

## Antimicrobial resistance at the human–animal–environment interface: A focus on antimicrobial-resistant *Escherichia coli* transmission dynamics, clinical implications, and future directions

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### Abstract

Understanding and combating antimicrobial resistance (AMR) is increasingly centered on the intricate relationship between humans, animals, and the environment, with *Escherichia coli* being the main source of AMR-related fatalities worldwide. *E. coli*, though prevalent in the intestines of humans and warm-blooded creatures, demonstrates wide ecological adaptability in both intestinal and extraintestinal habitats. This study explores the dynamics, implications, and future directions of antimicrobial-resistant *E. coli* (AREC) transmission and clinical significance. We investigated the spread of antibiotic-resistant strains among humans, animals, and the environment, illuminating the impact of healthcare and agriculture practices, as well as environmental contamination. The implications of AREC infections are addressed, emphasizing the challenges in treatment due to limited antibiotic options, increased morbidity and mortality rates, and economic burdens on healthcare systems and agriculture, as well as the urgent need for a One Health approach to combat AMR through collaborative efforts across disciplines. Proposed future directions encompass enhanced surveillance, innovative antimicrobial stewardship, and alternative treatment modalities.

**Keywords:** antimicrobial stewardship, antimicrobial-resistant *Escherichia coli*, clinical implications, One Health, surveillance strategies, transmission dynamics.

### Introduction

*Escherichia coli*, a Gram-negative bacterium with a rod shape, inhabits intestine of warm-blooded creatures, including humans and animals. It can also live in soil, plants, vegetables, water, and other environments [1, 2]. Some strains of *E. coli*, while generally harmless, are capable of producing virulence factors and causing disease. Some pathogenic strains can cause several illnesses in humans, ranging from mild gastrointestinal discomfort to severe infections such as urinary tract infections (UTIs), bloodstream infections, and meningitis [3].

Certain *E. coli* strains responsible for foodborne diseases are among the pathogenic types. These strains are known to generate toxins, resulting in symptoms such as abdominal pain, diarrhea, vomiting, and fever [3, 4]. Specific strains of *E. coli*, like Shiga toxin-producing *E. coli* (STEC), can lead to devastating consequences such as hemolytic uremic syndrome (HUS), a condition that can cause kidney failure and even death, primarily affecting young children and elderly [3–5].

*E. coli* as a major human bacterial infection causes, significantly burdens public health systems, particularly in resource-limited countries, with substantial morbidity and mortality [6, 7]. Furthermore, the incidence of antimicrobial resistance (AMR) in *E. coli* is increasing, and it ranks third among the 12 antibiotic-resistant priority pathogens identified by the World Health Organization [8]. In 2019, *E. coli*, alone among pathogens, accounted for the majority of AMR deaths globally [6]. Antimicrobial-resistant

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*E. coli* (AREC) have significant impacts on human, animal, and environmental health.

This review explores transmission dynamics among human and animal populations, environmental factors influencing resistance patterns, and clinical implications of AREC at the human–animal–environment interface, emphasizing their interconnectedness and calling for co-ordinated interventions.

### Overview of AMR and its Global Impact

AMR occurs as microbes develop abilities to withstand antibiotic treatments, diminishing their efficacy or even rendering them ineffective against infections [9, 10]. Misuse and overuse of antimicrobial drugs in human, veterinary, and agricultural medicine are fueling the emergence and spread of antibiotic-resistant bacteria, endangering global health [9, 11]. AMR compromises the efficacy of treatments, raises the risk of treatment failure, prolongs illness, and increases mortality from bacterial infections [6, 12, 13]. In 2019, an estimated 4.95 million deaths were associated with bacterial AMR, with *E. coli* being the leading cause [6]. The economic cost of antimicrobial-resistant infections and their management may reach US\$ 100 trillion globally by 2050 [14, 15].

### Importance of Understanding the Human–animal–environmental Interface in AMR Transmission

Addressing the emergence and spread of AMR requires recognizing the interconnectedness of

human health, animal health, and the environment (Figure-1) [16]. At the human-animal-environment interface, antimicrobial-resistant bacteria, genes, and residues circulate dynamically, promoting resistance dissemination across diverse ecosystems [17].

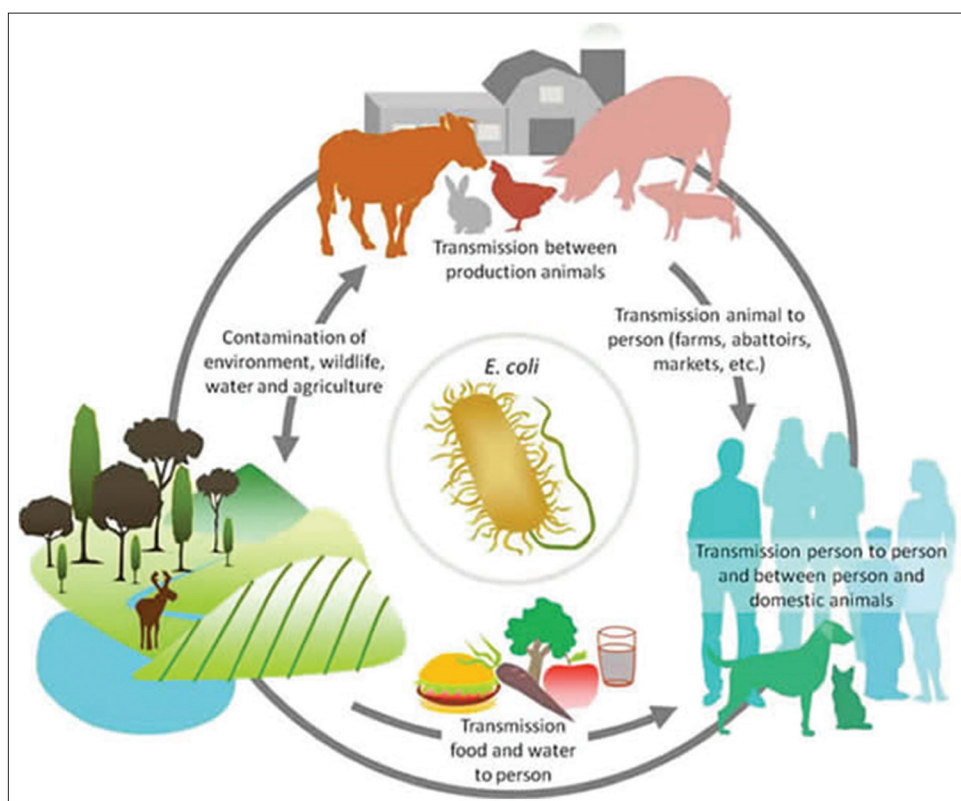
Antimicrobial use for livestock growth and disease control promotes bacterial resistance in both animals and their surroundings [11, 18]. These bacteria can contaminate animal food products and pose a risk to humans through consumption.

Improper disposal of pharmaceuticals, wastewater discharge, and agricultural runoff contributes to antimicrobial residues and resistant bacteria in the environment, adding complexity to AMR epidemiology [10, 18, 19]. Water bodies, soil, and vegetation function as reservoirs for antimicrobial-resistant pathogens, transmitting resistance determinants among humans, animals, and wildlife [20].

Comprehending the human-animal-environment interface is essential for creating comprehensive strategies to counteract AMR transmission [17]. By recognizing the interconnected nature of AMR dynamics and adopting collaborative approaches that involve stakeholders from multiple sectors, including human health, animal health, agriculture, environmental science, and policymaking, it is possible to mitigate the spread of AMR and safeguard public health on a global scale [17, 18].

### Mechanisms of AMR in *E. coli*

In *E. coli*, AMR is predominantly determined genetically, enabling the bacterium to evade



**Figure-1:** Transmission of antimicrobial resistance at the human-animal-environment interface [16].

antimicrobial agent impacts. These mechanisms consist of mutations in chromosomal genes, horizontal gene transfer (HGT) for resistance genes, and activation of resistance determinants by mobile genetic elements (MGEs) [3, 21, 22]. Devising effective strategies to combat AMR and preserve antimicrobial therapy efficacy necessitates a solid understanding of the genetic mechanisms of AMR in *E. coli*, the role of MGEs in dissemination, and the factors driving resistance gene development and spread.

#### Genetic mechanisms

Through spontaneous mutations in chromosomal genes related to drug targets or transport mechanisms, *E. coli* can acquire resistance to antimicrobial agents [3, 21]. These mutations can alter the structure or function of target sites, thereby reducing the binding affinity of antimicrobial agents and rendering them ineffective [21, 23]. Mutations in genes for bacterial ribosomal proteins or DNA gyrase confer antibiotic resistance, particularly to fluoroquinolones [24, 25].

Regulatory gene mutations leading to heightened efflux pump expression diminish intracellular antimicrobial agent concentrations [26, 27]. For instance, mutations in regulatory genes that control efflux pump expression can increase the efflux of antimicrobial agents, reducing intracellular drug concentrations and conferring resistance [26, 27].

#### Role of MGEs in AMR dissemination

MGEs (plasmids, transposons, and integrons) possess the ability to relocate within a genome or be transmitted between various strains. Plasmids, which are extrachromosomal DNA components, contain resistance genes to antimicrobial agents and accessory genes for virulence determinants and metabolic enzymes [28, 29]. *E. coli* can acquire resistance plasmids through conjugation, a process in which plasmid DNA is transferred from donor cells to recipient cells through direct cell-to-cell contact [30, 31]. Resistance genes from conjugative plasmids enable swift spread within bacterial populations, promoting AMR dissemination [28, 29].

Transposons are mobile DNA segments capable of transfer among various genomes, such as plasmids and chromosomes [29, 32]. AMR genes borne by transposons can transfer horizontally between bacterial strains through chromosomal or plasmid integration [32, 33]. Multiple resistance genes, enclosed in insertion sequences of composite transposons, facilitate the spread of intricate resistance traits [32, 34].

Integrons are genetic elements that capture and express gene cassettes encoding various functions, such as AMR [32, 35]. Integrons are often associated with MGEs such as transposons and plasmids, allowing the assembly and dissemination of multidrug resistance gene arrays [29, 32]. *E. coli* strains carrying integrons can acquire resistance gene cassettes through site-specific recombination events, contributing to the

diversification and dissemination of resistance determinants [36, 37].

### Factors Influencing the Development and Spread of Resistance Genes

#### Antimicrobial selection pressure

Antimicrobial agents exert pressure, causing the evolution and spread of resistance genes among bacterial populations [9, 18, 38]. Overuse and misuse of antibiotics across human, veterinary, and agricultural medicine contribute to the emergence and spread of AREC strains [39, 40].

#### HGT

*E. coli*'s resistance genes spread quickly among populations due to its proficiency in acquiring them through HGT mechanisms such as conjugation, transduction, and transformation [3, 21, 22]. Close proximity, high population densities, and selective conditions in bacterial populations favor HGT and the spread of AMR [41, 42].

#### Biofilm formation

On both biotic and abiotic surfaces, *E. coli* forms protective biofilms that promote bacterial survival and facilitate HGT [43, 44]. Biofilm-bound *E. coli* strains exhibit enhanced AMR due to drug penetration inhibition and metabolic dormancy, thereby perpetuating resistance gene propagation within biofilms [43–45].

#### Antimicrobial co-selection

The use of antimicrobial agents with distinct action mechanisms fosters the amassment of multiple resistance genes in *E. coli* populations [46, 47]. Exposure to one class of antimicrobial agents can select resistance traits conferring cross-resistance or co-resistance to other antimicrobial classes, leading to the emergence of multidrug-resistant (MDR) phenotypes [48].

### Transmission Dynamics of Human, Animal, and Environmental Reservoirs

ARECs spread is fueled by intricate exchanges among human, animal, and environmental reservoirs [18, 49]. Effectively addressing AMR dynamics is crucial for implementing successful strategies to contain its spread.

#### Zoonotic Transmission of Resistant *E. coli* Strains

The transmission of AREC from animals to humans poses a major public health risk [50]. Animals are the primary reservoirs of antibiotic-resistant *E. coli* strains, which result from the selective influence of antimicrobial application in veterinary medicine and agriculture [18, 39, 51]. Human contact with infected animals, consumption of contaminated animal products, or exposure to animal waste can lead to the acquisition of resistant strains [1, 18].

Human-animal interaction in communities such as agriculture, petting zoos, and pet households increases the risk of zoonotic transmission of antibiotic-resistant *E. coli* strains [1, 52]. Transmission

can occur through contaminated water or environmental reservoirs tainted with animal waste [18, 52, 53].

### **The Importance of Foodborne Transmission in Human Infection**

Uncooked meat, raw vegetables, and unpasteurized dairy products can harbor resistant *E. coli* strains and transmit them to humans [54, 55]. Consuming contaminated food with AREC causes gastrointestinal infections and related diseases [56, 57]. Incorrect food handling techniques, inadequate sanitation, and cross-contamination during food processing and distribution propagate AMR in the food supply chain [55, 57].

### **Environmental Contamination and its Role in Dissemination**

The spread of AMR determinants is facilitated by environmental contamination with AREC strains [53, 58]. Resistant strains have various ways, such as agricultural runoff, wastewater discharge, and improper disposal of animal waste, to contaminate environmental reservoirs such as water bodies, soil, and vegetation [16, 18]. AREC in humans, animals, and wildlife are spread through contaminated environmental reservoirs, propagating resistance determinants within and between ecosystems [53, 58]. Antimicrobial residues from agricultural practices and wastewater effluents can promote the survival and proliferation of antibiotic-resistant bacteria in the environment [59, 60].

Human, animal, and environmental health factors are intricately linked in the dissemination of AMR, as evidenced by the role of environmental contamination in the spread of resistant *E. coli* strains [20, 53, 58]. Efforts to mitigate environmental contamination and implement sustainable agricultural and wastewater management practices are essential for reducing the spread of AMR and preserving the efficacy of antimicrobial therapies [20, 61]. Strengthening surveillance and control over the food supply chain and environmental sources is essential to ward off resistant *E. coli* strains and safeguard public health.

### **Clinical Implications of MDR *E. coli***

According to the definition, MDR organisms do not respond to one antimicrobial agent in three or more antibiotic categories [62]. MDR *E. coli* strains, with resistance to multiple antimicrobial classes [35, 63], pose significant clinical challenges. The emergence and spread of MDR *E. coli* significantly impact patient outcomes, empirical antibiotic therapy, healthcare costs, and resource use [63, 64].

### **Increased morbidity and mortality associated with resistant strains**

Compared to susceptible strains, MDR *E. coli* infections lead to greater morbidity and mortality [6, 64]. Multiple antibiotic resistances can lead to treatment failure, prolonging illness, exacerbating infection severity, and increasing the likelihood of complications. Patients infected with MDR *E. coli*

are at a greater risk of developing severe infections, such as bloodstream infections [65], UTIs [35, 66, 67], and intra-abdominal infections [68].

Furthermore, MDR *E. coli* strains are often associated with healthcare-associated infections (HAIs) [69]. HAIs caused by MDR *E. coli* are particularly concerning because of the limited therapeutic options available and the potential for transmission to other patients, leading to outbreaks and increased healthcare burden [70].

### **Challenges in empirical antibiotic therapy and treatment options**

Antibiotics are often started for bacterial infections, including those caused by *E. coli*, based on clinical suspicion before identification of the causative agent. Due to rising resistance in MDR *E. coli* strains to fluoroquinolones, cephalosporins, and trimethoprim-sulfamethoxazole, empirical antibiotic therapy is complicated by their potential resistance to these commonly used antibiotics [71, 72].

MDR *E. coli* infections limited antibiotic treatment options pose challenges to clinical decision-making and raise the risk for inappropriate antibiotic therapy [71, 73]. Due to being more expensive and having a wider range of activity against various types of bacteria, clinicians may resort to prescribing carbapenems for serious infections [71, 74]. Excessive use of broad-spectrum antibiotics can lead to the development of extensively drug-resistant *E. coli* strains due to the promotion of AMR.

### **Impact of Healthcare Cost and Resource Use**

MDR *E. coli* infections significantly increase healthcare costs by requiring lengthy hospital stays and expensive antibiotic treatments. The healthcare costs for treating drug-resistant *E. coli* infections are increased due to the need for extensive therapies, including surgeries, intensive care unit stays, and intricate antibiotic treatments [75, 76].

To prevent the spread of resistant MDR *E. coli* strains within healthcare facilities, infectious disease consultation, antimicrobial stewardship programs, and infection control measures are essential [77]. Allocation of healthcare resources to address the challenges posed by MDR *E. coli* strains diverts resources from other essential healthcare services and contributes to the overall strain on healthcare systems [64].

### **Impact on animal health**

Animal health is significantly affected by AREC strains. Diseases including mastitis in dairy cows and colibacillosis in poultry and swine can infect livestock [39]. Disease transmission by *E. coli* has been observed in sheep, goats, deer, and certain bird species [39]. Ruminants are one of the most significant reservoirs of pathogenic *E. coli* and commonly infect animals and humans through the cross-contamination of water, food, drinks, and feces [78]. Severe infections and diarrhea, which often lead to animal death

and stunted growth, are common consequences of this condition [78].

AREC infections not only lead to individual animal suffering but also result in economic losses for farmers due to reduced productivity, increased veterinary costs, and the implementation of stringent management practices to control the spread of resistant strains among livestock populations [39]. The loss of effective antimicrobials due to resistance negatively influences livestock production and farmers' income [18].

#### **Impact on the environment**

The noteworthy environmental impact arises from AREC. *Escherichia* can persist in harsh environments for lengthy durations [79]. *E. coli* strains thrive in warm-blooded intestines and feces, spread through contaminated water and soil by fecal matter from infected humans and animals [80, 81]. The contamination poses a risk to wildlife, resulting in the proliferation of resistance in natural ecosystems.

MDR *E. coli* strains bring about increased morbidity, mortality, difficulties in empirical therapy, and substantial healthcare costs and resources. Combating MDR *E. coli* infections necessitates a multifaceted approach, which involves antimicrobial stewardship, infection prevention, and control measures, and the development of new antimicrobial agents and treatment strategies for the emerging threat of AMR.

#### **One Health Approach to Addressing AMR**

The One Health approach is a collaborative, multisectoral, and transdisciplinary approach that recognizes the interconnectedness of human beings, animal, and environmental health [82]. This holistic approach emphasizes the interdependence of humans, animals, and ecosystems and aims to address complex health challenges, including AMR, through integrated and coordinated actions [82, 83]. Strategies should encompass surveillance, judicious use of antimicrobials, stringent infection prevention, and exploration of alternative treatments.

#### **The concept of One Health and its relevance to AMR control**

The One Health approach recognizes AMR as not only a human health issue but also a multifaceted problem that transcends traditional disciplinary boundaries [84]. AMR emerges intricately from human, animal, and environmental interactions, fueled by medical, veterinary, and agricultural antimicrobial use, as well as environmental residues and resistant bacteria contamination.

Adopting a One Health approach encourages collaboration among sectors such as human health, animal health, agriculture, environmental science, and policymaking to comprehensively address AMR drivers and consequences [82–84]. This strategy recognizes the interdependent roles of various sectors in addressing AMR and advocates for holistic approaches that consider human-animal-environmental health connections.

#### **Collaborative surveillance and data sharing efforts**

Establishing collaborative surveillance systems and data-sharing mechanisms among humans, animals, and the environment is vital for the One Health approach to AMR control [85]. Surveillance programs gather information on AMR, usage, and mechanisms, offering insights on the emergence and dissemination of antibiotic-resistant bacteria. Collaborative surveillance efforts involve sharing surveillance data and information among human health agencies, veterinary health agencies, agricultural authorities, environmental agencies, and other relevant stakeholders [86, 87]. Sharing data about emerging resistance trends enables early detection, facilitates timely responses, and supports evidence-based decision-making.

#### **Interventions targeting human, animal, and environmental resistance sources**

The One Health approach aims to reduce the spread of resistant bacteria and preserve antimicrobial therapy efficacy by targeting sources of AMR in humans, animals, and the environment. Antimicrobial stewardship programs, infection prevention and control measures, responsible antimicrobial use in agriculture, and environmental management practices comprise these interventions [88–90].

The One Health approach strives to preserve antimicrobial effectiveness, safeguard public health, and sustain ecosystems through integrated and collaborative efforts across human, animal, and environmental sectors [82, 90].

#### **Strategies for the Surveillance, Prevention, and Control of AMR**

Addressing the global challenge of AMR necessitates the implementation of effective surveillance, prevention, and control measures. These strategies aim to monitor AMR patterns, promote judicious antimicrobial use, and reduce the spread of resistant bacteria across human, animal, and environmental sectors [91].

#### **Surveillance programs for monitoring AMR**

AMR surveillance programs are essential in tracking resistance trends and guiding informed decisions on AMR control [91, 92]. These programs analyze AMR data from human, animal, food, and environmental bacterial pathogens, offering insights into the epidemiology and dynamics of resistance. Surveillance programs include laboratory-based, sentinel, and antimicrobial consumption components [91, 93]. Continuous monitoring of AMR through surveillance programs allows for early detection of emerging resistance threats, enabling timely response to outbreaks, guiding antimicrobial stewardship efforts, and informing policy development for AMR control.

#### **Antimicrobial stewardship initiatives in healthcare and veterinary medicine settings**

Antimicrobial stewardship programs encompass guideline-prescribing, antimicrobial review and audits, education, and training, as well as antimicrobial

restriction and preauthorization [94, 95]. These initiatives foster appropriate antimicrobial prescription, provide stewardship education and training, and introduce interventions to optimize antimicrobial utilization. The key components of antimicrobial stewardship programs include guideline-based prescribing, antimicrobial review and audit, education and training, and antimicrobial restriction and preauthorization [94, 95]. Initiatives promoting responsible antimicrobial use and optimizing patient outcomes in healthcare and veterinary settings, while reducing the pressure for AMR, are crucial.

#### **Environmental management practices to reduce the dissemination of AMR**

By managing the environment using practices that limit the spread of AMR, we can decrease the prevalence of resistant bacteria and their genes [61, 96]. This practice aims to reduce the environmental impact of antimicrobial residues and antibiotic-resistant bacteria from humans, animals, and agriculture. Effective environmental management entails addressing wastewater treatment, managing manure, controlling agricultural runoff, and monitoring environmental reservoirs [18, 96, 97]. Effective environmental management is crucial in limiting the spread of AMR and maintaining environmental well-being.

Strategies for preventing, controlling, and monitoring AMR involve surveillance programs, antimicrobial stewardship initiatives, and environmental management practices. Integrated approaches are vital for fighting AMR and maintaining the potency of antimicrobial treatments in human, animal, and environmental realms.

#### **Future Directions and Challenges**

##### **Emerging trends in *E. coli* AMR**

*E. coli* continues to evolve and adapt, leading to emerging trends in AMR that pose significant challenges to public health. The key emerging trends in AMR in *E. coli* include the following:

##### *Increasing prevalence of multidrug resistance*

There has been a notable increase in the prevalence of MDR *E. coli* strains, which are resistant to multiple classes of antibiotics [48, 98]. This trend aggravates treatment options, contributes to higher rates of treatment failure, and increases healthcare costs.

##### *Rise of extended-spectrum beta-lactamase (ESBL)-producing *E. coli**

In healthcare settings, ESBL-producing *E. coli* strains have become more prevalent. These strains can hydrolyze and resist the effects of most penicillins and cephalosporins due to the production of antibiotic-degrading enzymes [99, 100].

##### *Emergence of carbapenem-resistant *E. coli* (CRE)*

CRE strains are resistant to carbapenem antibiotics and have emerged as a significant threat to public health [101]. CRE strains often carry carbapenemase

genes that confer resistance to carbapenems and other beta-lactam antibiotics.

##### *Global spread of hypervirulent *E. coli**

Severe infections like HUS and bloodstream infections are linked to hypervirulent *E. coli* strains, inclusive of specific STEC serotypes [3–5]. These strains often present with AMR, complicating clinical management.

##### **Novel approaches to combat MDR *E. coli***

Addressing the challenge of MDR *E. coli* requires innovative approaches to develop new antimicrobial agents, enhance infection prevention and control measures, and optimize antimicrobial stewardship practices [102, 103]. To fight MDR *E. coli*, new strategies are proposed;

##### *New antibiotics*

New antibiotics with unique modes of action are urgently required to overcome MDR *E. coli* strains [103, 104]. Research efforts are focused on identifying new antibiotic targets, discovering antimicrobial agents with improved efficacy and safety profiles, and developing combination therapies to overcome resistance mechanisms [104].

##### *Antimicrobial peptides and bacteriophages*

Antimicrobial peptides and bacteriophages offer potential as alternative therapies against MDR *E. coli* [105, 106]. These agents have unique mechanisms of action and may offer new strategies for combating resistant bacteria [107].

##### *Precision medicine approaches*

Optimizing treatment regimens for MDR infections can be achieved through precision medicine methods such as genomic sequencing and customized antimicrobial therapy [108, 109]. Precision medicine, through characterization of resistance profiles of infecting strains and identification of targeted therapies based on genetic determinants of resistance, can improve treatment outcomes and limit resistance spread.

##### **Policy implications and the need for global cooperation**

The urgent need for global action and policy interventions to address the increasing AMR in *E. coli* is emphasized by its growing prevalence. Implications from the key policy areas require global cooperation.

##### *Enhanced surveillance and data sharing*

Effective surveillance and international data sharing are imperative for identifying AMR trends, emerging threats, and guiding evidence-based interventions [91, 92]. To ensure uniform surveillance practices, standard data collections, and seamless data sharing among nations, international collaboration is pivotal [91].

##### *Antimicrobial stewardship policies*

Policies for antimicrobial stewardship should be implemented by governments and international

organizations across healthcare, veterinary medicine, and agriculture sectors [94, 95, 110]. Regulating antimicrobial usage, encouraging prudent prescribing, and rewarding the creation of new antimicrobial agents are necessary actions.

#### Research and innovation

To combat MDR *E. coli*, investing further in research and innovation for new antimicrobial agents, diagnostics, and treatment methods is essential. Global collaboration and funding support are essential for advancing research efforts and translating scientific discoveries into clinical applications [111, 112].

#### International collaboration and capacity building

International collaboration and capacity building are essential for building global partnerships, sharing best practices, and enhancing the capacity of low- and middle-income countries to address AMR [113, 114]. Global cooperation is needed to support resource-limited settings in implementing effective infection prevention and control measures, strengthening laboratory capacity, and promoting antimicrobial stewardship initiatives [115].

To effectively combat the emerging trends in antibiotic resistance in *E. coli*, it is necessary to develop new therapeutic strategies, implement evidence-based policies, and foster international cooperation. Collaboration among sectors and borders worldwide can reduce the threat of AMR, securing health for future generations.

#### Conclusion

The growing threat of AMR in *E. coli* requires thorough approaches for monitoring, prevention, and management in public health. This review highlights the pressing requirement for innovative methods to overcome MDR *E. coli*, such as the creation of new antibiotics, antimicrobial peptides, and precision medicine techniques. The presence of MDR *E. coli* in clinical settings leads to elevated mortality rates, complications in initial antibiotic treatment, and substantial financial and resource burdens for healthcare. MDR strains pose challenges to treatment, potentially leading to treatment failure, and inflicting significant economic costs on healthcare systems. To combat the challenges associated with AMR, a multifaceted approach is necessary, including antimicrobial stewardship, infection prevention, and environmental management practices.

The significance of implementing integrated strategies to tackle AMR at the human-animal-environment interface cannot be ignored. Collaborative efforts across human, animal, and environmental sectors are crucial to address AMR's transmission dynamics interconnections. Adopting a One Health approach enables stakeholders to collaborate in monitoring AMR trends, promoting responsible use, and preventing the spread of antibiotic-resistant bacteria among humans, animals, and the environment. The

significance of implementing integrated strategies to tackle AMR at the human-animal-environment interface cannot be ignored. Collaborative efforts across human, animal, and environmental sectors are crucial to address AMR's transmission dynamics interconnections. Adopting a One Health approach enables stakeholders to collaborate in monitoring AMR trends, promoting responsible use, and preventing the spread of antibiotic-resistant bacteria among humans, animals, and the environment.

Combating MDR *E. coli* strains necessitates collective efforts and international cooperation. At the human-animal-environmental interface, integrated strategies can reduce the clinical effect of antimicrobial-resistant infections, maintain antimicrobial therapy effectiveness, and secure public health for future generations.

#### Authors' Contributions

OF: Conceptualization, project administration, and writing of the original draft. OF, MS, and HA: Methodology, formal analysis, and review and editing of the manuscript. MS, HA, TZMTJ, SNSI, RM, SAS, and NO: Review and editing of the manuscript. OF, HA, TZMTJ, SNSI, RM, and SAS: Funding acquisition. All authors have read, reviewed, and approved the final manuscript.

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#### Competing Interests

The authors declare that they have no competing interests.

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