found. However, bacteria carrying other resistance genes, including genes conferring resistance to tetracyclines and macrolides, were present in both animal groups, suggesting that feral swine could theoretically contribute to the exchange of resistant bacteria or resistance determinants with cattle.

In South Africa, Van den Honert et al. [132] compared antimicrobial resistance patterns of *E. coli* isolates from co-grazing and non-co-grazing livestock and wildlife species. Their results suggested that antimicrobial-resistant *E. coli* and resistance genes may be exchanged between livestock and wildlife sharing grazing areas, although clear evidence of ESBL transmission was not demonstrated. Similarly, Kozak et al. [133] showed that wild small mammals trapped on farms were five times more likely to carry tetracycline-resistant *E. coli* than animals trapped in natural areas, supporting the influence of livestock-associated environments on wildlife exposure to resistant bacteria.

At the buffalo–cattle interface in Southern Africa, Mercat et al. [134] found differences in antimicrobial resistance among *E. coli* isolates from buffalo populations with and without contact with cattle. No resistant *E. coli* strains were isolated from buffalo without cattle contact, whereas resistance was detected in buffalo sharing areas with cattle. A narrow-spectrum beta-lactamase-producing *E. coli* isolate carrying TEM-1 was found in both cattle and the in-contact buffalo population. In contrast, Navarro-González et al. [135] found no correlation between antimicrobial resistance in *E. coli* isolated from free-ranging cattle and cohabiting wild ungulates, including Iberian ibex and wild boar, in a natural environment.

Other studies have highlighted the role of anthropogenic pressure in shaping bacterial exchange among humans, livestock and wildlife. In Uganda, Rwego et al. [136] analyzed *E. coli* transmission among mountain gorillas, livestock and humans. Gorillas living in anthropogenically influenced areas harbored *E. coli* strains genetically similar to those from livestock and humans, whereas isolates from gorillas that did not share habitat with humans or livestock were genetically distinct. Although ESBL production was not investigated, this study illustrates how human and livestock proximity may influence bacterial exchange in wildlife populations.

More recent genomic approaches have provided stronger evidence for local circulation of ESBL-producing *E. coli* among domestic and wild animals. Using whole-genome sequencing, Hayer et al. [137] studied ESBL-producing *E. coli* transmission dynamics in livestock, dogs and wild rodents in Chile. Nearly identical clones, carrying similar antimicrobial resistance genes, heavy metal resistance genes and virulence-associated genes, were detected in dogs, cattle and sheep from the same farm, as well as in a dog and a wild rodent from a nearby farm located approximately 15 km away. These findings support the possibility that resistant clones and plasmids may circulate among livestock, companion animals and wildlife in agricultural landscapes.

Overall, current evidence indicates that the wildlife–livestock interface can contribute to the circulation of multidrug-resistant bacteria and resistance determinants, but the magnitude and direction of transmission remain difficult to establish. Wildlife may act as a reservoir, spillover host, sentinel or disperser of antimicrobial resistance depending on the species, habitat, degree of human influence and type of contact with livestock. However, the mere detection of resistant bacteria in wildlife should not be interpreted as proof of effective transmission to livestock or humans. Future studies should move beyond prevalence data and combine simultaneous sampling of livestock, wildlife and environmental matrices with genomic analysis, ecological information and epidemiological modeling. Such integrated One Health approaches are needed to determine whether resistance dissemination at the wildlife–livestock interface occurs through clonal transmission, plasmid exchange, shared environmental contamination or broader anthropogenic pressure.

6. Public Health Implications

Although this review focuses on ESBL-producing E. coli, selected examples involving other antimicrobial-resistant bacteria are mentioned when they illustrate shared transmission routes, biosecurity challenges or One Health mechanisms relevant to the wildlife–livestock interface.

 doi:10.20944/preprints202605.2038.v1

6.1. Risks of Transmission to Humans Through Direct Contact or Food

The public health relevance of antimicrobial-resistant bacteria at the wildlife–livestock–human interface lies in their capacity to circulate among food-producing animals, humans and the environment [138]. Food-producing animals may contribute to the emergence, maintenance and dissemination of resistant bacteria, which can subsequently reach humans through contaminated food products, direct animal contact or environmental exposure [138]. In the case of ESBL-producing Escherichia coli, livestock and food products represent relevant sources of concern, as human exposure may occur through contact with colonized animals or through the consumption or handling of contaminated food [139]. Similarly, human colonization or infection with multidrug-resistant bacteria may occur through foods of animal origin, including meat, milk and eggs, as well as through direct contact with animals [140].

Occupationally exposed populations, such as farmers, farm workers and slaughterhouse personnel, are particularly relevant because resistant bacteria may circulate between animals, farm environments and humans. Although most evidence at this interface concerns ESBL-producing Enterobacterales, studies in pig production have also shown that livestock-associated resistant bacteria can be detected in animals, barn air, abattoir environments and farm workers. Schmithausen et al. reported livestock-associated methicillin-resistant Staphylococcus aureus (MRSA) in pigs, barn air and humans, while evidence for ESBL-producing Enterobacterales transmission from pigs to humans was less conclusive. These findings illustrate that farm and slaughterhouse environments may act as relevant interfaces for the dissemination of antimicrobial-resistant bacteria, including ESBL-producing E. coli [141].

Foodborne exposure is a major route by which resistant bacteria from animals may reach humans [140]. Although ESBL-producing E. coli is the focus of this review, other foodborne pathogens illustrate the public health relevance of this pathway. For example, multidrug-resistant ESBL-producing Salmonella enterica serovar Infantis has been epidemiologically linked to contaminated chicken meat and human infections, supporting the need for control measures at both livestock and food-chain levels [142].

The public health significance of ESBL-producing E. coli is further increased when these isolates also harbor resistance determinants against critically important antimicrobials, such as fluoroquinolones or colistin. The detection of mobile colistin resistance genes, including mcr, in bacteria from food-producing animals is particularly concerning because these determinants may be transferred between commensal E. coli and other foodborne bacteria [139,143].

Wildlife may contribute indirectly to human exposure by acting as a reservoir, sentinel or disperser of resistant bacteria across natural, livestock-associated and human-associated environments. Plaza-Rodríguez et al. [79] detected ESBL-/AmpC-producing E. coli in wild boars, roe deer, wild ducks and geese, although the overall prevalence of resistant bacteria in the selected wildlife species in Germany was low. Importantly, the authors cautioned that the carriage of resistant bacteria by wildlife does not necessarily demonstrate that wild animals are effective vehicles of transmission to humans or livestock. Nevertheless, wild birds may act as long-distance disseminators of resistant bacteria because of their migratory behavior and broad spatial range.

Brendecke et al. [144] identified ESBL-producing E. coli and Klebsiella pneumoniae in black-headed gulls, including high-risk E. coli lineages such as ST131, ST38 and ST58. The detection of strains combining antimicrobial resistance and virulence-associated genes in wildlife supports the inclusion of wild animal populations in One Health surveillance frameworks.

At the same time, transmission should not be interpreted as universally direct or unidirectional. Genomic One Health studies may identify shared resistance determinants or mobile genetic elements without demonstrating direct animal-to-human strain transmission. Nguyen et al. [145] reported distinct blaCTX-M-harboring E. coli strains and plasmids in food animals and humans with community-acquired urinary tract infections, suggesting the existence of evolutionary barriers to direct strain or plasmid transfer across host species. However, the same study identified common

 doi:10.20944/preprints202605.2038.v1

insertion sequence elements flanking blaCTX-M variants across different sample sources, supporting the potential dissemination of resistance genes within or between habitats.

Overall, current evidence indicates that humans may be exposed to antimicrobial-resistant and zoonotic bacteria through direct animal contact, animal-associated environments and contaminated foods. However, the relative contribution of each pathway depends on the bacterial species involved, the production system, hygiene and biosecurity standards, food-chain controls and local environmental conditions [139,145,146].

6.2. Public Health Implications and One Health Relevance of Antimicrobial Resistance

Antimicrobial resistance at the wildlife–livestock–human interface represents a major public health concern because resistant bacteria and mobile resistance determinants can circulate among humans, animals, food products and the environment [146]. This problem is no longer confined to healthcare settings, as ESBL-producing Enterobacteriaceae have increasingly been reported in the community, including in healthy humans, food-producing animals, companion animals, wildlife and environmental reservoirs [144,147,148].

Food-producing animals constitute important reservoirs of antimicrobial resistance, since ESBL-producing and multidrug-resistant E. coli have been repeatedly detected in cattle, pigs, poultry and their associated production environments [149]. The public health significance of these reservoirs is reinforced by the possibility that resistant bacteria may reach humans through direct contact with animals, contaminated food products or environmental pathways [150].

Foodborne exposure is particularly relevant because ESBL/AmpC-producing E. coli and Klebsiella pneumoniae can contaminate food products during production, slaughter and processing. The detection of ESBL/AmpC-producing bacteria in meat and vegetables, especially in broiler meat subsamples, supports the need to consider the food chain as an important route of human exposure [151].

Direct contact with animals and their environments also represents a relevant transmission pathway. ESBL-producing E. coli have been identified in livestock workers, and similar resistance genes or sequence types have been reported in humans and animals from farm settings [149]. Nevertheless, direct animal-to-human transmission should not be assumed in all cases. Some genomic One Health studies have identified distinct human and animal lineages despite the presence of shared resistance determinants, indicating that transmission dynamics may be complex and shaped by ecological, bacterial and host-related barriers [145].

Wildlife may contribute to the environmental ecology of antimicrobial resistance by acting as reservoirs, sentinels or dispersers of resistant bacteria across natural and human-associated ecosystems [79,149]. The detection of ESBL-producing E. coli and high-risk K. pneumoniae lineages in wild birds further supports the inclusion of wildlife in integrated antimicrobial resistance surveillance systems [144].

A One Health approach is therefore essential, because antimicrobial resistance emerges and disseminates through interconnected human, animal, food-production and environmental reservoirs. At the local scale, One Health surveillance enables the comparative analysis of resistant bacteria, resistance genes and mobile genetic elements from humans, animals, food products and environmental samples, thereby helping to identify possible transmission routes and shared sources [146,152]. At the global scale, this approach is equally important, as international travel, food trade and the movement of animals and goods may facilitate the transboundary dissemination of resistant bacteria, plasmids and resistance genes [151].

Mobile genetic elements play a central role in this process. Plasmids, integrons, transposons and insertion sequences can mobilize resistance genes, such as blaCTX-M, across bacterial populations, host species and ecological compartments [148]. Consequently, surveillance should not be limited to bacterial species alone, but should also include resistance genes, plasmid lineages and other mobile genetic elements that may link animal, human and environmental reservoirs [139,151].

 doi:10.20944/preprints202605.2038.v1

Overall, the available evidence supports integrated surveillance across livestock, wildlife, companion animals, food products, humans and environmental matrices as a core public health strategy [148]. Mitigation efforts should combine prudent antimicrobial use, improved hygiene and biosecurity, better sanitation, safe food-handling practices, environmental control and genomic surveillance within a coordinated One Health framework [139,151].

6.3. Potential of Wildlife as a Source of Reintroduction of Resistance into Controlled Environments

Wildlife may act as a potential source of reintroduction of antimicrobial-resistant bacteria into controlled or partially controlled environments, particularly when livestock, companion animals, wild animals and environmental matrices share water sources, soil, pasture, feed, manure or peri-farm spaces. This risk is especially relevant because, although wild animals are not usually exposed to antimicrobial treatment, they can acquire antimicrobial-resistant bacteria from contaminated environments and subsequently transfer them to livestock or other animals through direct or indirect contact [149].

External biosecurity in animal production is intended to prevent the introduction of pathogens from the surrounding environment through vectors such as humans, vehicles, companion animals, wild animals, rodents, water and feed [153]. Therefore, even in farms or facilities where antimicrobial use, cleaning and disinfection are strictly controlled, wildlife and environmental reservoirs may compromise biosecurity by reintroducing resistant bacteria or resistance genes from outside the managed system. The farm environment itself provides multiple interfaces for this process, as ESBL-producing E. coli have been reported in manure-amended soil, barn dust, feed mixers, animal feed, bedding material and water troughs. Wild birds are particularly relevant in this context because their mobility enables them to acquire resistant bacteria in anthropogenically impacted areas and disseminate them to farms, natural habitats or remote environments [149].

Fuentes-Castillo et al. provided genomic evidence that migratory and resident gulls in Patagonia can carry multidrug-resistant E. coli producing CTX-M-type ESBLs. In that study, gull isolates belonged to international E. coli sequence types ST295 and ST388 and carried clinically relevant blaCTX-M genes. Phylogenomic analysis clustered these gull isolates with E. coli strains from environmental, companion animal and livestock sources in the United States, suggesting the possible transhemispheric movement of international ESBL-producing clones along migratory routes [56].

Similarly, Brendecke et al. detected ESBL-producing E. coli and Klebsiella pneumoniae in black-headed gulls from German conservation islands, including strains phylogenetically related to isolates from humans, livestock, food and environmental sources. These findings support the concept that wild birds may connect anthropogenic and natural ecosystems and contribute to the long-distance dissemination of multidrug-resistant bacteria [144].

Hayer et al. provided direct local evidence that ESBL-producing E. coli can circulate among domestic and wild animals in agricultural settings. In their study in Chile, nearly identical ESBL-producing E. coli clones were identified in dogs, cattle or sheep from the same farm, as well as in a dog and a wild rodent living in close proximity. These findings support the possibility that wildlife and peri-domestic animals may participate in the maintenance and re-entry of resistant clones into farms after control measures have been implemented. The same study showed that dissemination across animal species may occur through both clonal transmission and plasmid spread, which is particularly relevant because plasmids can maintain and disseminate resistance genes even when bacterial lineages differ. The presence of clinically relevant lineages, such as ST410, ST58, ST88 and ST617, in animals without apparent signs of disease further indicates that resistant clones with pathogenic potential may circulate silently in animal populations [137].

Wildlife should therefore be considered in surveillance and control programs not only as a passive indicator of environmental contamination, but also as a potential ecological bridge for the reintroduction of resistance into livestock, companion animal or managed wildlife settings [154]. Nevertheless, the role of wildlife should not be overgeneralized, as the detection of resistant bacteria in wild animals does not, by itself, demonstrate efficient transmission to livestock or humans [79].

 doi:10.20944/preprints202605.2038.v1

For this reason, integrated One Health surveillance should combine wildlife sampling, livestock monitoring, environmental sampling and genomic analysis to determine whether reintroduction occurs through the movement of bacterial clones, plasmids or shared resistance genes [137].

From a control perspective, these findings support the reinforcement of perimeter biosecurity, restriction of wildlife access to feed and water, improved manure and waste management, systematic monitoring of rodents and wild birds, and the incorporation of wildlife into antimicrobial resistance surveillance programs [149].

7. Strategies for Mitigation and Control

7.1. Reduction of Antimicrobial Use in Livestock

Reducing antimicrobial use in livestock is a central component of AMR mitigation because antimicrobial use in food-producing animals is recognized as a significant contributor to the development and spread of resistant bacteria and resistance genes. The intensive use of antibiotics in food-producing animals can select resistant bacteria that may subsequently reach humans through food products, direct animal contact or environmental pathways. Antimicrobial use in livestock is not limited to therapeutic treatment, as antimicrobials may also be used for metaphylaxis, prophylaxis and growth promotion [138].

Inappropriate and excessive antimicrobial use is a recognized driver of AMR, and the use of antimicrobials for prophylaxis or growth promotion may also compensate for poor hygiene or suboptimal management conditions [154]. Therefore, reduction strategies should prioritize the elimination of unnecessary antimicrobial use while preserving appropriate therapeutic treatment when animal health and welfare require it [155]. The restriction of medically important antimicrobials for growth promotion is consistent with international recommendations aimed at reducing selection pressure in food-producing animals [154].

Within a One Health framework, reducing unnecessary antibiotic use in food-producing animals and restricting medically important antimicrobials are key measures to limit AMR dissemination across animal, human and environmental reservoirs [138]. Evidence reviewed by Olaru et al. indicates that interventions restricting antimicrobial use in animals can reduce the burden of AMR in animals and are likely to reduce AMR in humans [154]. However, reduction should not be interpreted only as a quantitative decrease in antimicrobial consumption, because antimicrobial stewardship also requires appropriate selection, dosage and duration of treatment. Antimicrobial stewardship in livestock should therefore promote evidence-based treatment, avoidance of unnecessary group medication, and limitation of prophylactic or growth-promoting uses [149].

The implementation of antibiotic-free or organic production systems may contribute to lower resistance to some antimicrobials, as Musa et al. observed lower levels of cefotaxime-, ceftazidime- and ciprofloxacin-resistant E. coli in organic broiler systems compared with conventional systems. Nevertheless, the same study found higher prevalence of tigecycline-, azithromycin- and gentamicin-resistant E. coli in organic samples, suggesting that reducing on-farm antimicrobial use does not fully prevent the occurrence of resistant bacteria. This finding supports the view that antimicrobial reduction must be accompanied by environmental control and production-chain monitoring, because external contamination may contribute to resistant strains even in systems with limited antimicrobial use [155].

Preventive strategies that reduce disease pressure are also needed, since poor biosecurity, low vaccination coverage and inadequate nutrition can favor disease outbreaks and increase reliance on preventive antibiotic use [140].

Subramanya et al. recommend immunization, public awareness and education, improved hygiene standards, antibiotic stewardship, genomic surveillance, reduced antibiotic use in agriculture and livestock, and good husbandry practices as part of AMR mitigation [148].

Alternative approaches such as prebiotics, probiotics, phage therapy, vaccines, antimicrobial peptides and antimicrobial polymers may help reduce dependence on antibiotics, although their

 doi:10.20944/preprints202605.2038.v1

effectiveness has not yet been fully evaluated. Consequently, these alternatives should be incorporated cautiously as part of broader prevention programs rather than presented as universally validated replacements for antibiotics [149].

Reliable antimicrobial-use data are also essential, because current estimates of antimicrobial consumption in animals remain uncertain and are affected by limited standardization across studies and countries. For this reason, antimicrobial reduction policies should include farm-level recording systems, monitoring of veterinary prescriptions and integration of antimicrobial-use data with AMR surveillance [154].

At the environmental level, reducing antibiotic use in animals is also relevant because antimicrobial residues and resistant bacteria can enter soil and water through animal waste and food-production systems. Martak et al. identify reducing antibiotic use in humans and animals, regulating antibiotic distribution, and prioritizing less environmentally persistent antibiotics as key levers to reduce AMR in environmental reservoirs [146].

Overall, reduction of antimicrobial use in livestock should be framed as an integrated One Health intervention combining prudent use, restriction of non-essential indications, disease prevention, improved husbandry, vaccination, environmental management and continuous surveillance [148].

7.2. Biosecurity Measures on Farms

Farm biosecurity is a key component of AMR mitigation because it reduces the introduction, persistence and spread of infectious agents within and between animal populations, thereby decreasing the need for therapeutic or prophylactic antimicrobial use. At farm level, infection control through biosecurity and disease-control programs is particularly relevant in intensive food-animal industries, especially poultry and swine production. However, the direct effectiveness of these programs in limiting antimicrobial resistance, particularly in non-pathogenic bacteria, is rarely evaluated, and this limitation should be acknowledged when interpreting biosecurity as an AMR-control measure [152].

Biosecurity measures should therefore be framed not as a stand-alone intervention, but as part of an integrated prevention strategy combining herd health, hygiene, environmental management, prudent antimicrobial use and surveillance. Established veterinary approaches to reduce infectious disease include improved husbandry, quarantine, biosecurity measures, vaccination, vector control, antiseptic practices and competitive-exclusion strategies. These interventions are relevant to AMR control because prevention of viral and bacterial disease can reduce secondary bacterial infections and decrease the need for antimicrobial therapy [152].

External biosecurity should aim to prevent the entry of resistant bacteria into farms through animals, people, vehicles, feed, water, wildlife, rodents, birds, insects and contaminated environmental matrices [156].

Internal biosecurity should limit the dissemination of resistant bacteria between groups of animals, pens, houses and production stages within the same farm. All-in, all-out management can help maintain physical separation between successive animal groups and reduce the dissemination of resistant bacteria and their resident microbiota [152].

Effective cleaning and disinfection of barns, pens and production sites after depopulation are additional measures to control infectious diseases and reduce pathogen spread. Specific measures described for preventing the introduction and spread of Salmonella include restricting farm access, requiring visitors to change clothing and boots, controlling birds and rodents, using Salmonella-free feed and applying disinfectant footbaths [152].

Environmental hygiene within the farm is also essential, because ESBL-producing E. coli have been detected in manure-amended soil, barn dust, feed mixers, animal feed, bedding and water troughs. The detection of resistant bacteria in these matrices supports the inclusion of manure management, dust control, water hygiene, feed hygiene and bedding management in farm biosecurity plans. The farm environment should be considered a potential reservoir and transmission

 doi:10.20944/preprints202605.2038.v1

interface, since ESBL-producing bacteria and resistance genes can move through manure, soil, water, air, wildlife and farm workers. Wildlife control is relevant because wild animals may acquire resistant bacteria from contaminated environments and transfer them to livestock through shared resources such as pasture, water or soil. Wild birds, rodents and flies should be considered in biosecurity planning because they may act as carriers or mechanical vectors of ESBL-producing bacteria in livestock-associated environments. This is particularly important in open or semi-open production systems, where contact between livestock, wildlife, insects and environmental reservoirs is more difficult to prevent [149].

Water and waste management are also central to farm biosecurity, as resistant microorganisms and ARGs may enter soil, air, water and sediments through agricultural waste, manure, wastewater and other environmental hotspots. Consequently, AMR-oriented biosecurity should include safe manure storage and treatment, prevention of runoff, protection of drinking-water sources and control of wastewater contamination [157].

For MRSA and other resistant staphylococci, general hygiene, infection-control routines, environmental disinfection, isolation and treatment of infected animals, and hygienic handling of milk and meat products are recommended control measures. Food-chain hygiene, including control measures during slaughter, processing and handling, is also relevant to reduce contamination with ESBL-producing E. coli and other antimicrobial-resistant bacteria [158].

The relevance of such measures is reinforced by the fact that MRSA is no longer an exclusively hospital-associated problem, as community-associated and livestock-associated MRSA lineages are also recognized [159].

Companion animals and peri-farm animals should not be ignored, because livestock-associated MRSA lineages have been detected in pets even without direct contact with livestock [147].

Biosecurity measures should also be linked to antimicrobial stewardship, because preventing disease reduces the need for routine prophylaxis, metaphylaxis and group antimicrobial treatments [152]. Lee et al. specifically indicate that improved farm hygiene and biosecurity may decrease the prevalence and concentration of antimicrobial-resistant microorganisms in livestock. Examples of farm-management practices associated with lower detection of resistant microorganisms include frequent cleaning of drinking-water troughs, quarantine programs and appropriate disposal of dead animals [149].

Nevertheless, disinfection practices should be used carefully because antimicrobial resistance genes and quaternary ammonium compound resistance genes may be genetically linked. This means that biosecurity should rely on well-designed hygiene protocols, rather than indiscriminate or excessive use of disinfectants [152].

Overall, biosecurity in livestock farms should combine controlled animal movements, visitor and vehicle management, quarantine, all-in/all-out systems, cleaning and disinfection, pest and wildlife control, feed and water hygiene, manure management, isolation of infected animals and integrated AMR monitoring [149,152].

7.3. Importance of Integrated Surveillance Across Livestock, Wildlife and the Environment

Integrated surveillance is essential for AMR mitigation because resistant bacteria and resistance determinants circulate across livestock, wildlife, food, humans and environmental compartments. From a One Health perspective, surveillance should not be restricted to clinical settings, but should also include farms, veterinary clinics, food products and environmental matrices such as wildlife, soil and water. Such surveillance is necessary to estimate the magnitude, distribution patterns and health burden of AMR at national, regional and international levels. It is also needed to detect emerging resistance trends of clinical relevance for humans and animals, guide antimicrobial-use policies and evaluate the effectiveness of control interventions [160].

At the local level, One Health surveillance should assess the genetic relatedness of antibiotic-resistant bacteria, resistance genes and mobile genetic elements isolated from humans, animals, food products and the environment. This approach makes it possible to distinguish between potential

 doi:10.20944/preprints202605.2038.v1

bacterial transmission and the dissemination of resistance determinants through genetic exchange. Environmental surveillance is particularly important because the environment can act both as a reservoir of resistance genes and as a niche in which antimicrobial resistance may emerge, persist and disseminate under anthropogenic pressure [146].

In livestock systems, surveillance should identify critical control points at which resistant microorganisms are likely to be transmitted between animals and the environment. Lee et al. emphasized that transmission rates through different vehicles or sources should be quantified and incorporated into transmission models to assess risks at the interface level. Integrated AMR surveillance should therefore combine microbiological isolation, antimicrobial susceptibility testing, molecular typing, genomic analysis, ecological data and epidemiological modelling [149].

Wildlife should be included because wild animals can act as bioindicators or sentinels of resistant bacteria present in the environment. Plaza-Rodríguez et al. found that, even when the overall prevalence of resistant bacteria in selected wild animals was low, wildlife isolates reflected resistance traits to high-priority substances such as third-generation cephalosporins, fluoroquinolones and colistin. Continuous monitoring of AMR in wildlife by selective isolation is therefore advisable, particularly when resistance to critically important antimicrobials may occur at low prevalence. However, the detection of resistant bacteria in wildlife should not automatically be interpreted as evidence that wild animals are efficient vehicles of transmission to livestock or humans. Surveillance programs should therefore be designed to determine whether wildlife acts as a reservoir, sentinel, spillover host or active disperser of AMR. Standardization and harmonization of sampling strategies, laboratory methods and antimicrobial susceptibility interpretation are also required to enable meaningful comparisons of wildlife AMR data between countries [79].

Highly mobile wildlife species deserve particular attention because birds and bats may disseminate resistant bacteria over long distances [154]. Genomic surveillance of wild birds can provide evidence of long-range dissemination. For example, Fuentes-Castillo et al. identified ESBL-producing E. coli ST295 and ST388 carrying clinically relevant blaCTX-M genes in migratory and resident gulls from Patagonia. The phylogenomic clustering of these gull isolates with strains from environmental, companion animal and livestock sources supports the value of wildlife genomic surveillance for detecting international AMR dissemination routes [56].

Local simultaneous sampling is also important, because studies restricted to a single population or broad spatial comparisons may fail to detect cross-species transmission at the farm interface. Hayer et al. showed that nearly identical ESBL-producing E. coli clones were present in dogs, cattle or sheep from the same farm, as well as in a dog and a wild rodent living in close proximity. These findings support the inclusion of livestock, dogs, peri-domestic animals and wildlife in farm-level AMR surveillance. The same study also showed that AMR spread across animal species may occur through both clonal transmission and plasmid dissemination [137].

Food-chain surveillance should also be integrated, because globally traded food products can carry ESBL/AmpC-producing E. coli and Klebsiella pneumoniae harboring multidrug resistance genes and potentially epidemic plasmids. Kurittu et al. reported similarities between food-derived plasmids and plasmids previously recovered from livestock-associated and human clinical sources from different countries. These findings support the need for One Health surveillance systems that include not only livestock and wildlife, but also food products and international trade pathways [151].

Human, animal and environmental sampling should be interpreted jointly. Subramanya et al. detected ESBL-producing Enterobacteriaceae in farmers, children, livestock and environmental samples in rural Nepal. The predominance of blaCTX-M-15 in human and animal isolates in that study illustrates the value of integrated molecular surveillance in rural farming communities [148].

Genomic surveillance is particularly useful because it can clarify whether resistance dissemination reflects direct clonal transmission, plasmid exchange or the spread of shared mobile genetic elements. Nguyen et al. illustrate this point, as their One Health surveillance study in Vietnam did not support direct food-animal-to-human transmission of blaCTX-M-harboring E. coli strains or plasmids, but did identify common genetic elements across habitats. This type of evidence helps

 doi:10.20944/preprints202605.2038.v1

avoid overinterpretation of animal-to-human transmission while still recognizing the importance of shared resistance determinants across reservoirs [145].

Properly designed monitoring programs are required to generate reliable data, including appropriate selection of sentinel organisms, sampling strategies, culture methods and antimicrobial susceptibility testing protocols. Lack of standardization may lead to misinterpretation, underreporting or unnecessary responses, with potential consequences for both animal and public health. Overall, integrated surveillance across livestock, wildlife and the environment should be considered a core mitigation tool, as it enables the identification of reservoirs, detection of emerging resistance, clarification of transmission pathways, implementation of targeted biosecurity measures and evaluation of antimicrobial-use reduction policies [152,160].

8. Conclusions and Future Perspectives

Antimicrobial resistance at the wildlife–livestock–human interface should be understood as a dynamic and bidirectional process rather than as a linear pathway from livestock to humans [149,157]. Resistant bacteria, resistance genes and mobile genetic elements may circulate among food-producing animals, wildlife, humans, food products and environmental matrices, and interventions implemented in one sector may influence the others [146,149,152].

This bidirectionality is particularly relevant because wildlife can acquire antimicrobial-resistant bacteria from contaminated environments and may subsequently transfer them to livestock. Conversely, livestock-associated bacteria and resistance determinants may reach wildlife through shared water sources, soil, pasture, manure or peri-farm habitats [149]. Evidence of both clonal and plasmid-mediated circulation of ESBL-producing E. coli among livestock, dogs and wildlife in agricultural settings reinforces the need to consider domestic animals, peri-domestic species and wildlife as interconnected components of the same epidemiological system [137].

However, the detection of resistant bacteria or shared resistance determinants in different reservoirs should not be automatically interpreted as evidence of direct transmission. Genomic studies may identify shared mobile genetic elements without demonstrating direct animal-to-human or wildlife-to-livestock strain transfer [145]. Future studies should therefore move beyond prevalence-based approaches and integrate epidemiological, ecological and genomic data to distinguish between clonal transmission, plasmid dissemination and broader environmental circulation of resistance genes [56,145,149].

The One Health approach provides the most appropriate framework for addressing this challenge, as it explicitly connects human health, animal health, wildlife, food systems and environmental quality [155]. Interdisciplinary research involving veterinarians, microbiologists, ecologists, epidemiologists, environmental scientists, food-safety specialists and public-health authorities is needed to understand how antimicrobial resistance emerges, persists and spreads across these interconnected reservoirs [146,155]. Such an approach is essential because the drivers of antimicrobial resistance include antimicrobial use in humans and animals, infection-control practices, farming systems, waste management, sanitation, environmental contamination, wildlife ecology and food-chain dynamics [146,149,155,157].

Future monitoring programs should combine livestock sampling, wildlife surveillance, food-chain monitoring and environmental sampling of water, soil, manure, wastewater and farm-associated matrices [149,151,155]. Surveillance should not focus solely on bacterial species, but should also include antimicrobial susceptibility profiles, resistance genes, plasmids, insertion sequences, transposons and other mobile genetic elements that may link different reservoirs [145,151,155]. Whole-genome sequencing and, when feasible, long-read or hybrid sequencing approaches should be prioritized because they can clarify whether resistance dissemination is driven by bacterial clones, epidemic plasmids or shared genetic platforms [56,145,151,153].

Wildlife should be incorporated into AMR monitoring programs as a potential reservoir, sentinel or disperser of resistant bacteria, particularly in species with high mobility, close contact with livestock or frequent exposure to anthropogenic environments [79,149,153]. Selective isolation may

 doi:10.20944/preprints202605.2038.v1

be especially useful in wildlife surveillance when the expected prevalence of resistant bacteria is low but resistance to critically important antimicrobials, such as third-generation cephalosporins, fluoroquinolones or colistin, is of particular concern [79]. Local and simultaneous sampling of livestock, companion animals, wildlife and the farm environment should also be encouraged, as broad spatial comparisons or studies restricted to a single population may miss transmission events occurring at farm level [56].

Monitoring programs should also collect data on antimicrobial use, animal movements, farm hygiene, biosecurity practices, manure management, water sources, wildlife access and food-production practices, because these variables are necessary to identify critical control points [149,155,160]. Control programs should combine prudent antimicrobial use, reduction of unnecessary prophylactic and growth-promoting uses, improved husbandry, vaccination, farm biosecurity, hygiene, pest and wildlife control, safe manure management and protection of water sources [149,155,160].

The effectiveness of these interventions should be evaluated through continuous surveillance, because antimicrobial resistance may persist or re-enter controlled systems through environmental reservoirs, mobile genetic elements, wildlife, food products or animal movements [56,149,151,155]. Standardized sampling strategies, harmonized laboratory methods and comparable antimicrobial susceptibility interpretation criteria are essential to generate reliable data and avoid underreporting, misinterpretation or disproportionate responses [79,155,160].

In conclusion, recognizing the bidirectional and ecological nature of antimicrobial resistance is essential for designing effective mitigation strategies at the livestock–wildlife–environment interface [149,155]. Future policies should prioritize integrated One Health surveillance, genomic epidemiology, environmental risk assessment and targeted farm-level interventions to reduce the emergence, persistence and reintroduction of resistant bacteria in animal production systems [56,149,155,160].

Author Contributions: Conceptualization, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; methodology, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; validation, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; formal analysis, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; investigation, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; resources, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; writing—original draft preparation, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; writing—review and editing, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; visualization, M.G.M., M.T.T.J., N.C.R.G. and J.A.C.; supervision, M.G.M., M.T.T.J., N.C.R.G. and J.A.C. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding

Institutional Review Board Statement: Not applicable

Informed Consent Statement: Not applicable.

Data Availability Statement: No new data were generated or analyzed in this study. Data sharing is not applicable to this article.

Acknowledgments: The authors have reviewed and edited the output and take full responsibility for the content of this publication.

Conflicts of Interest: The authors declare no conflicts of interest.

References

1. Meier, H.; Spinner, K.; Crump, L.; Kuenzli, E.; Schuepbach, G.; Zinsstag, J. State of Knowledge on the Acquisition, Diversity, Interspecies Attribution and Spread of Antimicrobial Resistance between Humans, Animals and the Environment: A Systematic Review. *Antibiotics* **2022**, *12*, 73, doi:10.3390/antibiotics12010073.

 doi:10.20944/preprints202605.2038.v1

2. Robinson, T.P.; Bu, D.P.; Carrique-Mas, J.; Fèvre, E.M.; Gilbert, M.; Grace, D.; Hay, S.I.; Jiwakanon, J.; Kakkar, M.; Kariuki, S.; et al. Antibiotic Resistance Is the Quintessential One Health Issue. *Trans. R. Soc. Trop. Med. Hyg.* **2016**, *110*, 377–380, doi:10.1093/trstmh/trw048.
3. Torres, R.T.; Carvalho, J.; Cunha, M. V.; Serrano, E.; Palmeira, J.D.; Fonseca, C. Temporal and Geographical Research Trends of Antimicrobial Resistance in Wildlife - A Bibliometric Analysis. *One Health* **2020**, *11*, 100198, doi:10.1016/j.onehlt.2020.100198.
4. Bueno, I.; Williams-Nguyen, J.; Hwang, H.; Sargeant, J.M.; Nault, A.J.; Singer, R.S. Impact of Point Sources on Antibiotic Resistance Genes in the Natural Environment: A Systematic Review of the Evidence. *Anim. Health Res. Rev.* **2017**, *18*, 112–127, doi:10.1017/S146625231700007X.
5. Dolejska, M.; Literak, I. Wildlife Is Overlooked in the Epidemiology of Medically Important Antibiotic-Resistant Bacteria. *Antimicrob. Agents Chemother.* **2019**, *63*, doi:10.1128/AAC.01167-19.
6. Huijbers, P.M.C.; Blaak, H.; De Jong, M.C.M.; Graat, E.A.M.; Vandenbroucke-Grauls, C.M.J.E.; De Roda Husman, A.M. Role of the Environment in the Transmission of Antimicrobial Resistance to Humans: A Review. *Environ. Sci. Technol.* **2015**, *49*, 11993–12004, doi:10.1021/acs.est.5b02566.
7. Tseng, C.-H.; Liu, C.-W.; Liu, P.-Y. Extended-Spectrum β-Lactamases (ESBL) Producing Bacteria in Animals. *Antibiotics* **2023**, *12*, 661, doi:10.3390/antibiotics12040661.
8. Magiorakos, A.P.; Srinivasan, A.; Carey, R.B.; Carmeli, Y.; Falagas, M.E.; Giske, C.G.; Harbarth, S.; Hindler, J.F.; Kahlmeter, G.; Olsson-Liljequist, B.; et al. Multidrug-Resistant, Extensively Drug-Resistant and Pandrug-Resistant Bacteria: An International Expert Proposal for Interim Standard Definitions for Acquired Resistance. *Clinical Microbiology and Infection* **2012**, *18*, 268–281, doi:10.1111/j.1469-0691.2011.03570.x.
9. WHO *Global Action Plan on Antimicrobial Resistance*; WHO Document Production Services, Ed.; Library Cataloguing-in-Publication Data: Geneva, 2016;
10. WHO *Monitoring and Evaluation of the Global Action Plan on Antimicrobial Resistance*; Geneve, 2019;
11. Haenni, M.; Métayer, V.; Jarry, R.; Drapeau, A.; Puech, M.P.; Madec, J.Y.; Keck, N. Wide Spread of BlaCTX–M–9/Mcr-9 IncHI2/ST1 Plasmids and CTX-M-9-Producing *Escherichia coli* and *Enterobacter cloacae* in Rescued Wild Animals. *Front. Microbiol.* **2020**, *11*, doi:10.3389/fmicb.2020.601317.
12. Mukerji, S.; Stegger, M.; Truswell, A.V.; Laird, T.; Jordan, D.; Abraham, R.J.; Harb, A.; Barton, M.; O'Dea, M.; Abraham, S. Resistance to Critically Important Antimicrobials in Australian Silver Gulls (*Chroicocephalus novaehollandiae*) and Evidence of Anthropogenic Origins. *Journal of Antimicrobial Chemotherapy* **2019**, *74*, 2566–2574, doi:10.1093/jac/dkz242.
13. Wang, J.; Ma, Z.-B.; Zeng, Z.-L.; Yang, X.-W.; Huang, Y.; Liu, J.-H. The Role of Wildlife (Wild Birds) in the Global Transmission of Antimicrobial Resistance Genes. *Zool. Res.* **2017**, *38*, 55–80, doi:10.24272/j.issn.2095-8137.2017.003.
14. Gambino, D.; Vicari, D.; Vitale, M.; Schirò, G.; Mira, F.; Giglia, M. La; Riccardi, A.; Gentile, A.; Giardina, S.; Carrozzo, A.; et al. Microorganisms Study on Bacteria Isolates and Antimicrobial Resistance in Wildlife in Sicily, Southern Italy. **2021**, doi:10.3390/microorganisms.
15. Kimani, T.; Kiambi, S.; Eckford, S.; Njuguna, J.; Makonnen, Y.; Rugulema, G.; Morzaria, S.P.; Lubroth, J.; Fasina, F.O. Expanding beyond Zoonoses: The Benefits of a National One Health Coordination Mechanism to Address Antimicrobial Resistance and Other Shared Health Threats at the Human–Animal–Environment Interface in Kenya. *Revue Scientifique et Technique de l'OIE* **2019**, *38*, 155–171, doi:10.20506/rst.38.1.2950.
16. Lagerstrom, K.M.; Hadly, E.A. The Under-Investigated Wild Side of Escherichia Coli: Genetic Diversity, Pathogenicity and Antimicrobial Resistance in Wild Animals. *Proceedings of the Royal Society B: Biological Sciences* 2021, *288*.
17. Cañada-García, J.E.; Moure, Z.; Sola-Campoy, P.J.; Delgado-Valverde, M.; Cano, M.E.; Gijón, D.; González, M.; Gracia-Ahufinger, I.; Larrosa, N.; Mulet, X.; et al. CARB-ES-19 Multicenter Study of Carbapenemase-Producing *Klebsiella pneumoniae* and *Escherichia coli* From All Spanish Provinces Reveals Interregional Spread of High-Risk Clones Such as ST307/OXA-48 and ST512/KPC-3. *Front. Microbiol.* **2022**, *13*, doi:10.3389/fmicb.2022.918362.
18. ECDC *Carbapenem-Resistant Enterobacteriaceae, Second Update*; Stockholm, 2019;

 doi:10.20944/preprints202605.2038.v1

19. ECDC *Increase in Escherichia Coli Isolates Carrying BlaNDM-5 in the European Union/European Economic Area, 2012–2022*; Stockholm, 2023;
20. Suay-García, B.; Pérez-Gracia, M.T. Present and Future of Carbapenem-Resistant Enterobacteriaceae (CRE) Infections. *Antibiotics* **2019**, *8*, 122, doi:10.3390/antibiotics8030122.
21. WHO *WHO Integrated Global Surveillance on ESBL-Producing E. Coli Using a One Health Approach: Implementation and Opportunities*; World Health Organization: Geneva, 2021;
22. Ramos, S.; Silva, V.; de Lurdes Enes Dapkevicius, M.; Caniça, M.; Tejedor-Junco, M.T.; Igrejas, G.; Poeta, P. *Escherichia coli* as Commensal and Pathogenic Bacteria among Food-Producing Animals: Health Implications of Extended Spectrum β-Lactamase (ESBL) Production. *Animals* **2020**, *10*, 1–15, doi:10.3390/ani10122239.
23. Vidal, A.; Baldomà, L.; Molina-López, R.A.; Martin, M.; Darwich, L. Microbiological Diagnosis and Antimicrobial Sensitivity Profiles in Diseased Free-Living Raptors. *Avian Pathology* **2017**, *46*, 442–450, doi:10.1080/03079457.2017.1304529.
24. Awad, W.S.; El-Sayed, A.A.; Mohammed, F.F.; Bakry, N.M.; Abdou, N.-E.M.I.; Kamel, M.S. Molecular Characterization of Pathogenic *Escherichia coli* Isolated from Diarrheic and In-Contact Cattle and Buffalo Calves. *Trop. Anim. Health Prod.* **2020**, *52*, 3173–3185, doi:10.1007/s11250-020-02343-1.
25. Fahim, K.M.; Ismael, E.; Khalefa, H.S.; Farag, H.S.; Hamza, D.A. Isolation and Characterization of *E. coli* Strains Causing Intramammary Infections from Dairy Animals and Wild Birds. *Int. J. Vet. Sci. Med.* **2019**, *7*, 61–70, doi:10.1080/23144599.2019.1691378.
26. Roussel, P.; Porcherie, A.; Répérant-Ferter, M.; Cunha, P.; Gitton, C.; Rainard, P.; Germon, P. *Escherichia coli* Mastitis Strains: In Vitro Phenotypes and Severity of Infection in Vivo. *PLoS One* **2017**, *12*, doi:10.1371/journal.pone.0178285.
27. Yadav, A.; Kumar, T.; Khohal, D.; Bagri, P.; Kumar, A.; Sindhu, N.; Joshi, V.G.; Jangir, B.L. Comprehensive Analysis of *Escherichia coli* in Bovine Urinary Tract Infections: Serotypes, Antibiotic Resistance, and Virulence Gene Profiles. *Sci. Rep.* **2025**, *15*, doi:10.1038/s41598-025-26316-2.
28. Bush, K. Past and Present Perspectives on β-Lactamases. *Antimicrob. Agents Chemother.* **2018**, *62*, doi:10.1128/AAC.01076-18.
29. Bush, K.; Jacoby, G.A. Updated Functional Classification of β-Lactamases. *Antimicrob. Agents Chemother.* **2010**, *54*, 969–976, doi:10.1128/AAC.01009-09.
30. Sawa, T.; Kooguchi, K.; Moriyama, K. Molecular Diversity of Extended-Spectrum β-Lactamases and Carbapenemases, and Antimicrobial Resistance. *J. Intensive Care* **2020**, *8*, 13, doi:10.1186/s40560-020-0429-6.
31. Bush, K.; Jacoby, G.A.; Medeiros, A.A. A Functional Classification Scheme for β-Lactamases and Its Correlation with Molecular Structure. *Antimicrob. Agents Chemother.* **1995**, *39*, 1211–1233, doi:10.1128/AAC.39.6.1211.
32. Carvalho, I.; Carvalho, J.A.; Martínez-álvarez, S.; Sadi, M.; Capita, R.; Alonso-Calleja, C.; Rabbi, F.; Dapkevicius, M. de L.N.E.; Igrejas, G.; Torres, C.; et al. Characterization of ESBL-Producing *Escherichia coli* and *Klebsiella pneumoniae* Isolated from Clinical Samples in a Northern Portuguese Hospital: Predominance of Ctx-m-15 and High Genetic Diversity. *Microorganisms* **2021**, *9*, doi:10.3390/microorganisms9091914.
33. Cristóvão, F.; Alonso, C.A.; Igrejas, G.; Sousa, M.; Silva, V.; Pereira, J.E.; Lozano, C.; Cortés-Cortés, G.; Torres, C.; Poeta, P. Clonal Diversity of Extended-Spectrum Beta-Lactamase Producing *Escherichia coli* Isolates in Fecal Samples of Wild Animals. *FEMS Microbiol. Lett.* **2017**, *364*, doi:10.1093/femsle/fnx039.
34. Castanheira, M.; Simner, P.J.; Bradford, P.A. Extended-Spectrum β -Lactamases: An Update on Their Characteristics, Epidemiology and Detection. *JAC. Antimicrob. Resist.* **2021**, *3*, doi:10.1093/jacamr/dlab092.
35. Liakopoulos, A.; Mevius, D.; Ceccarelli, D. A Review of SHV Extended-Spectrum β-Lactamases: Neglected Yet Ubiquitous. *Front. Microbiol.* **2016**, *7*, doi:10.3389/fmicb.2016.01374.
36. Yu, K.; Huang, Z.; Xiao, Y.; Bai, X.; Gao, H.; Wang, D. Epidemiology and Molecular Characterization of CTX-M-Type ESBLs Producing *Escherichia coli* Isolated from Clinical Settings. *J. Glob. Antimicrob. Resist.* **2024**, *36*, 181–187, doi:10.1016/j.jgar.2023.11.013.
37. Guitart-Matas, J.; Dias-Alves, A.; Marco, I.; Carrera-Faja, L.; Muro, J.; Tushabe, J.; Kayaga, E.; Ndoboli, D.; Babweteera, F.; Asiimwe, C.; et al. CTX-M Variants on the Move: Tracking Resistance in *Escherichia coli* and

 doi:10.20944/preprints202605.2038.v1

Klebsiella spp. across Humans, Livestock and Wildlife in Western Uganda. *One Health* **2026**, *22*, doi:10.1016/j.onehlt.2026.101407.

38. Bauernfeind, A.; Stemplinger, I.; Jungwirth, R.; Mangold, P.; Amann, S.; Akalin, E.; Anğ, O.; Bal, C.; Casellas, J.M. Characterization of Beta-Lactamase Gene BlaPER-2, Which Encodes an Extended-Spectrum Class A Beta-Lactamase. *Antimicrob. Agents Chemother.* **1996**, *40*, 616–620, doi:10.1128/AAC.40.3.616.
39. Naas, T.; Poirel, L.; Nordmann, P. Minor Extended-Spectrum β-Lactamases. *Clinical Microbiology and Infection* **2008**, *14*, 42–52, doi:10.1111/j.1469-0691.2007.01861.x.
40. Girlich, D.; Poirel, L.; Szczepanowski, R.; Schlüter, A.; Nordmann, P. Carbapenem-Hydrolyzing GES-5-Encoding Gene on Different Plasmid Types Recovered from a Bacterial Community in a Sewage Treatment Plant. *Appl. Environ. Microbiol.* **2012**, *78*, 1292–1295, doi:10.1128/AEM.06841-11.
41. Zhao, J.Y.; Zhu, Y.Q.; Li, Y.N.; Mu, X.D.; You, L.P.; Xu, C.; Qin, P.; Ma, J.L. Coexistence of SFO-1 and NDM-1 β-Lactamase Genes and Fosfomycin Resistance Gene FosA3 in an *Escherichia coli* Clinical Isolate. *FEMS Microbiol. Lett.* **2015**, *362*, doi:10.1093/femsle/fnu018.
42. Sirot, D.; Recule, C.; Chaibi, E.B.; Bret, L.; Croize, J.; Chanal-Claris, C.; Labia, R.; Sirot, J. A Complex Mutant of TEM-1 Beta-Lactamase with Mutations Encountered in Both IRT-4 and Extended-Spectrum TEM-15, Produced by an *Escherichia coli* Clinical Isolate. *Antimicrob. Agents Chemother.* **1997**, *41*, 1322–1325, doi:10.1128/AAC.41.6.1322.
43. Romero-Oraá, L.; Pulido, M.R.; Galán, F.; Palacios, M.V.G.; Pascual, A.; López-Cerero, L. Genetic Features of BEL-1-Producing and KPC-2-Producing *E. coli* from Hospital Wastewater: Human Source or Sewages Adaptation. *Environmental Science and Pollution Research* **2024**, *31*, 43896–43902, doi:10.1007/s11356-024-33875-w.
44. Abdullahi, I.N.; Juárez-Fernández, G.; Höfle, Ú.; Cardona-Cabrera, T.; Mínguez, D.; Pineda-Pampliega, J.; Lozano, C.; Zarazaga, M.; Torres, C. Nasotracheal Microbiota of Nestlings of Parent White Storks with Different Foraging Habits in Spain. *Ecohealth* **2023**, *20*, 105–121, doi:10.1007/s10393-023-01626-x.
45. Ahlstrom, C.A.; Bonnedahl, J.; Woksepp, H.; Hernandez, J.; Olsen, B.; Ramey, A.M. Acquisition and Dissemination of Cephalosporin-Resistant *E. coli* in Migratory Birds Sampled at an Alaska Landfill as Inferred through Genomic Analysis. *Sci. Rep.* **2018**, *8*, 7361, doi:10.1038/s41598-018-25474-w.
46. Atterby, C.; Börjesson, S.; Ny, S.; Järhult, J.D.; Byfors, S.; Bonnedahl, J. ESBL-Producing *Escherichia coli* in Swedish Gulls—A Case of Environmental Pollution from Humans? *PLoS One* **2017**, *12*, doi:10.1371/journal.pone.0190380.
47. Dolejska, M.; Papagiannitsis, C.C. Plasmid-Mediated Resistance Is Going Wild. *Plasmid* **2018**, *99*, 99–111, doi:10.1016/j.plasmid.2018.09.010.
48. Höfle, U.; Jose Gonzalez-Lopez, J.; Camacho, M.C.; Solà-Ginés, M.; Moreno-Mingorance, A.; Manuel Hernández, J.; De La Puente, J.; Pineda-Pampliega, J.; Aguirre, J.I.; Torres-Medina, F.; et al. Foraging at Solid Urban Waste Disposal Sites as Risk Factor for Cephalosporin and Colistin Resistant *Escherichia coli* Carriage in White Storks (Ciconia Ciconia). *Front. Microbiol.* **2020**, *11*, doi:10.3389/fmicb.2020.01397.
49. Woksepp, H.; Karlsson, K.; Börjesson, S.; Karlsson Lindsjö, O.; Söderlund, R.; Bonnedahl, J. Dissemination of Carbapenemase-Producing Enterobacterales through Wastewater and Gulls at a Wastewater Treatment Plant in Sweden. *Science of the Total Environment* **2023**, *886*, doi:10.1016/j.scitotenv.2023.163997.
50. Alcalá, L.; Alonso, C.A.; Simón, C.; González-Esteban, C.; Orós, J.; Rezusta, A.; Ortega, C.; Torres, C. Wild Birds, Frequent Carriers of Extended-Spectrum β-Lactamase (ESBL) Producing *Escherichia coli* of CTX-M and SHV-12 Types. *Microb. Ecol.* **2016**, *72*, 861–869, doi:10.1007/s00248-015-0718-0.
51. Blanco, G.; Bautista, L.M. Avian Scavengers as Bioindicators of Antibiotic Resistance Due to Livestock Farming Intensification. *Int. J. Environ. Res. Public Health* **2020**, *17*, 3620, doi:10.3390/ijerph17103620.
52. Carvalho, I.; Tejedor-Junco, M.T.; González-Martín, M.; Corbera, J.A.; Suárez-Pérez, A.; Silva, V.; Igrejas, G.; Torres, C.; Poeta, P. Molecular Diversity of Extended-Spectrum β-Lactamase-Producing *Escherichia coli* from Vultures in Canary Islands. *Environ. Microbiol. Rep.* **2020**, *12*, 540–547, doi:10.1111/1758-2229.12873.
53. Darwich, L.; Vidal, A.; Seminati, C.; Albamonte, A.; Casado, A.; López, F.; Molina-López, R.A.; Migura-Garcia, L. High Prevalence and Diversity of Extended-Spectrum β-Lactamase and Emergence of OXA-48 Producing Enterobacterales in Wildlife in Catalonia. *PLoS One* **2019**, *14*, doi:10.1371/journal.pone.0210686.

 doi:10.20944/preprints202605.2038.v1

54. Fuentes-Castillo, D.; Farfán-López, M.; Esposito, F.; Moura, Q.; Fernandes, M.R.; Lopes, R.; Cardoso, B.; Muñoz, M.E.; Cerdeira, L.; Najle, I.; et al. Wild Owls Colonized by International Clones of Extended-Spectrum β-Lactamase (CTX-M)-Producing *Escherichia coli* and *Salmonella* Infantis in the Southern Cone of America. *Science of the Total Environment* **2019**, *674*, 554–562, doi:10.1016/j.scitotenv.2019.04.149.
55. Fuentes-Castillo, D.; Esposito, F.; Cardoso, B.; Dalazen, G.; Moura, Q.; Fuga, B.; Fontana, H.; Cerdeira, L.; Dropa, M.; Rottmann, J.; et al. Genomic Data Reveal International Lineages of Critical Priority *Escherichia coli* Harbouring Wide Resistome in Andean Condors (*Vultur gryphus* Linnaeus, 1758). *Mol. Ecol.* **2020**, *29*, 1919–1935, doi:10.1111/mec.15455.
56. Fuentes-Castillo, D.; Castro-Tardón, D.; Esposito, F.; Neves, I.; Rodrigues, L.; Fontana, H.; Fuga, B.; Catão-Dias, J.L.; Lincopan, N. Genomic Evidences of Gulls as Reservoirs of Critical Priority CTX-M-Producing *Escherichia coli* in Corcovado Gulf, Patagonia. *Science of the Total Environment* **2023**, *874*, doi:10.1016/j.scitotenv.2023.162564.
57. Guitart-Matas, J.; Espunyes, J.; Illera, L.; Gonzalez-Escalona, N.; Ribas, M.P.; Marco, I.; Migura-Garcia, L. High-Risk Lineages of Extended Spectrum Cephalosporinase Producing *Escherichia coli* from Eurasian Griffon Vultures (*Gyps fulvus*) Foraging in Landfills in North-Eastern Spain. *Science of the Total Environment* **2024**, *909*, doi:10.1016/j.scitotenv.2023.168625.
58. Haenni, M.; Du Fraysseix, L.; François, P.; Drapeau, A.; Bralet, T.; Madec, J.Y.; Boulinier, T.; Duriez, O. Occurrence of ESBL- and AmpC-Producing *E. coli* in French Griffon Vultures Feeding on Extensive Livestock Carcasses. *Antibiotics* **2023**, *12*, doi:10.3390/antibiotics12071160.
59. Uslu, A.; Toslak, E.E.; Denizli, O.; Balevi, A.; Sayin, Z.; Erganis, O. Microbiological Analysis of Gut Flora and Determination of Antibiotic Resistance from White Storks (*Ciconia ciconia*) Resting Area during Migration in Türkiye. *Eurasian Journal of Veterinary Sciences* **2024**, *40*, 107–114, doi:10.15312/EurasianJVetSci.2024.434.
60. Blanco, G.; Junza, A.; Segarra, D.; Barbosa, J.; Barrón, D. Wildlife Contamination with Fluoroquinolones from Livestock: Widespread Occurrence of Enrofloxacin and Marbofloxacin in Vultures. *Chemosphere* **2016**, *144*, 1536–1543, doi:10.1016/j.chemosphere.2015.10.045.
61. Blanco, G.; Junza, A.; Barrón, D. Food Safety in Scavenger Conservation: Diet-Associated Exposure to Livestock Pharmaceuticals and Opportunist Mycoses in Threatened Cinereous and Egyptian Vultures. *Ecotoxicol. Environ. Saf.* **2017**, *135*, 292–301, doi:10.1016/j.ecoenv.2016.10.009.
62. Blanco, G.; Gómez-Ramírez, P.; Lambertucci, S.A.; Wiemeyer, G.M.; Plaza, P.I.; Hiraldo, F.; Donázar, J.A.; Sánchez-Zapata, J.A.; García-Fernández, A.J. Unexpected Exposure of Andean Condors (*Vultur gryphus*) to Pharmaceutical Mixtures. *Biol. Conserv.* **2023**, *280*, 109964, doi:10.1016/j.biocon.2023.109964.
63. Hamzaoui, Z.; Kilani, H.; Ferjani, S.; Maamar, E.; Fakhfakh, A.; Kanzari, L.; Boubaker, I.B.-B. NGS-Based Genomic Characterization of ESBL/AmpC-Producing Extraintestinal Pathogenic *Escherichia coli* from Captive Wildlife in Tunisia. *Antibiotics* **2026**, *15*, 449, doi:10.3390/antibiotics15050449.
64. Gonçalves, A.; Igrejas, G.; Radhouani, H.; Estepa, V.; Pacheco, R.; Monteiro, R.; Brito, F.; Guerra, A.; Petrucci-Fonseca, F.; Torres, C.; et al. Iberian Wolf as a Reservoir of Extended-Spectrum β-Lactamase-Producing *Escherichia coli* of the TEM, SHV, and CTX-M Groups. *Microbial Drug Resistance* **2012**, *18*, 215–219, doi:10.1089/mdr.2011.0145.
65. Sabença, C.; Igrejas, G.; Poeta, P.; Robin, F.; Bonnet, R.; Beyrouthy, R. Multidrug Resistance Dissemination in *Escherichia coli* Isolated from Wild Animals: Bacterial Clones and Plasmid Complicity. *Microbiol. Res. (Pavia).* **2021**, *12*, 123–137, doi:10.3390/microbiolres12010009.
66. Gonçalves, A.; Igrejas, G.; Radhouani, H.; Santos, T.; Monteiro, R.; Pacheco, R.; Alcaide, E.; Zorrilla, I.; Serra, R.; Torres, C.; et al. Detection of Antibiotic Resistant Enterococci and *Escherichia coli* in Free Range Iberian Lynx (*Lynx pardinus*). *Science of The Total Environment* **2013**, *456–457*, 115–119, doi:10.1016/j.scitotenv.2013.03.073.
67. Liu, T.; Lee, S.; Kim, M.; Fan, P.; Boughton, R.K.; Boucher, C.; Jeong, K.C. A Study at the Wildlife-Livestock Interface Unveils the Potential of Feral Swine as a Reservoir for Extended-Spectrum β-Lactamase-Producing *Escherichia coli*. *J. Hazard. Mater.* **2024**, *473*, doi:10.1016/j.jhazmat.2024.134694.
68. Bondo, K.J.; Pearl, D.L.; Janecko, N.; Boerlin, P.; Reid-Smith, R.J.; Parmley, J.; Jardine, C.M. Epidemiology of Antimicrobial Resistance in *Escherichia coli* Isolates from Raccoons (*Procyon lotor*) and the Environment

 doi:10.20944/preprints202605.2038.v1

on Swine Farms and Conservation Areas in Southern Ontario. *PLoS One* **2016**, *11*, doi:10.1371/journal.pone.0165303.

69. Orden, J.A.; García-Meniño, I.; Flament-Simon, S.C.; Blanco, J.; de la Fuente, R.; Martínez-Rodrigo, A.; Mas, A.; Carrión, J.; Sobrino, F.; Domínguez-Bernal, G. Raccoons (*Procyon lotor*) in the Madrid Region of Spain Are Carriers of Antimicrobial-Resistant *Escherichia coli* and Enteropathogenic *E. coli*. *Zoonoses Public Health* **2021**, *68*, 69–78, doi:10.1111/zph.12784.
70. Asai, T.; Sugiyama, M.; Omatsu, T.; Yoshikawa, M.; Minamoto, T. Isolation of Extended-Spectrum β-Lactamase-Producing *Escherichia coli* from Japanese Red Fox (*Vulpes vulpes* Japonica). *Microbiology open* **2022**, *11*, doi:10.1002/mbo3.1317.
71. O'Hagan, M.J.H.; Pascual-Linaza, A. V.; Couzens, C.; Holmes, C.; Bell, C.; Spence, N.; Huey, R.J.; Murphy, J.A.; Devaney, R.; Lahuerta-Marin, A. Estimation of the Prevalence of Antimicrobial Resistance in Badgers (*Meles meles*) and Foxes (*Vulpes vulpes*) in Northern Ireland. *Front. Microbiol.* **2021**, *12*, doi:10.3389/fmicb.2021.596891.
72. Alonso, C.A.; González-Barrio, D.; Tenorio, C.; Ruiz-Fons, F.; Torres, C. Antimicrobial Resistance in Faecal *Escherichia coli* Isolates from Farmed Red Deer and Wild Small Mammals. Detection of a Multiresistant *E. coli* Producing Extended-Spectrum Beta-Lactamase. *Comp. Immunol. Microbiol. Infect. Dis.* **2016**, *45*, 34–39, doi:10.1016/j.cimid.2016.02.003.
73. Ballash, G.A.; Dennis, P.M.; Mollenkopf, D.F.; Albers, A.L.; Robison, T.L.; Adams, R.J.; Li, C.; Tyson, G.H.; Wittum, T.E. Colonization of White-Tailed Deer (*Odocoileus virginianus*) from Urban and Suburban Environments with Cephalosporinase- and Carbapenemase-Producing Enterobacterales. *Appl. Environ. Microbiol.* **2022**, *88*, doi:10.1128/aem.00465-22.
74. Costa, D.; Poeta, P.; Saenz, Y.; Vinue, L.; Rojo-Bezares, B.; Jouini, A.; Zarazaga, M.; Rodrigues, J.; Torres, C. Detection of *Escherichia coli* Harbouring Extended-Spectrum beta-Lactamases of the CTX-M, TEM and SHV Classes in Faecal Samples of Wild Animals in Portugal. *Journal of Antimicrobial Chemotherapy* **2006**, *58*, 1311–1312, doi:10.1093/jac/dkl415.
75. Dias, D.; Fonseca, C.; Caetano, T.; Mendo, S. Oh, Deer! How Worried Should We Be about the Diversity and Abundance of the Faecal Resistome of Red Deer? *Science of the Total Environment* **2022**, *825*, doi:10.1016/j.scitotenv.2022.153831.
76. Homeier-Bachmann, T.; Schütz, A.K.; Dreyer, S.; Glanz, J.; Schaufler, K.; Conraths, F.J. Genomic Analysis of ESBL-Producing *E. coli* in Wildlife from North-Eastern Germany. *Antibiotics* **2022**, *11*, doi:10.3390/antibiotics11020123.
77. Katakweba, A.A.S.; Olsen, J.E. Quantification of Antibiotic Resistance Genes in Wildlife Ungulates in Ngorongoro Conservation Area and Mikumi National Park, Tanzania. *Tanzania Veterinary Journal* **2021**, *36*, 1–10, doi:10.4314/tvj.v36i2.1.
78. Konputtar, A.; Yossapol, M.; Phaechaiyaphum, T.; Manyuen, P.; Suetrong, N.; Ruksachat, N.; Purisotayo, T. Epidemiological Study of Antimicrobial-Resistant Bacteria in Healthy Free-Ranging Bantengs (*Bos javanicus*) and Domestic Cattle. *Vet. World* **2023**, *16*, 1796–1802, doi:10.14202/vetworld.2023.1796-1802.
79. Plaza-Rodríguez, C.; Alt, K.; Grobbel, M.; Hammerl, J.A.; Irrgang, A.; Szabo, I.; Stingl, K.; Schuh, E.; Wiehle, L.; Pfefferkorn, B.; et al. Wildlife as Sentinels of Antimicrobial Resistance in Germany? *Front. Vet. Sci.* **2021**, *7*, doi:10.3389/fvets.2020.627821.
80. Carvalho, I.; Tejedor-Junco, M.T.; González-Martín, M.; Corbera, J.A.; Silva, V.; Igrejas, G.; Torres, C.; Poeta, P. *Escherichia coli* Producing Extended-Spectrum β-Lactamases (ESBL) from Domestic Camels in the Canary Islands: A One Health Approach. *Animals* **2020**, *10*, 1–9, doi:10.3390/ani10081295.
81. Torres, R.T.; Fernandes, J.; Carvalho, J.; Cunha, M. V.; Caetano, T.; Mendo, S.; Serrano, E.; Fonseca, C. Wild Boar as a Reservoir of Antimicrobial Resistance. *Science of The Total Environment* **2020**, *717*, 135001, doi:10.1016/j.scitotenv.2019.135001.
82. Bonardi, S.; Cabassi, C.S.; Longhi, S.; Pia, F.; Corradi, M.; Gilioli, S.; Scaltriti, E. Detection of Extended-Spectrum Beta-Lactamase Producing *Escherichia coli* from Mesenteric Lymph Nodes of Wild Boars (*Sus scrofa*). *Ital. J. Food Saf.* **2018**, *7*, 213–216, doi:10.4081/ijfs.2018.7707.

 doi:10.20944/preprints202605.2038.v1

83. Formenti, N.; Calò, S.; Parisio, G.; Guarneri, F.; Birbes, L.; Pitozzi, A.; Scali, F.; Tonni, M.; Guadagno, F.; Giovannini, S.; et al. Esbl/Ampc-Producing *Escherichia coli* in Wild Boar: Epidemiology and Risk Factors. *Animals* **2021**, *11*, doi:10.3390/ani11071855.
84. Günther, T.; Kramer-Schadt, S.; Fuhrmann, M.; Belik, V. Environmental Factors Associated with the Prevalence of ESBL/AmpC-Producing *Escherichia coli* in Wild Boar (*Sus scrofa*). *Front. Vet. Sci.* **2022**, *9*, doi:10.3389/fvets.2022.980554.
85. Mercato, A.; Cortimiglia, C.; Abualsha'ar, A.; Piazza, A.; Marchesini, F.; Milani, G.; Bonardi, S.; Cocconcelli, P.S.; Migliavacca, R. Wild Boars as an Indicator of Environmental Spread of ESβL-Producing *Escherichia coli*. *Front. Microbiol.* **2022**, *13*, doi:10.3389/fmicb.2022.838383.
86. Poeta, P.; Radhouani, H.; Pinto, L.; Martinho, A.; Rego, V.; Rodrigues, R.; Gonçalves, A.; Rodrigues, J.; Estepa, V.; Torres, C.; et al. Wild Boars as Reservoirs of Extended-Spectrum Beta-Lactamase (ESBL) Producing *Escherichia coli* of Different Phylogenetic Groups. *J. Basic Microbiol.* **2009**, *49*, 584–588, doi:10.1002/jobm.200900066.
87. Selmi, R.; Tayh, G.; Srairi, S.; Mamlouk, A.; Ben Chehida, F.; Lahmar, S.; Bouslama, M.; Daaloul-Jedidi, M.; Messadi, L. Prevalence, Risk Factors and Emergence of Extended-Spectrum β-Lactamase Producing-, Carbapenem- and Colistin-Resistant Enterobacterales Isolated from Wild Boar (*Sus scrofa*) in Tunisia. *Microb. Pathog.* **2022**, *163*, doi:10.1016/j.micpath.2021.105385.
88. Abdallah, R.; Kuete Yimagou, E.; Hadjadj, L.; Mediannikov, O.; Ibrahim, A.; Davoust, B.; Barciela, A.; Hernandez-Aguilar, R.A.; Diatta, G.; Sokhna, C.; et al. Population Diversity of Antibiotic Resistant Enterobacterales in Samples From Wildlife Origin in Senegal: Identification of a Multidrug Resistance Transposon Carrying BlaCTX–M–15 in *Escherichia coli*. *Front. Microbiol.* **2022**, *13*, doi:10.3389/fmicb.2022.838392.
89. Bager, S.L.; Kakaala, I.; Kudirkiene, E.; Byarugaba, D.K.; Olsen, J.E. Genomic Characterization of Multidrug-Resistant Extended-Spectrum β-Lactamase–Producing *Escherichia coli* and *Klebsiella pneumoniae* from Chimpanzees (*Pan troglodytes*) from Wild and Sanctuary Locations in Uganda. *J. Wildl. Dis.* **2022**, *58*, 269–278, doi:10.7589/JWD-D-21-00068.
90. Janatova, M.; Albrechtova, K.; Petrzelkova, K.J.; Dolejska, M.; Papousek, I.; Masarikova, M.; Cizek, A.; Todd, A.; Shutt, K.; Kalousova, B.; et al. Antimicrobial-Resistant Enterobacteriaceae from Humans and Wildlife in Dzanga-Sangha Protected Area, Central African Republic. *Vet. Microbiol.* **2014**, *171*, 422–431, doi:10.1016/j.vetmic.2014.02.014.
91. Benavides, J.A.; Salgado-Caxito, M.; Opazo-Capurro, A.; González Muñoz, P.; Piñeiro, A.; Otto Medina, M.; Rivas, L.; Munita, J.; Millán, J. ESBL-Producing *Escherichia coli* Carrying CTX-M Genes Circulating among Livestock, Dogs, and Wild Mammals in Small-Scale Farms of Central Chile. *Antibiotics* **2021**, *10*, 510, doi:10.3390/antibiotics10050510.
92. Guenther, S.; Grobbel, M.; Beutlich, J.; Guerra, B.; Ulrich, R.G.; Wieler, L.H.; Ewers, C. Detection of Pandemic B2-O25-ST131 *Escherichia coli* Harbouring the CTX-M-9 Extended-Spectrum beta-Lactamase Type in a Feral Urban Brown Rat (*Rattus norvegicus*). *Journal of Antimicrobial Chemotherapy* **2010**, *65*, 582–584, doi:10.1093/jac/dkp496.
93. Guyomard-Rabenirina, S.; Reynaud, Y.; Pot, M.; Albina, E.; Couvin, D.; Ducat, C.; Gruel, G.; Ferdinand, S.; Legreneur, P.; Le Hello, S.; et al. Antimicrobial Resistance in Wildlife in Guadeloupe (French West Indies): Distribution of a Single BlaCTX–M–1/IncI1/ST3 Plasmid Among Humans and Wild Animals. *Front. Microbiol.* **2020**, *11*, doi:10.3389/fmicb.2020.01524.
94. Ho, P.L.; Chow, K.H.; Lai, E.L.; Lo, W.U.; Yeung, M.K.; Chan, J.; Chan, P.Y.; Yuen, K.Y. Extensive Dissemination of CTX-M-Producing *Escherichia coli* with Multidrug Resistance to "critically Important" Antibiotics among Food Animals in Hong Kong, 2008-10. *Journal of Antimicrobial Chemotherapy* **2011**, *66*, 765–768, doi:10.1093/jac/dkq539.
95. Ho, P.L.; Liu, M.C.J.; Lo, W.U.; Lai, E.L.Y.; Lau, T.C.K.; Law, O.K.; Chow, K.H. Prevalence and Characterization of Hybrid BlaCTX-M among *Escherichia coli* Isolates from Livestock and Other Animals. *Diagn. Microbiol. Infect. Dis.* **2015**, *82*, 148–153, doi:10.1016/j.diagmicrobio.2015.02.010.

 doi:10.20944/preprints202605.2038.v1

96. Literak, I.; Dolejska, M.; Cizek, A.; Ahmed, C.; Djigo, T.; Konecny, A.; Koubek, P. Reservoirs of Antibiotic-Resistant Enterobacteriaceae among Animals Sympatric to Humans in Senegal: Extended-Spectrum Beta-Lactamases in Bacteria in a Black Rat (*Rattus rattus*). *Advanced Journal of Microbiology Research* **2014**.
97. Uea-Anuwong, T.; Byers, K.A.; Wahl, L.C.; Nekouei, O.; Grohn, Y.T.; Magouras, I. Antimicrobial Resistance in Bacteria Isolated from Peridomestic *Rattus* Species: A Scoping Literature Review. *One Health* **2023**, *16*, 100522, doi:10.1016/j.onehlt.2023.100522.
98. de Carvalho, M.P.N.; Fernandes, M.R.; Sellera, F.P.; Lopes, R.; Monte, D.F.; Hippólito, A.G.; Milanelo, L.; Raso, T.F.; Lincopan, N. International Clones of Extended-Spectrum β-Lactamase (CTX-M)-Producing *Escherichia coli* in Peri-Urban Wild Animals, Brazil. *Transbound. Emerg. Dis.* **2020**, *67*, 1804–1815, doi:10.1111/tbed.13558.
99. Agustin, A.L.D.; Khairullah, A.R.; Effendi, M.H.; Tyasningsih, W.; Moses, I.B.; Budiastuti, B.; Plumeriastuti, H.; Yanestria, S.M.; Riwu, K.H.P.; Dameanti, F.N.A.E.P.; et al. Ecological and Public Health Dimensions of ESBL-Producing *Escherichia coli* in Bats: A One Health Perspective. *Vet. World* **2025**, *18*, 1199–1213, doi:10.14202/vetworld.2025.1199-1213.
100. Ahmed, T.; Ahsan, A.; Shahzad, M.A.; Irshad, H.; Ali, A.; Tahir, M.F.; Zaheer, M.U.; Kingston, T. Environmental Factors Driving Antimicrobial Resistance in Indian Flying Foxes (*Pteropus medius*): One Health Implications. *Sci. Rep.* **2025**, *15*, doi:10.1038/s41598-025-19738-5.
101. Benavides, J.A.; Godreuil, S.; Opazo-Capurro, A.; Mahamat, O.O.; Falcon, N.; Oravcova, K.; Streicker, D.G.; Shiva, C. Long-Term Maintenance of Multidrug-Resistant *Escherichia coli* Carried by Vampire Bats and Shared with Livestock in Peru. *Science of The Total Environment* **2022**, *810*, 152045, doi:10.1016/j.scitotenv.2021.152045.
102. Garcês, A.; Correia, S.; Amorim, F.; Pereira, J.E.; Igrejas, G.; Poeta, P. First Report on Extended-Spectrum Beta-Lactamase (ESBL) Producing *Escherichia coli* from European Free-Tailed Bats (*Tadarida teniotis*) in Portugal: A One-Health Approach of a Hidden Contamination Problem. *J. Hazard. Mater.* **2019**, 219–224, doi:10.1016/j.jhazmat.2017.12.053.
103. Sellera, F.P.; Fernandes, M.R.; Moura, Q.; Carvalho, M.P.N.; Lincopan, N. Extended-Spectrum-B-Lactamase (CTX-M)-Producing *Escherichia coli* in Wild Fishes from a Polluted Area in the Atlantic Coast of South America. *Mar. Pollut. Bull.* **2018**, *135*, 183–186, doi:10.1016/j.marpolbul.2018.07.012.
104. Brahmi, S.; Touati, A.; Dunyach-Remy, C.; Sotto, A.; Pantel, A.; Lavigne, J.P. High Prevalence of Extended-Spectrum β-Lactamase-Producing Enterobacteriaceae in Wild Fish from the Mediterranean Sea in Algeria. *Microbial Drug Resistance* **2018**, *24*, 290–298, doi:10.1089/mdr.2017.0149.
105. Cortés-Cortés, G.; Lozano-Zarain, P.; Torres, C.; Castañeda, M.; Sánchez, G.M.; Alonso, C.A.; López-Pliego, L.; Mayen, M.G.G.; Martínez-Laguna, Y.; Rocha-Gracia, R. del C. Detection and Molecular Characterization of *Escherichia coli* Strains Producers of Extended-Spectrum and CMY-2 Type Beta-Lactamases, Isolated from Turtles in Mexico. *Vector-Borne and Zoonotic Diseases* **2016**, *16*, 595–603, doi:10.1089/vbz.2014.1725.
106. Nieto-Claudin, A.; Esperón, F.; Blake, S.; Deem, S.L. Antimicrobial Resistance Genes Present in the Faecal Microbiota of Free-Living Galapagos Tortoises (*Chelonoidis porteri*). *Zoonoses Public Health* **2019**, *66*, 900–908, doi:10.1111/zph.12639.
107. Mengistu, T.S.; Garcias, B.; Castellanos, G.; Seminati, C.; Molina-López, R.A.; Darwich, L. Occurrence of Multidrug Resistant Gram-Negative Bacteria and Resistance Genes in Semi-Aquatic Wildlife - *Trachemys scripta*, *Neovison vison* and *Lutra lutra* - as Sentinels of Environmental Health. *Science of the Total Environment* **2022**, *830*, doi:10.1016/j.scitotenv.2022.154814.
108. Manageiro, V.; Clemente, L.; Jones-Dias, D.; Albuquerque, T.; Ferreira, E.; Caniça, M. CTX-M-15–Producing *Escherichia coli* in Dolphin, Portugal. *Emerg. Infect. Dis.* **2015**, *21*, 2249–2251, doi:10.3201/EID2112.141963.
109. Song, J.; Oh, S.S.; Kim, J.; Park, S.; Shin, J. Clinically Relevant Extended-Spectrum β-Lactamase–Producing *Escherichia coli* Isolates From Food Animals in South Korea. *Front. Microbiol.* **2020**, *11*, doi:10.3389/fmicb.2020.00604.
110. Miltgen, G.; Martak, D.; Valot, B.; Kamus, L.; Garrigos, T.; Verchere, G.; Gbaguidi-Haore, H.; Ben Cimon, C.; Ramiandrisoa, M.; Picot, S.; et al. One Health Compartmental Analysis of ESBL-Producing *Escherichia coli* on Reunion Island Reveals Partitioning between Humans and Livestock. *Journal of Antimicrobial Chemotherapy* **2022**, *77*, 1254–1262, doi:10.1093/jac/dkac054.

 doi:10.20944/preprints202605.2038.v1

111. Balázs, B.; Nagy, J.B.; Tóth, Z.; Nagy, F.; Károlyi, S.; Turcsányi, I.; Bistyák, A.; Kálmán, A.; Sárközi, R.; Kardos, G. Occurrence of *Escherichia coli* producing Extended Spectrum β-Lactamases in Food-Producing Animals. *Acta Vet. Hung.* **2021**, *69*, 211–215, doi:10.1556/004.2021.00036.
112. Gruel, G.; Sellin, A.; Riveiro, H.; Pot, M.; Breurec, S.; Guyomard-Rabenirina, S.; Talarmin, A.; Ferdinand, S. Antimicrobial Use and Resistance in *Escherichia coli* from Healthy Food-Producing Animals in Guadeloupe. *BMC Vet. Res.* **2021**, *17*, doi:10.1186/s12917-021-02810-3.
113. Chai, M.H.; Sukiman, M.Z.; Jasmy, N.; Zulkifly, N.A.; Mohd Yusof, N.A.S.; Mohamad, N.M.; Ariffin, S.M.Z.; Ghazali, M.F. Molecular Detection and Antibiogram of ESBL-Producing and Carbapenem Resistant *Escherichia coli* from Rabbit, Swine, and Poultry in Malaysia. *Tropical Animal Science Journal* **2022**, *45*, 16–23, doi:10.5398/tasj.2022.45.1.16.
114. Giufrè, M.; Mazzolini, E.; Cerquetti, M.; Brusaferro, S.; Accogli, M.; Agnoletti, F.; Agodi, A.; Alborali, G.L.; Arghittu, M.; Auxilia, F.; et al. Extended-Spectrum β-Lactamase-Producing *Escherichia coli* from Extraintestinal Infections in Humans and from Food-Producing Animals in Italy: A 'One Health' Study. *Int. J. Antimicrob. Agents* **2021**, *58*, doi:10.1016/j.ijantimicag.2021.106433.
115. Peyser, A. V.; Gonçalves, A.; Haisi, A.; Araújo, J.P.; Raimondo, R.F.S.; Heinemann, M.B.; Cortez, A.; Gaeta, N.C. First Pandemic BlaCTX-M-8-Producing ST224 *E. coli* in Brazilian Sheep: Resistance and Genomic Traits. *Ecohealth* **2025**, doi:10.1007/s10393-025-01767-1.
116. Kirat, H.; Rahab, H.; Chekroud, Z.; Abbassi, M.S.; Basher, N.S.; Ibrahim, N.A.; Touati, A. Fecal Carriage of Resistant *Escherichia coli* in Livestock in Algeria: Emergence of NDM and OXA-181. *BMC Microbiol.* **2025**, *25*, doi:10.1186/s12866-025-04174-2.
117. Ramos, S.; Igrejas, G.; Silva, N.; Jones-Dias, D.; Capelo-Martinez, J.L.; Caniça, M.; Poeta, P. First Report of CTX-M Producing *Escherichia coli*, Including the New ST2526, Isolated from Beef Cattle and Sheep in Portugal. *Food Control* **2013**, *31*, 208–210, doi:10.1016/j.foodcont.2012.10.011.
118. Seni, J.; Falgenhauer, L.; Simeo, N.; Mirambo, M.M.; Imirzalioglu, C.; Matee, M.; Rweyemamu, M.; Chakraborty, T.; Mshana, S.E. Multiple ESBL-Producing *Escherichia coli* Sequence Types Carrying Quinolone and Aminoglycoside Resistance Genes Circulating in Companion and Domestic Farm Animals in Mwanza, Tanzania, Harbor Commonly Occurring Plasmids. *Front. Microbiol.* **2016**, *7*, doi:10.3389/fmicb.2016.00142.
119. Taghadosi, R.; Shakibaie, M.R.; Hosseini-Nave, H. Antibiotic Resistance, ESBL Genes, Integrons, Phylogenetic Groups and MLVA Profiles of *Escherichia coli* Pathotypes Isolated from Patients with Diarrhea and Farm Animals in South-East of Iran. *Comp. Immunol. Microbiol. Infect. Dis.* **2019**, *63*, 117–126, doi:10.1016/j.cimid.2019.01.004.
120. Shi, L.; Xu, M.; Tang, S.; Cai, Q.; Chen, H.; Xu, D.; Qin, H.; Long, B.; Tian, W.; Liu, B.; et al. Study on Drug Resistance, Biofilm Formation, Phylogenetic and Virulence Gene Analysis of *Escherichia coli* from Diarrheic Lambs. *BMC Vet. Res.* **2026**, *22*, doi:10.1186/s12917-026-05296-z.
121. Shnaiderman-Torban, A.; Navon-Venezia, S.; Dor, Z.; Paitan, Y.; Arielly, H.; Ahmad, W.A.; Kelmer, G.; Fulde, M.; Steinman, A. Extended-Spectrum β-Lactamase-Producing Enterobacteriaceae Shedding in Farm Horses versus Hospitalized Horses: Prevalence and Risk Factors. *Animals* **2020**, *10*, doi:10.3390/ani10020282.
122. Yiğin, A. Antimicrobial Resistance and Extended-Spectrum Beta-Lactamase (ESBL) Genes in *E. coli* Isolated from Equine Fecal Samples in Turkey. *J. Equine Vet. Sci.* **2021**, *101*, 103461, doi:10.1016/j.jevs.2021.103461.
123. Vicente, J.; Höfle, U. *Mitigating Disease Transmission Risk at the Wildlife–Livestock Interface to Facilitate Safe Trade*; 2025;
124. Marín-Rojo, Á.; Herrero-García, G.; Herranz-Benito, C.; Barroso, P.; Relimpio, D.; García-Seco, T.; Perelló, A.; Díez-Guerrier, A.; Pozo, P.; Balseiro, A.; et al. Wildlife Risk Mitigation Protocols Reduce Risk Species Visits and Pathogen Marker Detection in Open-Air Farms. *Vet. Res.* **2025**, *56*, 237, doi:10.1186/s13567-025-01671-0.
125. Martínez-Guijosa, J.; Lima-Barbero, J.F.; Acevedo, P.; Cano-Terriza, D.; Jiménez-Ruiz, S.; Barasona, J.Á.; Boadella, M.; García-Bocanegra, I.; Gortázar, C.; Vicente, J. Description and Implementation of an On-Farm Wildlife Risk Mitigation Protocol at the Wildlife-Livestock Interface: Tuberculosis in Mediterranean Environments. *Prev. Vet. Med.* **2021**, *191*, doi:10.1016/j.prevetmed.2021.105346.

 doi:10.20944/preprints202605.2038.v1

126. Jori, F.; Hernandez-Jover, M.; Magouras, I.; Dürr, S.; Brookes, V.J. Wildlife–Livestock Interactions in Animal Production Systems: What Are the Biosecurity and Health Implications? *Animal Frontiers* **2021**, *11*, 8–19, doi:10.1093/af/vfab045.
127. Kauer, L.; Sapountzis, P.; Imholt, C.; Berens, C.; Kuehn, R. Microbial Exchange at the Wildlife-Livestock Interface: Insights into Microbial Composition, Antimicrobial Resistance and Virulence Factor Gene Dynamics in Grassland Ecosystems. *Anim. Microbiome* **2025**, *7*, doi:10.1186/s42523-025-00448-2.
128. Jiménez-Ruiz, S.; Laguna, E.; Vicente, J.; García-Bocanegra, I.; Martínez-Guijosa, J.; Cano-Terriza, D.; Risalde, M.A.; Acevedo, P. Characterization and Management of Interaction Risks between Livestock and Wild Ungulates on Outdoor Pig Farms in Spain. *Porcine Health Manag.* **2022**, *8*, doi:10.1186/s40813-021-00246-7.
129. Kukielka, E.; Barasona, J.A.; Cowie, C.E.; Drewe, J.A.; Gortazar, C.; Cotarelo, I.; Vicente, J. Spatial and Temporal Interactions between Livestock and Wildlife in South Central Spain Assessed by Camera Traps. *Prev. Vet. Med.* **2013**, *112*, 213–221, doi:10.1016/j.prevetmed.2013.08.008.
130. Lee, S.; Fan, P.; Liu, T.; Yang, A.; Boughton, R.K.; Pepin, K.M.; Miller, R.S.; Jeong, K.C. Transmission of Antibiotic Resistance at the Wildlife-Livestock Interface. *Commun. Biol.* **2022**, *5*, doi:10.1038/s42003-022-03520-8.
131. Smith, O.M.; Snyder, W.E.; Owen, J.P. Are We Overestimating Risk of Enteric Pathogen Spillover from Wild Birds to Humans? *Biological Reviews* **2020**, *95*, 652–679, doi:10.1111/brv.12581.
132. van den Honert, M.S.; Gouws, P.A.; Hoffman, L.C. Escherichia Coli Antibiotic Resistance Patterns from Co-Grazing and Non-Co-Grazing Livestock and Wildlife Species from Two Farms in the Western Cape, South Africa. *Antibiotics* **2021**, *10*, 618, doi:10.3390/antibiotics10060618.
133. Kozak, G.K.; Boerlin, P.; Janecko, N.; Reid-Smith, R.J.; Jardine, C. Antimicrobial Resistance in *Escherichia coli* Isolates from Swine and Wild Small Mammals in the Proximity of Swine Farms and in Natural Environments in Ontario, Canada. *Appl. Environ. Microbiol.* **2009**, *75*, 559–566, doi:10.1128/AEM.01821-08.
134. Mercat, M.; Clermont, O.; Massot, M.; Ruppe, E.; De Garine-Wichatitsky, M.; Miguel, E.; Fox, H.V.; Cornelis, D.; Andremont, A.; Denamur, E.; et al. *Escherichia coli* Population Structure and Antibiotic Resistance at a Buffalo/Cattle Interface in Southern Africa. *Appl. Environ. Microbiol.* **2016**, *82*, 1459–1467, doi:10.1128/AEM.03771-15.
135. Navarro-Gonzalez, N.; Porrero, M.C.; Mentaberre, G.; Serrano, E.; Mateos, A.; Domínguez, L.; Lavína, S. Antimicrobial Resistance in Indicator *Escherichia coli* Isolates from Free-Ranging Livestock and Sympatric Wild Ungulates in a Natural Environment (Northeastern Spain). *Appl. Environ. Microbiol.* **2013**, *79*, 6184–6186, doi:10.1128/AEM.01745-13.
136. Rwego, I.B.; Isabirye-Basuta, G.; Gillespie, T.R.; Goldberg, T.L. Gastrointestinal Bacterial Transmission among Humans, Mountain Gorillas, and Livestock in Bwindi Impenetrable National Park, Uganda. *Conservation Biology* **2008**, *22*, 1600–1607, doi:10.1111/j.1523-1739.2008.01018.x.
137. Hayer, J.; Salgado-Caxito, M.; Opazo-Capurro, A.; Muñoz, P.G.; Millán, J.; Piñeiro, A.; Munita, J.M.; Rivas, L.; Benavides, J.A. Multiple Clonal Transmissions of Clinically Relevant Extended-Spectrum Beta-Lactamase–Producing *Escherichia coli* among Livestock, Dogs, and Wildlife in Chile. *J. Glob. Antimicrob. Resist.* **2023**, *34*, 247–252, doi:10.1016/j.jgar.2023.07.009.
138. Silva, A.; Silva, V.; Pereira, J.E.; Maltez, L.; Igrejas, G.; Valentão, P.; Falco, V.; Poeta, P. Antimicrobial Resistance and Clonal Lineages of *Escherichia coli* from Food-Producing Animals. *Antibiotics* **2023**, *12*, 1061, doi:10.3390/antibiotics12061061.
139. Juraschek, K.; Malekzadah, J.; Malorny, B.; Käsbohrer, A.; Schwarz, S.; Meemken, D.; Hammerl, J.A. Characterization of QnrB-Carrying Plasmids from ESBL- and Non-ESBL-Producing *Escherichia coli. BMC Genomics* **2022**, *23*, doi:10.1186/s12864-022-08564-y.
140. Islam, M.A.; Bose, P.; Rahman, M.Z.; Muktaruzzaman, M.; Sultana, P.; Ahamed, T.; Khatun, M.M. A Review of Antimicrobial Usage Practice in Livestock and Poultry Production and Its Consequences on Human and Animal Health. *J. Adv. Vet. Anim. Res.* **2024**, *11*, 675–685, doi:10.5455/javar.2024.k817.
141. Schmithausen, R.M.; Schulze-Geisthoevel, S.V.; Stemmer, F.; El-Jade, M.; Reif, M.; Hack, S.; Meilaender, A.; Montabauer, G.; Fimmers, R.; Parcina, M.; et al. Analysis of Transmission of MRSA and ESBL-E among Pigs and Farm Personnel. *PLoS One* **2015**, *10*, doi:10.1371/journal.pone.0138173.

 doi:10.20944/preprints202605.2038.v1

142. Martínez-Puchol, S.; Riveros, M.; Ruidias, K.; Granda, A.; Ruiz-Roldán, L.; Zapata-Cachay, C.; Ochoa, T.J.; Pons, M.J.; Ruiz, J. Dissemination of a Multidrug Resistant CTX-M-65 Producer *Salmonella enterica* Serovar Infantis Clone between Marketed Chicken Meat and Children. *Int. J. Food Microbiol.* **2021**, *344*, doi:10.1016/j.ijfoodmicro.2021.109109.
143. Alba, P.; Leekitcharoenphon, P.; Franco, A.; Feltrin, F.; Ianzano, A.; Caprioli, A.; Stravino, F.; Hendriksen, R.S.; Bortolaia, V.; Battisti, A. Molecular Epidemiology of Mcr-Encoded Colistin Resistance in Enterobacteriaceae from Food-Producing Animals in Italy Revealed through the EU Harmonized Antimicrobial Resistance Monitoring. *Front. Microbiol.* **2018**, *9*, doi:10.3389/fmicb.2018.01217.
144. Brendecke, J.; Homeier-Bachmann, T.; Schmitz Ornés, A.; Guenther, S.; Heiden, S.E.; Schwabe, M.; Eger, E.; Schaufler, K. Multidrug-Resistant High-Risk *Escherichia coli* and *Klebsiella pneumoniae* Clonal Lineages Occur in Black-Headed Gulls from Two Conservation Islands in Germany. *Antibiotics* **2022**, *11*, doi:10.3390/antibiotics11101357.
145. Nguyen, M.N.; Hoang, H.T.T.; Xavier, B.B.; Lammens, C.; Le, H.T.; Hoang, N.T.B.; Nguyen, S.T.; Pham, N.T.; Goossens, H.; Dang, A.D.; et al. Prospective One Health Genetic Surveillance in Vietnam Identifies Distinct BlaCTX-M-Harbouring Escherichia coli in Food-Chain and Human-Derived Samples. *Clinical Microbiology and Infection* **2021**, *27*, 1515.e1-1515.e8, doi:10.1016/j.cmi.2021.01.006.
146. Martak, D.; Henriot, C.P.; Hocquet, D. Environment, Animals, and Food as Reservoirs of Antibiotic-Resistant Bacteria for Humans: One Health or More? *Infect. Dis. Now* **2024**, *54*, doi:10.1016/j.idnow.2024.104895.
147. Kaspar, U.; von Lützau, A.; Schlattmann, A.; Roesler, U.; Köck, R.; Becker, K. Zoonotic Multidrug-Resistant Microorganisms among Small Companion Animals in Germany. *PLoS One* **2018**, *13*, doi:10.1371/journal.pone.0208364.
148. Subramanya, S.H.; Bairy, I.; Metok, Y.; Baral, B.P.; Gautam, D.; Nayak, N. Detection and Characterization of ESBL-Producing Enterobacteriaceae from the Gut of Subsistence Farmers, Their Livestock, and the Surrounding Environment in Rural Nepal. *Sci. Rep.* **2021**, *11*, doi:10.1038/s41598-021-81315-3.
149. Lee, S.; Mir, R.A.; Park, S.H.; Kim, D.; Kim, H.-Y.; Boughton, R.K.; Morris, J.G.; Jeong, K.C. Prevalence of Extended-Spectrum β-Lactamases in the Local Farm Environment and Livestock: Challenges to Mitigate Antimicrobial Resistance. *Crit. Rev. Microbiol.* **2020**, *46*, 1–14, doi:10.1080/1040841X.2020.1715339.
150. Shafiq, M.; Rahman, S.U.; Bilal, H.; Ullah, A.; Noman, S.M.; Zeng, M.; Yuan, Y.; Xie, Q.; Li, X.; Jiao, X. Incidence and Molecular Characterization of ESBL-Producing and Colistin-Resistant *Escherichia coli* Isolates Recovered from Healthy Food-Producing Animals in Pakistan. *J. Appl. Microbiol.* **2022**, *133*, 1169–1182, doi:10.1111/jam.15469.
151. Kurittu, P.; Khakipoor, B.; Aarnio, M.; Nykäsenoja, S.; Brouwer, M.; Myllyniemi, A.L.; Vatunen, E.; Heikinheimo, A. Plasmid-Borne and Chromosomal ESBL/AmpC Genes in *Escherichia coli* and *Klebsiella pneumoniae* in Global Food Products. *Front. Microbiol.* **2021**, *12*, doi:10.3389/fmicb.2021.592291.
152. McEwen, S.A.; Collignon, P.J. Antimicrobial Resistance: A One Health Perspective. *Microbiol. Spectr.* **2018**, *6*, doi:10.1128/microbiolspec.arba-0009-2017.
153. Becker, E.; Projahn, M.; Burow, E.; Käsbohrer, A. Are There Effective Intervention Measures in Broiler Production against the ESBL/AmpC Producer *Escherichia coli*? *Pathogens* **2021**, *10*, 608, doi:10.3390/pathogens10050608.
154. Olaru, I.D.; Walther, B.; Schaumburg, F. Zoonotic Sources and the Spread of Antimicrobial Resistance from the Perspective of Low and Middle-Income Countries. *Infect. Dis. Poverty* **2023**, *12*, doi:10.1186/s40249-023-01113-z.
155. Musa, L.; Proietti, P.C.; Marenzoni, M.L.; Stefanetti, V.; Kika, T.S.; Blasi, F.; Magistrali, C.F.; Toppi, V.; Ranucci, D.; Branciari, R.; et al. Susceptibility of Commensal *E. coli* Isolated from Conventional, Antibiotic-Free, and Organic Meat Chickens on Farms and at Slaughter toward Antimicrobials with Public Health Relevance. *Antibiotics* **2021**, *10*, doi:10.3390/antibiotics10111321.
156. Phillips, I.; Casewell, M.; Cox, T.; De Groot, B.; Friis, C.; Jones, R.; Nightingale, C.; Preston, R.; Waddell, J. Does the Use of Antibiotics in Food Animals Pose a Risk to Human Health? A Critical Review of Published Data. *Journal of Antimicrobial Chemotherapy* **2004**, *53*, 28–52, doi:10.1093/jac/dkg483.

 doi:10.20944/preprints202605.2038.v1

157. Samreen; Ahmad, I.; Malak, H.A.; Abulreesh, H.H. Environmental Antimicrobial Resistance and Its Drivers: A Potential Threat to Public Health. *J. Glob. Antimicrob. Resist.* **2021**, *27*, 101–111, doi:10.1016/j.jgar.2021.08.001.
158. Algammal, A.M.; Hetta, H.F.; Elkelish, A.; Alkhalifah, D.H.H.; Hozzein, W.N.; Batiha, G.E.S.; Nahhas, N. El; Mabrok, M.A. Methicillin-Resistant *Staphylococcus aureus* (MRSA): One Health Perspective Approach to the Bacterium Epidemiology, Virulence Factors, Antibiotic-Resistance, and Zoonotic Impact. *Infect. Drug Resist.* **2020**, *13*, 3255–3265, doi:10.2147/IDR.S272733.
159. Stefani, S.; Chung, D.R.; Lindsay, J.A.; Friedrich, A.W.; Kearns, A.M.; Westh, H.; MacKenzie, F.M. Methicillin-Resistant *Staphylococcus aureus* (MRSA): Global Epidemiology and Harmonisation of Typing Methods. *Int. J. Antimicrob. Agents* **2012**, *39*, 273–282, doi:10.1016/j.ijantimicag.2011.09.030.
160. McEwen, S.A.; Fedorka-Cray, P.J. Antimicrobial Use and Resistance in Animals. *Clinical Infectious Diseases* **2002**, *34*, S93–S106, doi:10.1086/340246.