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Drift of antibiotic resistance genes in pathogenic *Enterobacteriaceae*: a case study of *Escherichia coli*

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ABSTRACT

Introduction. The widespread antibiotic resistance among representatives of the *Escherichia coli* species is an acute problem for livestock and poultry farms, since this pathogen is the most frequently registered component of the etiological structure of gastrointestinal diseases in young farm animals and poultry, and is also often detected in diseases of other organs and systems. Even now, in many farms, the use of antibacterial drugs to treat diseases caused by this pathogen is difficult due to the circulation of strains with multiple resistance to most antibiotics used in veterinary practice. It is known that over time, the sensitivity of a microorganism to various groups of antibacterial drugs changes, often quite significantly. Sensitivity monitoring can help contain the spread of antibiotic resistance and optimally select drugs for use in therapy.

Objective. Analysis and systematization of the research results presented in the scientific literature on the resistance of *Escherichia coli* to antibacterial drugs.

Materials and methods. A search was conducted for scientific papers on this topic in scientific journals and materials of scientific and practical conferences.

Results. This article presents and summarizes literature data on trends in *Escherichia coli* resistance to antibacterial drugs.

Conclusion. *Escherichia coli* resistance is most often demonstrated to *β*-lactam antibacterial drugs, aminoglycosides, as well as tetracyclines, macrolides (erythromycin) and lincosamides (lincomycin). In almost all studies, *Escherichia coli* exhibits polyresistance (resistance to two or more drugs) and in some cases, multiresistance (resistance to at least one drug from three or more groups). The results of susceptibility determination in many studies differ significantly from each other, which is associated with different conditions for the formation of antibiotic resistance in bacteria on different livestock enterprises. For a more accurate assessment of the dynamics of the spread of antibiotic resistance within the *Escherichia coli* species, it is necessary to continue studying the sensitivity to antimicrobial drugs of various strains detected in livestock and poultry farms, as well as from environmental objects.

Keywords: review, antibiotics, resistance, *Escherichia coli*, colibacteriosis

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Дрейф генов антибиотикорезистентности патогенных энтеробактерий на примере *Escherichia coli*

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РЕЗЮМЕ

Введение. Широкое распространение антибиотикорезистентности среди представителей вида *Escherichia coli* является острой проблемой животноводческих и птицеводческих хозяйств, поскольку этот возбудитель является наиболее часто регистрируемым компонентом этиологической структуры желудочно-кишечных заболеваний молодняка сельскохозяйственных животных и птицы, а также нередко выявляется при заболеваниях других органов и систем. Уже сейчас во многих хозяйствах затруднено применение антибактериальных препаратов для лечения заболеваний, вызванных данным патогеном, ввиду циркуляции штаммов, обладающих множественной устойчивостью к большинству применяемых в ветеринарной практике антибиотиков. Известно, что со временем чувствительность микроорганизма к различным группам антибактериальных препаратов изменяется, и нередко весьма значительно. Мониторинг чувствительности может помочь в сдерживании распространения антибиотикорезистентности и оптимальном подборе препаратов для применения их в терапии.

Цель исследования. Анализ и систематизация представленных в научной литературе результатов исследований по изучению устойчивости *Escherichia coli* к антибактериальным препаратам.

Материалы и методы. Проведен поиск работ по заявленной теме в научных журналах и материалах научно-практических конференций.

Результаты. В статье представлены и обобщены литературные данные о тенденциях в резистентности *Escherichia coli* к антибактериальным препаратам.

Заключение. Устойчивость *Escherichia coli* чаще проявляется к *β*-лактамным антибактериальным препаратам, аминогликозидам, а также тетрациклинам, макролидам (эритромицину) и линкозамидам (линкомицину). Практически во всех исследованиях установлено, что выделенные изоляты *Escherichia coli* характеризуются полирезистентностью (устойчивостью к двум и более препаратам), а в некоторых случаях и мультирезистентностью (устойчивостью по крайней мере к одному препарату из трех и более групп). Результаты определения чувствительности во многих исследованиях значительно отличаются друг от друга, что связано с неодинаковыми условиями формирования антибиотикорезистентности у бактерий на разных животноводческих предприятиях. Для более точной оценки динамики распространения антибиотикорезистентности внутри вида *Escherichia coli* необходимо продолжать изучение чувствительности к антимикробным препаратам различных штаммов, выявляемых в животноводческих и птицеводческих хозяйствах, а также из объектов окружающей среды.

Ключевые слова: обзор, антибиотики, резистентность, *Escherichia coli*, колибактериоз

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INTRODUCTION

Escherichia coli is a significant opportunistic pathogen in animals, often causing colibacillosis, but its role extends beyond this primary disease. This microorganism is frequently found in diseased animals and humans, particularly in gastrointestinal, obstetric, gynecological, respiratory, and urinary tract infections. *E. coli* are categorized into 7 pathotypes, including enterotoxigenic (ETEC), enteropathogenic (EPEC), enterohemorrhagic (EHEC), and shigatoxin-producing (STEC). Additionally, there's a category for strains that are pathogenic to birds.

Colibacillosis remains a major challenge in animal husbandry, particularly in industrial poultry farming, where it ranks among the most prevalent bacterial infections in birds (is detected in 40–70% of disease cases). A critical complicating factor is the widespread antimicrobial resistance (AMR) in *E. coli* isolates, with resistance observed against all major classes of antibacterial drugs – in some cases reaching 100% [1, 2, 3].

The significance of this study is underscored by two critical factors: the substantial economic losses inflicted on livestock production by colibacillosis, and the escalating global prevalence of antimicrobial-resistant *E. coli* strains associated with this disease. The sensitivity of pathogens to antibiotics can change over time, making ongoing monitoring of antimicrobial resistance crucial, especially for pathogens like *E. coli*.

This study summarizes the data available in the literature on the resistance dynamics of *E. coli* isolated from different farm animal species to antibacterial drugs.

Antimicrobial resistance is the ability of microorganisms to resist the effects of antimicrobial agents, including antibiotics. The early years 1945–1963 following Fleming's 1945 discovery were marked by a belief that the pharmaceutical industry could constantly develop new antibiotics faster than bacteria could develop resistance. Later, the discovery of plasmids, which can transfer resistance genes between bacteria, highlighted a major route for resistance spread and increased concern (1963–1981). This concern grew into a global problem perception from 1981–1992, leading to increased research and funding (1992–2013). Since 2013 the problem continues to worsen due to the emergence of new resistance mechanisms and the increasing spread of resistant microorganisms among populations [4, 5].

The use of alternative products like bacteriophages, probiotics, phytobiotics, and antimicrobial peptides is increasingly important in the treatment of bacterial diseases. However, antibacterial drugs are still very widely used for treatment in livestock and poultry farming. Moreover, the use of antibiotics to prevent disease and boost productivity in agriculture is the reason for the creation and accumulation of AMR genetic determinants in *Escherichia* species. This, in turn, leads to AMR developement and contamination of raw materials and food products [6, 7].

The purpose of this study was to summarize the scientific literature data on *E. coli* AMR resistance dynamics.

MATERIALS AND METHODS

This study was conducted through systematic analysis of literature data on antibiotic resistance patterns in diverse *E. coli* strains isolated from pathological specimens and biological samples obtained from companion animals, livestock, and poultry.

RESULTS AND DISCUSSION

In 2011 N. N. Shkil presented the results of testing of 21 pathological and biological samples from aborted and stillborn bovine fetuses; 71 samples from newborn calves; 67 samples from calves aged 10 days to 1 month; 47 samples from 1–3-month-old calves and 18 samples from > 3 month old calves. Pathogenic microorganisms were isolated in 32% of samples from animals exhibiting clinical signs of gastrointestinal disease, while respiratory syndrome was observed in 68% of affected calves. *Escherichia* were isolated from 38% of the samples. Isolation tests were conducted annually from 2001 to 2010. As established by the author, in 2001, 50% of the isolated *Escherichia* bacteria exhibited high sensitivity to aminoglycosides. In subsequent years, the increased sensitivity to quinolone/fluoroquinolone drugs was established, which peaked in 2006 (66%). By 2007, resistance rates to these agents had reached parity with aminoglycosides. Subsequently, in 2009–2010, bacterial isolates demonstrated significantly greater sensitivity to aminoglycosides (50%) compared to fluoroquinolones (15%). The author observed a consistent inverse relationship in antimicrobial susceptibility patterns, where increased sensitivity to one drug class frequently corresponds with decreased sensitivity to another class within the same temporal period. Furthermore, these susceptibility trends demonstrate cyclical fluctuations, characterized by multi-year periods of increasing sensitivity followed by subsequent declines in subsequent years [8]. *E. coli* have, apparently, developed a robust mechanism for acquiring resistance to fluoroquinolone antibiotics. Antisense RNA produced by the *micF* gene does indeed inhibit porin protein synthesis at the translation level. This has a positive effect on the sigma factor content related to multiple stress resistance σ^S in cells. The most significant fluctuations in *E. coli* resistance are associated with this phenomenon [9].

The analysis of dynamics in sensitivity of *E. coli* strains from diseased calves to antimicrobial drugs by N. E. Gorkovenko and Yu. A. Makarov revealed resistance to enrofloxacin in 6.5% isolates in 2006; by 2007 their number increased to 36.4%, and in 2010 reached 90.0%. The number of polymyxin-resistant *E. coli* isolates in 2006 was 23.3%, in 2010 – 75%. Neomycin resistance was revealed in 64.0 and 81.8% in 2006 and 2010, respectively. Thus, an increasing resistance to enrofloxacin, polymyxin and neomycin, which significantly reduces the therapeutic effectiveness of these antibiotics is observed. Tetracycline resistance in 2006–2008 was approximately 70%, in 2009 it decreased to 60%, and in 2010 it reached 100%. Resistance to chloramphenicol in 2006 and 2007 was 60 and 55%, respectively; in 2008–2009 it increased to 80%, and then decreased significantly. Resistance to streptomycin and kanamycin was increasing from 2006 to 2008, an then decreased in 2009. It reached 100% for both drugs in 2010.

Consistent with previous findings, these data reveal cyclical fluctuations in antibacterial resistance patterns. Despite these periodic variations, the overall trend demonstrates progressive escalation of resistance, ultimately culminating in pan-resistance and complete loss of clinical efficacy for some antimicrobial agents [10].

The research presented by D. A. Zhelyabovskaya et al. in 2017 suggests that 71.4% of the studied *E. coli* strains (O15, O18, O26) isolated from the intestines of newborn calves are polyresistant. These isolates demonstrated resistance to erythromycin (95.2%), tetracycline and penicillin (90.5%), kanamycin (85.7%), ampicillin (76.2%), streptomycin and gentamicin (71.4%) [11].

Analysis by N. M. Al-Hammash and A. V. Ignatenko of *E. coli* isolates from a dairy farm revealed high resistance prevalence: 94% to benzylpenicillin, erythromycin, and lincomycin; 83% to tetracycline; 61% to ampicillin; 56% to neomycin; 44% to chloramphenicol; 37% to pefloxacin; 33% to polymyxin; and 28% to cephalexin. The isolates demonstrated intermediate susceptibility to neomycin (55%), polymyxin (50%), furadonin (27%), chloramphenicol (16%), and kanamycin (14%). They were susceptible to the following antibacterials: gentamicin (83%), kanamycin (78%), cephalexin (74%), furadonin (72%), pefloxacin (62%), chloramphenicol (39%), neomycin (39%), ampicillin (33%). Isolates showed 100% susceptibility only to ceftriaxone, while absolute resistance was observed to oleandomycin, clindamycin, and oxacillin [12].

In the study by S. N. Zolotukhin et al. 34.8% of *E. coli* isolates showed susceptibility to gentamicin, 34.2% were resistant and 31.5% were moderately resistant. Ampicillin was active against 57.8% of *E. coli* isolates, 27.3% were resistant to it, and 14.4% showed moderate resistance. The highest sensitivity was found to ceftriaxone (84.7%), ciprofloxacin (74.2%) and chloramphenicol (60.6%). The test results demonstrated that none of the antibiotics completely inhibited microbial growth (100% inhibition). Most strains were polyresistant to erythromycin, chloramphenicol, streptomycin, tetracycline, neomycin, ampicillin, gentamicin, and penicillin [13].

Between 2016 and 2020, M. E. Ostyakova and I. S. Shul'ga examined the gut microbiota (enterobiocenosis) of newborn calves affected by gastrointestinal disorders. In the course of this work, the resistance of *E. coli* strains to certain antibacterials was analyzed. The results of the study are the following: isolates showed resistance to benzylpenicillin, ofloxacin, ciprofloxacin and erythromycin. This suggests multidrug resistance of the isolated strains. 91.7% of the isolates were sensitive to polymyxin, 70.6% to cefazolin, 65.5% to streptomycin, 62.5% to amoxicillin / clavulanic acid combination. Therefore, these antibiotics are the drugs of choice for the treatment of intestinal infection caused by *E. coli* [14].

In the characterization of diarrheagenic *E. coli* museum strains for pathotypes and AMR genes by Yu. I. Pobolelova and S. P. Yatsentyuk, EPEC *E. coli* was the most prevalent pathotype, accounting for 29% of cases relative to other pathotypes. The determination relied on fragments of AMR determinants to *β*-lactam atibiotics (*blaTEM*, *blaSHV* genes), florfenicol (*floR*), chloramphenicol (*cat1*, *cml*A), streptomycin (*aadA1* gene), gentamicin (*aac3-IV* gene). Among the studied strains, 36% had resistance genes to at least one of the antimicrobials under study, and 5 strains demonstrated resistance to two antibiotics simultaneously: 2 strains to chloramphenicol and streptomycin, 2 more to streptomycin and florfenicol, and 1 strain to chloramphenicol and florfenicol. In total, the chloramphenicol resistance genes *cat1* and *cmlA* were identified in 3 and 4 strains, respectively; the streptomycin resistance gene *aadA1* was identified in 17 strains, and the florfenicol resistance gene *floR* was identified in 4 strains. Resistance genes to gentamicin and *β*-lactams were not detected [15].

Researchers A. A. Golikova and O. A. Manzhurina conducted experiments on susceptibility of *E. coli* strains isolated from colibacillosis-affected calves to 16 antimicrobials of various pharmacological classes. The authors established the susceptibility of *E. coli* O20 strain to the following antibiotics: ampicillin, amoxicillin, tetracycline, chloramphenicol, gentamicin, polymyxin, norfloxacin, enrofloxacin and streptomycin. Strain O33 showed sensitivity to the same antimicrobials as O22, but was resistant to gentamicin and streptomycin and sensitive to furazolidone and furadonin. *E. coli* O137 demonstrated susceptibility to ampicillin, amoxicillin, tetracycline, chloramphenicol, gentamicin, polymyxin, furazolidone, furadonin, norfloxacin, enrofloxacin, and streptomycin [16].

According to E. A. Sazonova, in 2020–2022, *E. coli* strains tended to develop multidrug resistance to first-generation cephalosporins, penicillins, tetracyclines, macrolides, lincosamides, sulfonamides, and streptomycin. Antimicrobial resistance was reveled in O2, O78, O115, O126, O15, O18, O119, O33, O41, O101, O137, O157:H7 serovariants isolated from swine colibacillosis cases.

At the same time, the *E. coli* resistance to various antibacterial drugs changed as follows: 44.0% to cephalexin in 2020, 71.4% in 2021, 100.0% in 2022; 29.1% to cefazolin in 2020, 50.0% in 2021, 31.5% in 2022; 6.9, 14.3, 15.3% to ceftriaxone; 73.7, 50.0, 48.7% to amoxicillin; 73.7, 78.7, 81.3% to ampicillin; 80.5, 57.1, 64.3% to tetracycline; 84.5, 100.0, 99.1% to doxycycline; 30.9, 71.4, 72.5% to streptomycin; 83.4, 100.0, 92.3% to erythromycin; 85.7, 92.8, 91.3% to rifampicin; 11.4, 7.1, 10.6% to norfloxanin; 18.3, 7.4, 2.3% to enrofloxacin; 10.3, 7.2, 11.3% to ciprofloxacin in 2020, 2021 and 2022 accordingly. These figures demonstrate that antibiotic-resistant *E. coli* strains are highly prevalent. Moreover, the antimicrobial resistance increases over time, sometimes (for example, to cephalexin, doxycycline, erythromycin) reaching 100% [17].

Tishchenko A. S. et al. reported that *E. coli* strains (K99:O141, F41:O26, F41, K88:O157) from calves and piglets with enteric diseases exhibited resistance to amoxiclav, tetracycline, gentamicin, oxacillin, azithromycin, and ceftazidime, highlighting challenges in veterinary antimicrobial therapy. While fluoroquinolones (ciprofloxacin and pefloxacin) demonstrated the highest antibacterial activity among tested agents, the observed intermediate resistance levels diminish their clinical efficacy. Amoxiclav, oxacillin, gentamicin, and azithromycin demonstrated the lowest antibacterial effect [18].

According to I. N. Zhdanova et al., *E. coli* strains O8, O15, O20, O101, O115, O157 were isolated from calves and adult cattle in the farms of the Perm Krai in 2020–2021. These strains revealed resistance to ampicillin and cefazolin (61.5% for each) and high resistance to ceftriaxone (23.1%), cefoxitin (30.7%), chloramphenicol (61.5%) and tetracycline (79.5%). The isolates were sensitive to imipenem and tobramycin (100%), meropenem (97.4%), amikacin and moxifloxacin (92.3%) [19].

Makavchik S. A. and Sukhinin A. A. studied microorganisms isolated from the milk of mastitic cows in 2021–2022. *E. coli* cultures were susceptible to neomycin and carbapenems (100%) and resistant to cephalexin (75%), tetracycline (30%), cefotaxime (30%), gentamicin (14%) and ciprofloxacin (7%). The collected data demonstrate a concerning trend of rapidly increasing resistance to cephalosporins, tetracyclines, and aminoglycosides among clinical isolates [20].

The results of studies conducted by A. S. Lokteva et al. demonstrated that *E. coli* O141 and O33 strains isolated from samples from dead pigs in 2017–2022 turned out to be pan-resistant. Over 90% of pathogenic isolates exhibited polyresistance, with this concerning prevalence persisting throughout the entire study period [21].

The article by I. M. Donnik describes that the majority of bacteria isolated from samples of cervical scrapings, from mammary secretions, nasal and oral swabs of animals, manure, feed and contact surfaces and equipment were resistant to antimicrobials. *Escherichia* were resistant to rifampicin, semi-synthetic penicillins and tetracyclines (64–67%); approximately 44% of isolates demonstrated low sensitivity to 3–5 antibiotics of different classes; 28% among them to third-generation cephalosporins: ceftriaxone and cefotaxime. The bacteria exhibited high sensitivity to fluoroquinolones: ciprofloxacin, enrofloxacin, and ofloxacin (82%) [22].

Kochkina E. E. and Morozova N. V. assessed antimicrobial resistance in *E. coli* strains isolated from cats with genitourinary tract disorders. The study revealed that isolates exhibited the sensitivity to cephalosporins (71 ± 10.7%), moderate resistance was observed to aminoglycosides (83.3 ± 8.8%) and synthetic penicillins (66 ± 11.1%) and resistance to macrolides and fluoroquinolones. The sensitivity of the strains to individual antibiotics is presented as follows: all studied cultures were sensitive to cefepime; 83.3 ± 8.8% were sensitive to ceftriaxone and cefazolin; 83.3 ± 8.8% showed moderate resistance to cefotaxime, enrofloxacin, and gentamicin; 66.7 ± 11.1% showed moderate resistance to amoxiclav; and 50 ± 11.8% showed moderate resistance to ciprofloxacin; 16.7 ± 8.8% exhibited moderate resistance to ceftriaxone and cefazolin. The authors report the absolute resistance to tylosin [23].

When assessing antibiotic resistance before using antibacterial drugs, N. N. Muzyka and A. V. Beletskaya isolated *E. coli* from various bird species. The isolates exhibited sensitivity to gentamicin (19.0%), florfenicol (16.6%), enrofloxacin (14.3%), spectomycin (14.3%), norfloxacin (7.1%), trimethoprim (4.7%), tilmicosin (4.7%), doxycycline (2.4%) and lincomycin (2.4%). Moderate sensitivity was observed for tilmicosin (11.9%), doxycycline, florfenicol, norfloxacin and spectinomycin (4.7% each), trimethoprim, lincomycin and gentamicin (2.4% each). Thus, the overall sensitivity rate to antibacterial drugs was 20% or lower [24].

In 2023, A. S. Krivonogova et al. published the article "Antibiotic resistance of *Enterobacteriacea* in the microbiomes associated with poultry farming". In this study, the minimum inhibitory concentration (MIC) was determined for the reference strain *E. coli* ATCC 25922 against ciprofloxacin, meropenem, cefepime, and ampicillin. The control strains were cultured during 37 days. This period corresponds to the period of broiler raising in commercial poultry farms from hatching to slaughter. The study demonstrated that the reference strain *E. coli* ATCC 25922 exhibited resistance to ciprofloxacin (MIC = 0.06–0.12 mg/L), meropenem (MIC = 0.12 mg/L), ampicillin (MIC = 2–4 mg/L), and cefepime (MIC = 0.5 mg/L). Under these conditions, antibiotic resistance did not arise because the studied microorganisms lacked active resistance determinants in their genomes and had no opportunity for horizontal gene transfer due to isolation from other microbes.

The sensitivity to antibacterial drugs of microflora isolated from chicken cloacal swabs and litter at different stages of poultry rearing was also analyzed. All *E. coli* isolates exhibited sensitivity to ampicillin (MIC: 2.0–4.0 mg/L) and ciprofloxacin (MIC: 0.06–0.12 mg/L). Meropenem was active against 74% of isolates at MIC 0.06 mg/L and against all isolates at MIC 0.12 mg/L. 50% of isolates were resistant to cefepime at MIC 0.125 mg/L, while 100% of isolates were susceptible to it at MIC 0.5 mg/L [25].

The results demonstrate that subinhibitory antibiotic concentrations promote pathogen survival and facilitate the development of resistance through vertical gene transfer. These studies demonstrate that carbapenem resistance in pathogenic *E. coli* serotypes severely limits therapeutic options, underscoring their critical status in clinical management and necessitating improved antimicrobial stewardship and infection control measures.

A group of authors studied the antibiotic sensitivity of pathogenic coliform cultures circulating in a commercial poultry farm in the Omsk Oblast. *E. coli* O37, O115, and O2 serovariants were isolated from pathological samples from chickens and chicks of different ages in 2018. These isolates exhibited 100% sensitivity to fluoroquinolone formulated into "Triflon" and "Enroflon K" drugs. At the same time, the strains showed absolute resistance to tetracycline, and most strains were resistant to tylosin, gentamicin, doxycycline, and chloramphenicol [26].

Isakova M. N. et al. studied 127 *E. coli* isolates from bovine mammary secretions and cervical swabs. Phenotypic resistance to rifampicin, semi-synthetic penicillins, and tetracyclines was prevalent among the studied isolates. The cultures showed a weaker resistance to azithromycin, chloramphenicol and tobramycin. Among the tested isolates, 28.46% demonstrated intermediate resistance to third-generation cephalosporins, while 49.02% carried the *blaDHA* resistance gene [27].

In 2023 M. S. Alexyuk et al. conducted the monitoring of *E. coli* antimicrobial resistance in the Republic of Kazakhstan. During 3 months, fecal samples from calves with escherichiosis clinical signs were collected on private farms in the Almaty region. 30 *E. coli* isolates were recovered from the biological samples; 6 of them were presumably identified as O157:H7. Study results revealed that only 4 isolates were susceptible to all tested antibiotic classes, while 7 isolates exhibited resistance to a single antibiotic. The majority demonstrated multidrug resistance (defined as non-susceptibility to ≥ 3 antibiotic classes). Five isolates showed resistance to 7 antibiotic classes, and one of the isolates proved to be resistant to all 8 classes of antibiotics. Most isolates were resistant to ampicillin, tetracycline, gentamicin, florfenicol, and trimethoprim. Resistance to enrofloxacin and amoxicillin / clavulanic acid combination was less prevalent. Almost all isolates were found to be sensitive to colistin. Some strains exhibited intermediate resistance to gentamicin and amoxicillin / clavulanic acid combination [28].

In the study by M. Yu. Syromyatnikov et al. the antimicrobial resistance genes of *E. coli* isolated from the intestines of 2–5-day-old diarrheic piglets were analyzed. Bioinformatic analysis identified 26 antibiotic resistance genes, including: aminoglycoside resistance (*Aac6-Aph2*, *Aac6-If*; *StrA*, *StrB*); *β*-lactam resistance (*AmpC1_Ecoli*; *OXA-10*, *OXA-14*, *OXA-16*, *Penicillin_Binding_Protein_Ecoli*, *TEM-143*, *TEM-166*, *TEM-215*, *TEM-76*, *TEM-95*); quinolone resistance (*QnrB19*, *QnrB5*, *QnrD*, *QnrVC4*); sulfonamide resistance (*SulI*); tetracycline resistance (*TetD*); trimethoprim resistance (*DfrA1*, *DfrA14*, *DfrA27*); phenicol resistance (*CmlA5*, *CmlA1*; *FloR*). Among 4 detected quinolone resistance genes, *QnrD* turned out to be prevalent: almost 60% of the genes in this sample. *E. coli* strains harboring this resistance plasmid are predicted to exhibit broad-spectrum resistance to most antimicrobial agents commonly used in veterinary practice. Among 10 identified *β*-lactam resistance genes, *Penicillin_Binding_Protein_Ecoli* was the most prevalent (24%). The prevalence of *OXA-16* was 9%, *AmpC1_Ecoli* – 15%, *OXA-10* – 12%, *OXA-14* – 11%. The prevalence of *TEM-143*, *TEM-166*, *TEM-76*, and *TEM-95* genes was 6% in total and only 1% of the findings were for *TEM-215*. Among the phenicol resistance genes, *CmlA5* (52%) and *CmlA1* (44%) were most prevalent. The most common trimethoprim resistance determinant was *DfrA14* gene (64%). Among the aminoglycoside-associated genes, *StrA* (35%) and *StrB* (31%) were the most prevalent. Tetracycline and sulfonamide resistance genes collectively represented 3% of the total relative abundance of resistance genes. Among the remaining sequences, no individual resistance group exceeded 10% in relative abundance. Specifically, resistance genes for tetracyclines, aminoglycosides, and sulfonamides each accounted for less than 1% of the total [29].

High-throughput sequencing revealed that *QnrD*, encoding quinolone resistance, was the most prevalent resistance gene identified.

CONCLUSION

The literature review indicates that *E. coli* frequently demonstrates resistance to: *β*-lactam antibiotics (particularly benzylpenicillin, penicillin, and cephalexin); aminoglycosides (primarily streptomycin and gentamicin);

tetracyclines, macrolides (erythromycin) and lincosamides (lincomycin). The majority of studies demonstrate that *E. coli* exhibit polyresistance (resistance to ≥ 2 antimicrobial agents), with many strains showing multiresistance (non-susceptibility to ≥ 1 agent from ≥ 3 antimicrobial classes).

Nevertheless, antibiogram results can vary significantly between studies. This can be attributed to the uneven distribution of antibiotic resistance mechanisms within the microbial populations (microbiocenosis) of individual livestock farms. The specific combination of resistance mechanisms in *E. coli* populations varies between farms and depends on multiple factors: circulating serovars and their genetic backgrounds; spectrum of antibiotics used and their application methods; presence of resistance determinants in farm environments; disinfection efficacy, as subinhibitory disinfectant concentrations may promote microbial adaptation. These factors collectively shape: the specific array of antibiotic resistance genes circulating within the farm's microbial community; phenotypic resistance mechanisms (including biofilm formation and bacterial persistence) and adaptive resistance (transient survival advantages under antimicrobial pressure). This represents one of the most critical challenges in treating *E. coli* infections, as the expanding resistance profile increasingly compromises optimal antimicrobial selection.

The literature review revealed key trends in *E. coli* antimicrobial resistance and confirmed the escalating challenge of antibiotic resistance in animal production systems. Consequently, comprehensive antimicrobial resistance surveillance is required, encompassing both livestock production facilities and their surrounding environments where resistant microorganisms may persist and spread. Monitoring of antimicrobial susceptibility trends will enable evidence-based updates to therapeutic guidelines for *E. coli* infections in livestock. In addition, it's crucial to continue the development and implementation of alternative therapies for infectious diseases that don't rely on antibiotics.

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