

Antimicrobial Resistance in Enterobacteriaceae from Veterinary Farms: Current Trends, Challenges, and One Health Implications

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DOI:10.5281/zenodo.17170555

ARTICLE INFO

Article history:

Received : 14-09-2025

Accepted : 17-09-2025

Available online : 21-09-2025

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Citation: Al-Ramadi, M. K. (2025). Antimicrobial Resistance in Enterobacteriaceae from Veterinary Farms: Current Trends, Challenges, and One Health Implications. *IKR Journal of Agriculture and Biosciences (IKRJAB)*, 1(2), 62-65.



ABSTRACT

Original research paper

Antimicrobial resistance (AMR) among Enterobacteriaceae is a global health crisis that threatens the effectiveness of antibiotics in both human and veterinary medicine. Veterinary farms represent important reservoirs for resistant bacteria, particularly multidrug-resistant (MDR) and extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus* spp., and *Enterobacter* spp. These pathogens are capable of disseminating resistance determinants such as blaCTX-M, blaSHV, blaNDM, and mcr genes through horizontal transfer in farm environments, the food chain, and human-animal interfaces. Evidence from Iraq and other regions demonstrates the high prevalence of β -lactamase genes in clinical, foodborne, and animal isolates, underscoring the interconnectedness of human and veterinary health (1–5). The increasing detection of carbapenem- and colistin-resistant isolates in livestock, despite the restricted use of these antibiotics in animals, highlights the complexity of AMR spread and its environmental dimension. This mini-review synthesizes current knowledge on the drivers of resistance in veterinary farms, key resistant Enterobacteriaceae, molecular mechanisms of resistance, zoonotic and environmental transmission, global surveillance trends, and mitigation strategies. Strengthened stewardship programs and integrated One Health approaches are urgently required to slow the emergence and dissemination of resistant Enterobacteriaceae.

Keywords: Antimicrobial resistance, Enterobacteriaceae, veterinary farms, β -lactamases, One Health.

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1. Introduction

Antimicrobial resistance (AMR) has emerged as one of the most critical threats to global health, food security, and sustainable development. According to the World Health Organization (WHO), resistant Enterobacteriaceae, especially carbapenem-resistant and ESBL-producing *Escherichia coli* and *Klebsiella pneumoniae*, are classified among the highest priority pathogens due to their clinical significance and limited treatment options (6). The misuse and overuse of antibiotics in agriculture and animal husbandry have accelerated the selection of resistant strains, leading to their persistence in veterinary farms. This is particularly concerning because livestock are not only a source of food but also a potential reservoir for resistance genes that can disseminate to humans and the environment.

Enterobacteriaceae, including *E. coli*, *K. pneumoniae*, *Proteus* spp., and *Enterobacter* spp., are ubiquitous organisms frequently associated with both animal and human infections. These bacteria possess remarkable genetic flexibility, enabling them to acquire multiple resistance determinants. Regional studies from Iraq have provided valuable insights into this issue. Multidrug-resistant *Proteus* spp. carrying β -lactamase genes were identified in clinical isolates (1), while ESBL-producing *E. coli* strains were reported in urinary tract infections (2). Resistant *E. coli* and *Staphylococcus* spp. isolated from raw meat further demonstrated the potential for zoonotic transmission through food (3). The discovery of novel blaSHV variants in *K. pneumoniae* in Sulaimani reflects the ongoing evolution of resistance mechanisms (4). In addition, investigations into enteric infections in children have shown quantitative

associations with leukocyte profiles, highlighting the clinical burden of resistant Enterobacteriaceae in the region (5). These findings emphasize the importance of addressing AMR from a One Health perspective, integrating human, animal, and environmental health.

2. Sources and Drivers of Resistance in Veterinary Farms

The development and spread of resistant Enterobacteriaceae in farm settings are driven by a combination of factors, primarily linked to antibiotic practices and environmental conditions. The routine use of antimicrobials for prophylaxis, metaphylaxis, and therapy is widespread in livestock production. In many countries, antibiotics are also used at sub-therapeutic doses as growth promoters, creating sustained selective pressure that encourages resistance (7,8). Poor farm hygiene, overcrowding, and inadequate biosecurity measures further contribute to bacterial persistence and transmission. Importantly, antibiotics excreted in animal feces contaminate manure, soil, and water sources, leading to environmental reservoirs of resistance (9).

The global movement of animals, feed, and meat also facilitates the transboundary dissemination of resistant strains. For example, ESBL-producing *E. coli* has been detected in poultry farms worldwide, and similar resistance genes have been identified in both animal and human isolates, suggesting interspecies transmission (10,11). These drivers underscore the role of intensive farming practices in accelerating AMR and highlight the need for stricter regulation of veterinary antibiotic use.

3. Resistant Enterobacteriaceae of Concern in Veterinary Farms

Among Enterobacteriaceae, *E. coli* is the most frequently reported resistant pathogen in livestock. ESBL-producing strains, often carrying blaCTX-M and blaTEM genes, are particularly widespread in poultry and swine (9,12). These bacteria pose a direct zoonotic risk, as they can be transmitted to humans through the food chain and direct contact. *K. pneumoniae* is another major concern; although carbapenems are not commonly used in animals, carbapenem-resistant strains harboring blaNDM and blaOXA-48 have been increasingly detected in farm environments (13). The identification of novel blaSHV variants in Iraq (4) illustrates the ongoing evolution of *K. pneumoniae* under selective pressures.

Proteus spp., while less studied in veterinary settings compared to *E. coli*, are clinically significant pathogens associated with urinary tract and wound infections. Resistant isolates carrying β -lactamase genes have been reported in Iraqi hospitals (1). *Enterobacter* spp. also present a concern, as they are opportunistic pathogens capable of harboring carbapenemases and plasmid-mediated colistin resistance

genes. Collectively, these bacteria illustrate the broad spectrum of resistance challenges emerging in veterinary farms.

4. Mechanisms of Resistance

Resistant Enterobacteriaceae employ diverse mechanisms to survive antibiotic pressure. The most significant include enzymatic inactivation of antibiotics through ESBLs such as blaCTX-M, blaSHV, and blaTEM, and carbapenemases including blaNDM, blaKPC, and blaOXA-48 (9,13,14). The emergence of plasmid-mediated colistin resistance genes (mcr-1 to mcr-10) further threatens last-resort therapies (15). Beyond enzymatic activity, bacteria utilize efflux pumps to expel antimicrobials, reduce outer membrane permeability by porin loss, and alter target binding sites such as penicillin-binding proteins. Importantly, these resistance determinants are frequently located on plasmids, integrons, and transposons, allowing horizontal gene transfer between species in the same farm ecosystem (16). The coexistence of multiple resistance genes within a single isolate accelerates the spread of multidrug resistance in both veterinary and human populations.

5. Zoonotic and Environmental Transmission

The transmission of resistant Enterobacteriaceae from veterinary farms to humans occurs through multiple interconnected pathways. Direct contact between farmers, veterinarians, and livestock provides a route for colonization and infection. The food chain is another critical route, as contaminated meat, milk, and eggs can harbor resistant bacteria. In Sulaimani, resistant *E. coli* and *Staphylococcus* spp. were recovered from raw meat, underscoring the foodborne risk (3). Environmental dissemination through manure, farm effluents, and irrigation water further spreads resistant organisms into surrounding ecosystems (17).

The human–animal interface is particularly concerning, as genetic studies have revealed the presence of identical ESBL genes in human clinical isolates and livestock-associated bacteria (11,12). Such findings illustrate the porous boundaries between veterinary and human medicine, highlighting the need for integrated surveillance systems.

6. Surveillance and Global Trends

International organizations such as the WHO, FAO, and OIE have recognized AMR as a top global health priority and have called for enhanced surveillance in livestock (6,7). Global analyses indicate that antimicrobial use in food animals is projected to rise, particularly in low- and middle-income countries where regulations are limited (8). The widespread detection of ESBL-producing *E. coli* in poultry farms worldwide illustrates the scale of the problem (9,12).

Regional evidence from Iraq confirms the circulation of β -lactamase-producing Enterobacteriaceae in clinical and food-related settings (1–4), while studies from Europe and Asia report the emergence of carbapenem- and colistin-resistant strains in livestock (13,15,18).

The convergence of resistance in both veterinary and human populations suggests that AMR is no longer confined to hospitals but has become entrenched in community and agricultural environments. This reinforces the urgency of adopting One Health approaches to AMR surveillance and control.

7. Control and Mitigation Strategies

Addressing AMR in veterinary farms requires multifaceted interventions. Antimicrobial stewardship programs are essential to restrict the prophylactic and growth-promoting use of antibiotics in livestock (7,19). Alternatives such as vaccines, probiotics, bacteriophages, and plant-derived antimicrobials offer promising options to reduce antibiotic dependence (12,20). Improvements in farm hygiene, housing conditions, and biosecurity practices can lower infection rates and reduce the need for antimicrobials.

Robust surveillance systems are also necessary to detect emerging resistance and monitor trends across regions. Collaboration across veterinary, medical, and environmental sectors is critical for effective One Health strategies. Finally, education and awareness programs targeting farmers, veterinarians, and policymakers are essential to ensure sustainable changes in antibiotic use.

8. Conclusion and Future Perspectives

Resistant Enterobacteriaceae in veterinary farms represent a major public health challenge with far-reaching consequences for food safety, animal health, and human medicine. Regional findings, particularly from Iraq, highlight the molecular diversity of β -lactamase genes and the interconnectedness of clinical, foodborne, and environmental reservoirs. Globally, the continued rise of ESBL-producing *E. coli* and the emergence of carbapenem- and colistin-resistant isolates emphasize the urgent need for coordinated responses. Future efforts must prioritize antimicrobial stewardship, alternative interventions, and integrated One Health surveillance systems. Without such measures, resistant Enterobacteriaceae will continue to undermine both veterinary productivity and human therapeutic options.

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