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Antimicrobial Resistance in *Escherichia coli* in Indonesia: A One Health Perspective

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Abstract

Antimicrobial resistance has become a major global health concern affecting humans, animals, and the environment. The increasing occurrence of antibiotic resistant bacteria threatens the effectiveness of antimicrobial therapy and poses serious public health risks. This review aims to describe the occurrence and distribution of antimicrobial resistant Escherichia coli across humans, animals, wildlife, and environmental sources using a One Health perspective. A literature review approach was conducted by collecting scientific articles published between 2015 and 2025 from international and national databases including PubMed, Scopus, and Google Scholar. Articles were selected based on relevance to antimicrobial resistance in Escherichia coli within human, animal, and environmental contexts. The reviewed studies indicate that Escherichia coli isolates frequently show resistance to commonly used antibiotics such as ampicillin, tetracycline, fluoroquinolones, and third generation cephalosporins. Multidrug resistant strains and extended spectrum beta lactamase producing bacteria have been reported in clinical samples, livestock, companion animals, wildlife, and environmental samples including wastewater and river water. These findings highlight the interconnected nature of antimicrobial resistance transmission between humans, animals, and the environment. Integrated surveillance and responsible antibiotic use are essential to control the spread of antimicrobial resistance through the One Health approach.

Keywords: *Antimicrobial Resistance, Escherichia coli, Indonesia, One Health*

INTRODUCTION

Antibiotic resistance (AMR) is a problem faced by every country on every continent (Bronzwaer et al., 2022; Wozniak et al., 2022; Gandra et al., 2020; Kariuki et al., 2022). Low- and lower-middle-income countries have a higher burden of antibiotic resistance compared to upper-middle-income or high-income countries (Pokharel et al., 2019). Low levels of knowledge about AMR, low levels of AMR awareness, inadequate education regarding antimicrobial use, low adherence to antimicrobial guidelines, and a lack of commitment to antimicrobial management contribute to the high incidence of AMR in developing countries (Coyne et al., 2019; Dewi et al., 2023). The indiscriminate use of antimicrobials in animal and human health encourages the development of AMR in various bacterial species in the environment (Coyne et al., 2020).

The increasing incidence of AMR in a country is correlated with increasing human population (Ikhimiukor et al., 2022), meat consumption (Ma et al., 2021; Anelia et al., 2023), and increasing waste contaminating the environment (Wu et al., 2023). Indonesia and other Southeast Asian countries are considered AMR “hot spots” due to their high human populations, which are not supported by economic development, limited health systems, a high variety of infectious diseases, and weak antibiotic policies (Limato et al., 2022). Indonesia has a large population of around 260 million people (Mboi et al., 2022) with a consumption requirement of animal protein from meat, milk, fish, chicken, and eggs reaching 11.49 kg/capita/year for beef, 94.55 kg/capita/year for fish, 49.55 kg/capita/year for chicken, 30.77 kg/capita/year for milk, and egg consumption of 37.07 kg/capita/year (Suryana et al., 2021; Anindita et al., 2022). Indonesians contribute 381 million tons of plastic waste annually, which can pollute soil, groundwater, surface water, rivers, and the sea (Luqman et al., 2021). In Indonesia, people can easily buy antibiotics without a prescription, there are more than 5,000 licensed drug stores operating in Indonesia that provide medicines for humans and animals (Kimura et al., 2020; Ferdiana et al., 2021).

Data in Indonesia shows that inappropriate antibiotic use occurs not only in humans but also in the livestock and fisheries sectors (Efendi et al., 2022; Fahmi et al., 2024). Unfortunately, data on antibiotic use in lower-middle-income countries is still very limited, making it difficult to prevent the spread of AMR (Cardinal et al., 2019; Yanestria et al., 2022). To date, AMR data in Indonesia has only been based on the Global Antimicrobial Resistance and Use Surveillance System (GLASS), which only provides data from 20 selected hospitals in Indonesia (WHO, 2022).

A comprehensive AMR monitoring system is needed to support the One Health system nationally and globally so that transmission from and to human-animal populations can be identified. In this review, we focus on antimicrobial-resistant *Escherichia coli* (*E. coli*) bacteria to monitor the level of AMR incidence in humans, animals, and the environment. The occurrence of AMR in *E. coli* bacteria is important to monitor because they can transfer genes horizontally which makes them able to spread antibiotic resistance to other bacteria in the wider environment (Mangroliya et al., 2025).

Compared with other pathogenic bacteria such as *Staphylococcus aures, Salmonella spp., and Pseudomonas aeruginosa, Eschericia coli* is more frequently used as an indicator bacteroim in AMR surveillance because of its widespread presence in humans, animals, food, and environmental source. *E. coli* is considered highly representative for describing the transmission dynamic of AMR within the One Health framework (Anjum et al., 2021; Smit et al., 2023). Furthermore, *E. coli* has a high capacity to acquire and transfer resistance gene through horizontal gene transfer mechanisms, particularly via plasmids carrying resistance genes such as blaCTX-M, thereby facilitating the rapid dissemination of antimicrobial resistance among bacterial populations (Mwakyoma et al., 2023). The study by Iryawati et al. (2025) also demonstrated similiarities in genotypic and phenotypic resistance patterns among *E. coli* isolates originating from humans and animals, indicating the potential for cross sector transmission of resistant bacteria.

This review aims to synthesize available evidence on antimicrobial resistant *Escherichia* *coli* in humans, livestock, companion animals, wildlife, and the environment in Indonesia using a One Health perspective to identify knowledge gaps and policy priorities.

MATERIALS AND METHODS

This study used a literature review approach to collect and analyze scientific publications related to antimicrobial resistance in *Escherichia coli*. Literature was obtained from several scientific databases including PubMed, Scopus, and Google Scholar. Articles published between 2015 and 2025 were included in this review. The search was conducted using keywords such as antimicrobial resistance, antibiotic resistance, *Escherichia coli*, One Health, livestock, wildlife, and environmental contamination.

The inclusion criteria were as follows, (1) articles reporting antimicrobial resistance in *Escherichia coli*, (2) studies conducted in humans, animals, wildlife, or environmental samples, (3) articles published in peer reviewed journals. Articles were excluded if they did not report antimicrobial susceptibility testing results or if the full text was unavailable.

A total of 101 articles met the inclusion criteria and were included in the final analysis. Data extracted from each article included bacterial species, sample source, antibiotic resistance profile, and study location..

RESULTS

Several studies have reported increasing antimicrobial resistance among bacterial isolates obtained from human clinical samples. The most frequently reported bacterial species associated with resistant infections is *Escherichia coli*. In addition, other opportunistic pathogens such as Klebsiella pneumoniae are also commonly detected in hospital environments. Table 1 presents research data on antibiotic resistance in *E. coli* bacteria in humans in Indonesia.

The studies summarized in Table 1 indicate that antibiotic-resistant strains of *Escherichia coli* are widely distributed across clinical settings, livestock production systems, and environmental sources. This widespread occurrence suggests that antimicrobial resistance can circulate between different sectors, reflecting the interconnected transmission pathways emphasized in the One Health framework. The presence of resistant bacteria in these sectors indicates that antimicrobial resistance is not confined to healthcare settings but is influenced by interactions among humans, animals, and the surrounding environment.

In clinical settings, bacterial pathogens such as *Escherichia coli* and Klebsiella pneumoniae are frequently reported as major contributors to antimicrobial resistance. Several studies have demonstrated that clinical isolates of *Escherichia coli* often exhibit resistance to β-lactam antibiotics, including ampicillin and third-generation cephalosporins. The emergence of strains producing extended-spectrum β-lactamases further increases resistance to antibiotics that are commonly used for the treatment of bacterial infections (Maharani et al., 2021). This situation is supported by the detection of multidrug-resistant isolates in patients with urinary tract infections as well as in hospitalized individuals (Prastiyanto et al., 2024).

Table 1. Reported antibiotic resistance profiles of *Escherichia coli* isolates from human, animal, and environmental sources based on various studies within the One Health framework

Bacteria	Sector	Sample Source	Resistant antibiotics	Reference
ESBL-producing *E. coli*	Human	Clinical samples	Cefotaxime, ceftazidime, ceftriaxone, ampicilin	Azizah et al., 2025
E. coli	Human	Urinary tract infection patients	Ampicillin, tetracycline, ciprofloxacin	Hasanah and Dewi, 2024
E. coli	Human	Gut flora of hospitalized patients	Ampicillin, trimethoprim sulfamethoxazole	Hidayah et al., 2020

Escherichia coli and *Klebsiella pneumoniae* producing ESBL	Human	Hospital Patients	Fluoroquinolones, cephalosporins	Sanjaya et al., 2025
ESBL-producing *E. coli*	Human	Pneumonia patients	Cefotaxime, ceftazidime, ceftriaxone	Manuaba et al., 2021
E. coli	Human	Urinary tract infection patients	Ampicillin, ciprofloxacin, trimethoprimsulfamethoxazole	Prastiyanto et al., 2024
E. coli	Animal	Dairy farm environments	Ampicillin, tetracycline, streptomycin, sulfamethoxazole	Widodo et al., 2023a
E. coli	Environment	Dairy farm wastewater	Ampicillin, tetracycline, chloramphenicol, sulfamethoxazole	Widodo et al., 2023b
E. coli	Environment	Dairy cattle wastewater	Ampicillin, tetracycline, cefotaxime	Yanestria et al., 2026
ESBL-producing *Escherichia coli* (blaTEM, blaCTX-M genes)	Animal	Milk from dairy cattle	β-lactam antibiotics including ampicillin and cephalosporins	Widodo et al., 2023c
E. coli	Animal	Poultry bacterial isolate	Tetracycline, ampicillin	Hilmi et al., 2024

Beyond human clinical cases, resistant *Escherichia coli* has also been identified in livestock production systems such as dairy cattle and poultry farms. The presence of multidrug-resistant strains in animal-derived samples suggests that the use of antibiotics in livestock production may contribute to the selection and persistence of resistant bacteria. These bacteria can potentially be transmitted to humans through direct contact with animals, consumption of contaminated animal products, or exposure to contaminated environments.

Environmental compartments also play an important role in the dissemination of antimicrobial resistance. Wastewater generated from hospitals and livestock production systems has been reported to contain resistant bacterial populations carrying antimicrobial resistance genes. These environmental reservoirs may facilitate the spread of resistance determinants through water systems, soil, and agricultural environments. Consequently, bacteria originating from these sources may re-enter human populations through multiple transmission pathways, including contaminated water, food chains, and environmental exposure (Kunarisasi et al., 2025).

Overall, the distribution of antibiotic-resistant bacteria across human, animal, and environmental sources highlights the complex ecology of antimicrobial resistance. These findings emphasize the importance of integrated surveillance and control strategies involving medical, veterinary, and environmental sectors to effectively address the growing challenge of antimicrobial resistance.

DISCUSSION

AMR in *Escherichia coli*

AMR in *E. coli* has become an important global public health concern due to its increasing prevalence in humans, animals, food products, and enviromental sources. Compared with many other bacterial species, *E. coli* is frequently used as an indicator organism in AMR surveillance because of its widespread distribution and its ability to reflect antimicrobial exposure across multiple sectors within the One Health framework (Anjum et al., 2021; Smit et al., 2023). In Indonesia, the emergence of antimicrobial resistant *E. coli* has been increasingly reported in clinical settings, livestock production systems, and environmental reservoirs, indicating the growing complexity of AMR transmission pathways (Dharmayanti et al., 2025)

One of the major factors contributing to the persistence of AMR in *E. coli* is its ability to acquire and disseminate resistance genetic such as blaCTX-M enables rapid disssemination of AMR between bacterial populations originating from human, animals, and environmental source (Mwakyoma et al., 2023). This Characteristic makes *E. coli* not only an opportunistic pathogen but also an important reservoir of resistance genes.

Enviromental contamination also contributes substantially to the dissemination of Antimicrobial resistant *E. coli*. Wastewater from hospital, households, farms, and slaugterhouse may contain both antimicrobial residue and resistant bacteria, facilitating the persistance of resistance determinants in enviromental reservoirs. Recent One health studies in Indonesia demonstrated the presence of multidrug resistant. *E. coli* in broiler chickens, market environments, and human associated surfaces, suggesting that traditional markets may function as important transmission interfaces for resistant bacteria (Ferasyi et al., 2025).

Antibiotic Resistance in Humans

Easy access to antibiotics has prevented AMR control from being optimal in Indonesia. People can easily purchase antibiotics at pharmacies without a prescription (Siahaan et al., 2022). COVID-19 has triggered increased antibiotic consumption, resulting in increased antimicrobial resistance in Indonesia (Subagdja et al., 2022). *Escherichia coli* in the blood, urinary tract infections (UTIs), wounds, and stool are commonly used as indicators of AMR in humans (Sunarsi et al., 2023). Table 1 presents research data on antibiotic resistance in *E. coli* bacteria in humans in Indonesia.

Clinical studies conducted in Indonesia healthcare facilities further demonstrate that *Escherichia coli* remains one of the most frequently isolated pathogens associated with urinary tract infections and blood stream infections. The bacterium is widely used as an epidemiological indicator to evaluate antibiotic resistance trends because its resistance profile reflects antibiotic exposure within healthcare settings. Several hospital-based investigations have reported increasing resistance to commonly prescribed antibiotics, indicating growing selective pressure resulting from empirical antibiotic use. These findings reinforce the importance of continuous surveillance of clinical isolates to understand resistance dynamics and to support evidence base antibiotic policies in human healthcare systems (Adhima et al., 2022; Hidayah et al., 2020)

The emergence of multidrug resistant isolates and ESBL producing *E. coli* has also been increasingly documented in clinical settings. Such resistance mechanisms reduce the effectiveness of first line antibiotic therapy and complicate infection management strategies. The presence of resistant strains contributes to prolonged hospitalization and increased treatment complexity, highlighting the need for strengthened antimicrobial stewardship programs and improved diagnostic guided therapy in Indonesian healthcare facilities (Effendi et al., 2024; Hasanah & Dewi, 2024; Perdana et al., 2023)

Based on our data, research on antibiotic resistance in humans in Indonesia was conducted in 2020 and 2021. This antibiotic susceptibility testing was conducted because 2020 and 2021 were the post-COVID-19 era (Kabiri-Samani et al., 2022). During the COVID-19 pandemic, many patients with respiratory infections received antibiotic therapy (Mahida et al., 2022) due to concerns about secondary infections in COVID-19 patients, especially in low- and lower-middle-income countries (Lucien et al., 2021).

The COVID-19 era saw an increase in antibiotic prescriptions, changes in antibiotics, and longer parenteral antibiotic administration in patients with severe infections (Sinto et al., 2024). During the COVID-19 period in Indonesia, it was very common for pharmacy technicians to sell drugs directly to clients without a doctor's prescription (Ferdiana et al., 2021). Clients generally purchased the antibiotic azithromycin because it was included in the management guidelines for patients infected with COVID-19 (Haryanto & Sari, 2022). The antibiotic azithromycin is recommended for COVID-19 patients because the antibiotic has shown the ability to reduce the production of pro-inflammatory cytokines (IL-8, IL-6, and TNF α), modulate T-helper, and reduce oxidative stress (Pani et al., 2020).

On the other hand, the use of antibiotics in Indonesia has not been balanced with an adequate level of knowledge by the public, the level of knowledge of Indonesian people regarding antibiotics is closely related to economic background, education and gender (Widayati et al., 2012). In Boyolali for example, 50% of respondents considered stopping the use of antibiotics when the symptoms that occurred in themselves disappeared, the findings showed that male respondents with low income and education levels and respondents living in rural areas did not have sufficient knowledge about the side effects of inappropriate antibiotic use (Karuniawati et al., 2021) in contrast to the results of a survey conducted by Yunita et al., (2022) on female respondents who were highly educated, who lived in urban areas, and had experience in using antibiotics with easy access to health workers, they tended to have good knowledge of using antibiotics, women were family caregivers who were believed to have better knowledge of compliance with the completion of antibiotic regimens.

The inappropriate use of antibiotic can lead to antimicrobial resistance, which may have significant consequences for public health. Therefore, it is essential to understand how communities consume antibiotics and to evaluate the patterns of bacterial resistance occurring within the community. Such understanding is important to support effective education, communication, and dissemination of accurate information to the public regarding the prevention of increasing antimicrobial resistance, the spread of resistant bacteria, and the public health risks associated with antimicrobial resistance in the community (Mangunsong et al., 2025). In addition, the use of educational videos addressing the danger of antimicrobial resistance has been considered an effective approach for improving public knowledge. Compared with printed educational materials and the traditional lectures, video based education is generally more cost effective and can be accepted by a broader range of age groups (Syam et al., 2025).

Escherichia coli bacteria in Indonesia have been proven to be resistant to 4th generation cephalosporin antibiotics (Marzah et al., 2024; Pradnyana et al., 2025). bacterial resistance to various antibiotics can result in low levels of therapeutic success against infectious agents, new antimicrobials are needed that have better mechanisms and efficacy against resistant bacteria, in addition, antimicrobial resistance can have an impact on the decline in the economy due to disrupted productivity and increased treatment costs if wounds occur due to longer hospitalizations, long-term antibiotic therapy, and special wound care products.

Antibiotic Resistance in Animals

The presence of antimicrobial resistance in livestock farming is closely related to livestock management (Sawodogo et al., 2023). Antibiotic use in pig and poultry farming has led to increased antibiotic use in low- and lower-middle-income countries (Muloi et al., 2025). Farmers' knowledge, awareness, and vigilance regarding antibiotic use, antibiotic residues, and antibiotic resistance are crucial to preventing antibiotic resistance in livestock (Suherman et al., 2023). Animal products are one factor contributing to increased resistance in humans due to exposure to low levels of antibiotics as residues in animal products such as eggs, milk, and meat (Dyar et al., 2020). In addition, farmers who use antibiotics to promote animal health as antibiotic growth promoters (AGP) with the aim of improving livestock health add to the burden of increasing antibiotic resistance in bacteria in livestock (Sudarnika et al., 2023). The Indonesian government has issued regulations prohibiting the use of AGP, but research results by Widiasih et al. (2024) show that there are still antibiotic residues in livestock products in fish (15.65%, 18/115), chicken meat (11.3%, 13/115), and eggs (0.87%, 1/114). Administering antibiotics to livestock through injection has been shown to produce residues that exceed the standard compared to oral or parenteral administration (Katz and Brady, 2000).

Studies conducted in animal production systems in Indonesia further indicate that *Escherichia coli* isolated from livestock frequently exhibits resistance to multiple classes of antibiotics commonly used in veterinary practice. The occurrence of resistant isolates reflects cumulative antibiotic exposure within intensive farming systems and highlights the role of livestock as an important reservoir of antimicrobial resistance. Surveillance findings demonstrate that resistance patterns observed in animal isolates often overlap with resistance profiles detected in human clinical settings, suggesting potential transmission pathways through direct contact, food chains, or shared environmental reservoirs. These findings emphasize the need for strengthened antibiotic stewardship and routine monitoring programs within animal health sectors to reduce the emergence and dissemination of resistant bacteria (Agatha et al., 2023; Maulana et al., 2021)

Easy access to antibiotics for livestock farmers, inadequate sanitation on farms, and unhygienic environmental conditions have led to increased antibiotic resistance in livestock in Indonesia (Suherman et al., 2023). Livestock live in groups, facilitating the spread of bacterial resistance from one animal to another, the environment, and the community (Karuniawati et al., 2021). The use of antibiotics in humans and animals has driven the spread of AMR in wildlife, where wildlife has the potential to spread AMR to the wider environment, triggered by anthropogenic human activities (Agustin et al., 2024a). It is believed that wildlife in the same environment can carry similar bacteria that have become resistant to humans, animals, and the environment (Lee et al., 2022). Understanding the spread of AMR in animals requires interdisciplinary collaboration within the One Health sector to control its wider spread (Caudell et al., 2020).

In addition to livestock management practices, molecular studies have demonstrated that horizontal gene transfer contributes substantially to the persistence and dissemination of resistance determinants among bacterial populations in animal environments. Mobile genetic elements enable resistant bacteria originating from farms to persist in surrounding ecosystems and potentially reenter animal populations. This dynamic exchange highlights that antimicrobial resistance in animal is not confined to farm boundaries but forms part of broader ecological network linking humans, animals, and environmental reservoirs (Neil et al., 2021)

Veterinarians' knowledge of antibiotic use is closely related to the incidence of resistance in pets, aquatic animals, and livestock (Wangmo et al., 2021). Penicillin antibiotics are the antibiotics most commonly resistant in animals in Indonesia, as they are in humans, followed by macrolide antibiotics, tetracyclines, quinolones, second-generation fluoroquinolones, aminoglycosides, and chloramphenicol. In a study by Jannah et al., (2024), veterinarians in Indonesia stated that medicines are easily accessible to farmers without contacting animal health professionals. Farmers will only call a veterinarian if their livestock does not recover after several days of treatment.

Antibiotic Resistance in Companion Animals

The close relationship between pets and their owners results in shared antibiotic resistance and extended-spectrum beta-lactamase (ESBL) genes in both (Naziri et al., 2022). Pet owner compliance with antibiotic use influences pet resistance. Owners face challenges when administering antibiotic therapy to their pets, including difficulty administering medication, timing, uncommon tablet sizes, and cost during therapy (Candellone et al., 2023). In Indonesia, there has been no research on pet owners' awareness and vigilance regarding pet care, or on veterinarians' perceptions of drug therapy and antibiotic prescriptions for pets. The knowledge of veterinarians in Indonesia regarding the use of antibiotics from research data by Wijayanti et al. (2023) is quite good, from 101 veterinarians working as independent practices, animal clinics, animal hospitals, and joint practices, the results obtained were that the rational use of antibiotics based on diagnostic results was 48.25%, based on laboratory test results was 34.32%, and based on personal experience was 17.41%.

Microbiological investigations have demonstrated that companion animals may harbor antimicrobial resistant bacteria that are genetically similar to isolates identified in humans. Resistant strains of *E. coli* and other gram-negative bacteria isolated from dogs and cats frequently carry resistance genes that are also present in clinical isolates from human infections. The presence of these shared resistance determinants suggest that close physical contact between pets and their owners may facilitate the bidirectional exchange of resistant bacteria within household environments. This interaction highlights the importance of considering companion animals as part of the epidemiological network of antimicrobial resistance within the One Health framework (Khairullah et al., 2024)

The challenge of increasing antibiotic resistance in pets can be seen from how good the owners' compliance and knowledge regarding the use of antibiotics, in Singapore, dog owners who are mostly women (63.9%) who are highly educated (86.9%) and a worker (76.4%) have poor knowledge about the use of antibiotics for pets (46.3%) while cat owners have worse knowledge about the use of antibiotics than dog owners (55.2%) where 67.1% of both showed poor knowledge about AMR (Aithal et al., 2025). In contrast to the results of research in the United States, the results of research by Frey et al. (2024) on pet owners concluded that (1) the educational background of pet owners influences their knowledge regarding antibiotic use, (2) compliance with recommendations for antibiotic use in pets can occur if owners have confidence in veterinarians, (3) owners tend to prefer to hear about successful experiences of therapy carried out by veterinarians in similar cases regarding the absence of the need for antibiotic use.

The growing number of companion animal in urban environments further increase the frequency oh human animal interaction, which may facilitate the circulation of resistant bacteria between domestic settings and broader community environments. Since companion animals commonly share household environments with humans, resistant microorganisms originating from veterinary treatment or environmental exposure may persist in domestic settings and contribute to the broader dissemination of antimicrobial resistance. Therefore, the prudent use of antibiotics in veterinary practice, along with effective communication between veterinarians and pet owners, represents a critical component of antimicrobial stewardship strategies within the companion animal sector (Frey et al., 2024).

Antibiotic Resistance in Livestock

In Indonesia, there is no comprehensive data recording antibiotic use in every livestock that produces animal products. Only a few sectors have recorded antibiotic use, such as in the cattle farming sector (Triadi et al., 2022; Rahim et al., 2023; Zulfanisa et al., 2024; Pratama et al., 2025). iSIKHNAS (National Animal Health System) is a website portal reporting on livestock health that lists the therapies used by veterinarians or Paravets when treating cattle in Indonesia. There is no comprehensive national data in Indonesia regarding antibiotic use in broiler chickens, layers, goats, buffalo, and pigs. Scientific publications in 2017 derived from iSIKHNAS data show that the highest antibiotic consumption in cattle is in East Java, in fact, 30.49% of antibiotics used for cattle therapy in Indonesia are applied by veterinarians and 67.57% of antibiotics for therapy are applied by Paravets, these antibiotics are widely used for the treatment of viral infections (30.17%), parasitic infections (17.74%), bacterial infections (8.60%), and used for others (29.77%) (Yusuf et al., 2017; Nastiti et al., 2024). In Indonesia, antibiotic use in chickens reaches 99% in one production cycle, farmers are not accustomed to recording antibiotic administration as a daily routine, they often give doses deviating from veterinarian recommendations (Sani et al., 2023). On broiler chicken farms, antimicrobials are given for an average of 12 days of treatment in one production cycle (30 days) with a range of administration from 4 to 22 days (Sani et al., 2024).

The livestock sector represents one of the major contributors to the emergence of antibiotic resistance due to the relatively intensive use of antimicrobials within animal production systems. Antibiotics are commonly administered for therapeutic as wel as disease prevention in high density livestock populations, creating selective pressure that promotes the emergence of resistant bacterial strains. Studies conducted in Indonesia have reported that *E. coli* isolates obtained from livestock exhibit resistance to multiple antibiotics commonly used in veterinary practice (Agatha et al., 2023).

Beyond the occurrence of resistant bacteria in live animals, resistant microorganisms have also been identified in animal derived food product such as meat and milk, indicating that animal product may serve as potential transmission pathways for AMR bacteria along the food chain (Rahim et al., 2023). The presence of resistant bacteria in the products suggests that the food production and distributing system can facilitate transmission pathways linking livestock reservoirs and human exposure (Hosain et al., 2021). These findings emphasize the importance of implementing prudent antibiotic use and strengthening food safety surveillance systems to reduce the risk of antimicrobial resistance dissemination through the consumption of animal derived food (Ningtyas et al., 2024). From a One Health perspective, the control of antibiotic resistance in livestock production therefore requires coordinated interventions that integrate animal health management, food safety regulation, and public health monitoring systems (Caudell et al., 2020; Dyar et al., 2020).

The spread of antibiotic resistance between livestock and humans is closely related to farmer knowledge, antibiotic prescribing policies by veterinarians, and the food chain (Malik et al., 2023). Most developing countries have not implemented measures to prevent the spread of AMR from livestock products to the dinner table, thus threatening global public health (Hosain et al., 2021; Ningtyas et al., 2024). In Indonesia, antibiotic use tends to be greater in intensive livestock farming than in small-scale livestock farming (Dewi et al., 2024). The limited research data related to AMR in livestock in Indonesia does not clearly describe the level of AMR in livestock in Indonesia. Based on the data above, the antibiotics commonly studied are the beta-lactam group, primarily penicillin. Penicillin antibiotics can be easily purchased by farmers at poultry shops without a prescription from a veterinarian.

Antibiotic Resistance in Wildlife

Wildlife is widely considered to be carriers and spreaders of AMR from the human environment to the natural environment, as sentinels of antibiotic resistance in a region, and as agents that transfer AMR between other species (Puarada et al., 2024; Agustin et al., 2024c). AMR bacteria in wildlife are closely related to environmental pollution (Laborda et al., 2022). The interaction between wildlife and various environments leads to the development of resistant bacteria in their bodies (Soto-Lopez et al., 2024). The development of AMR in wildlife is quite dynamic, so preventing the unwise use of antibiotics in humans and animals can facilitate the transmission of resistant bacteria in wildlife. Wildlife commonly sampled to serve as sentinels for environmental AMR include wildlife in zoos, wildlife in the wild, and wildlife in human environments (Ramey and Ahlstrom, 2020). AMR investigations were tested using a molecular approach to observe taxonomic diversity, estimate mutations, and estimate the distribution that occurred (Smoglica et al., 2023).

Notably, the detection of ESBL genes in bacterial isolates obtained from bats indicates that wildlife may function as indicator of antimicrobial resistance dissemination at the ecosystem level (Agustin et al., 2024c). The presence of these resistance determinants suggests that environmental contamination and ecological interactions between humans, domestic animals, and wildlife may facilitate the circulation of resistant bacteria across ecological boundaries (Mustika et al., 2024).

Exposure due to anthropogenic activities such as waste disposal, wastewater management, livestock farming, and agriculture can contaminate wildlife with AMR bacteria (Navarro-Gonzalez et al., 2018). However, unlike captive wildlife or zoos, they receive antibiotic therapy when needed, resulting in higher AMR bacterial levels compared to non-captive wildlife (Min et al., 2023). Wildlife living far from human environments, on the other hand, receive less exposure to humans and livestock, resulting in significantly lower bacterial resistance, except for those animals that can migrate from the wild to forage in human environments and return to the wild to sleep and reproduce (Mbehang Nguema et al., 2021). Fecal-oral transmission is the most common mechanism, but the rise of extreme culinary trends has increased the estimated risk of AMR transmission from wildlife to humans (Morrison and Rubin, 2020).

Antibiotic Resistance in the Environment

Research on antibiotic resistance in *Escherichia coli* in environmental settings in Indonesia has primarily focused on the presence of antibiotic residues in soil and water originating from agricultural and hospital activities. Various source of waste, including household waste (Benitez-Rico et al., 2023), agricultural waste (Zalewska and Popowska, 2020), livestock waste (Robles-Jimenez et al., 2021), fisheries waste (Koike et al., 2021), hospital waste (Ahmad et al., 2021), industrial waste (Wang et al., 2021), and wastewater treatment plant (WWTP) effluents (Rodriuez-Mozaz et al., 2020), contribute to the accumulation of antibiotic residues in environmental compartments such us soil, air, and water (Zhuang et al., 2021). The accumulation of antibiotics in the environment increases the risk of harm to soil microorganisms and plants (Carballo et al., 2022). Several articles have reported the transfer of resistance genes in the environment (Li and Zhang, 2022; Alduina, 2020; Sanderson et al., 2016). The highest levels of antibiotic residues come from agricultural waste, farmland that uses animal feces as fertilizer, and vegetable fields have the highest capacity to accumulate antibiotics because the soil used for growing vegetables has good absorbent properties (Lavrukhina et al., 2022).

The findings from the reviewed studies demonstrate that antimicrobial resistant *Escherichia coli* is widely distributed across multiple ecological sectors including humans, animals, wildlife, and environmental systems. Clinical isolates from human patients frequently exhibit resistance to beta lactam antibiotics, tetracycline, and fluoroquinolones. Similar resistance patterns have also been reported in livestock and companion animals, suggesting that antibiotic use in veterinary practices contributes to the selection of resistant bacterial strains. In addition, environmental samples such as river water and hospital wastewater have been identified as reservoirs of resistant bacteria and resistance genes. These environmental reservoirs may facilitate the dissemination of antimicrobial resistance through water systems, agricultural activities, and human contact. The interconnected occurrence of resistant bacteria across these sectors highlights the importance of understanding antimicrobial resistance through the One Health framework.

Recent studies conducted in Indonesia further demonstrate that *Escherichia coli* isolates obtained from river water and market environments exhibit resistance profiles comparable to those observed in human clinical isolates, indicating potential connectivity between environmental reservoir, humans, and animals in the dissemination of antibiotic resistance (Fahmi et al., 2024). Therefore, effective antimicrobial resistance control requires cross sectoral approaches integrating waste management practices, antibiotic use monitoring, and environmental surveillance systems within the One Health framework (Putri et al., 2023; Fahmi et al., 2024).

CONCLUSION

Antimicrobial resistance in *Escherichia coli* has been widely reported in humans, animals, wildlife, and environmental samples. The reviewed studies demonstrate that resistance to commonly used antibiotics such as beta lactam antibiotics, tetracycline, and fluoroquinolones is increasingly observed across different ecological sectors. The presence of multidrug resistant and extended spectrum beta lactamase producing strains further complicates the management of bacterial infections.

The interconnected occurrence of antimicrobial resistant bacteria highlights the importance of implementing the One Health approach to monitor and control antimicrobial resistance. Integrated surveillance, responsible antibiotic use, and improved public awareness are essential strategies to reduce the spread of resistant bacteria and protect the effectiveness of antimicrobial therapy in the future.

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