Slov Vet Res
DOI 10.26873/SVR-1630-2025
UDC 579:604.4:614.33:614:631.11:636.5/.58(497.6)
Pages: 259–68

Original Research Article

Antimicrobial Resistance Profiling of Selected *E. coli* Isolates and Detection of ESBL/pAmpC-encoding Genes in Broiler Flocks in Bosnia and Herzegovina Using Real-Time PCR

Key words

antimicrobial resistance;
E. coli;
broilers;
Bosnia and Herzegovina

Amira Koro-Spahić[1], Sead Hadžiabdić[2], Teufik Goletić[1], Amer Alić[3], Aida Kustura[4], Adis Softić[4], Emina Rešidbegović[1]*

[1]Department of Animal Production and Biotechnology and Department of Pathobiology and Epidemiology, [3]Department of Clinical Sciences of Veterinary Medicine, [4]Department of Animal Production and Biotechnology, Veterinary Faculty, University of Sarajevo, Zmaja od Bosne 90, 71 000, Sarajevo, Bosnia and Herzegovina, [2]German Federal Institute for Risk Assessment, Unit Food Hygiene and Technologies, Supply Chains, Food Defense, Department of Biological Safety, Max-Dohrn-Str.8-10, 10589 Berlin, Germany

***Corresponding author:** residbegovic.emina@gmail.com

Abstract: Antimicrobial resistance (AMR) is a growing global issue, driven by the nontargeted use of antimicrobials in livestock. Poultry, particularly broilers, may serve as significant reservoirs for resistant *Escherichia (E.) coli strains*. This study aimed to isolate *E. coli* from broiler flocks and evaluate their *in vitro* susceptibility towards β-lactams, cephalosporins, carbapenems, tetracyclines, and fluoroquinolones. Additionally, a multiplex real-time PCR assay was used to detect extended-spectrum β-lactamase (ESBL)- and carbapenemase-encoding genes. A total of 48 commensal *E. coli* isolates from broiler flocks in Bosnia and Herzegovina (BiH) were analyzed. Phenotypic resistance, determined using the disc diffusion method, was observed for ampicillin (87.5%), amoxicillin/clavulanic acid (62.5%), cefepime (41.7%), cefoxitin (45.8%), cefotaxime (50.0%), ceftazidime (47.9%), azithromycin (58.3%), ciprofloxacin (66.7%), and tetracycline (72.9%). PCR analysis confirmed bla_{TEM}, bla_{CTX-M} and bla_{CMY} genes in 24 isolates (50%), whereas bla_{SHV} and carbapenemase-encoding genes (bla_{KPC}, bla_{NDM}, bla_{OXA-48}, bla_{VIM} and bla_{GES}) were not detected. The high prevalence of multidrug-resistant *E. coli* strains highlights the need for enhanced antimicrobial stewardship in poultry production. Reducing antibiotic use, promoting alternative disease control measures, and implementing systematic resistance monitoring programs are crucial to reduce AMR in broiler farms and potential spill over to public health.

Received: 7 November 2022
Accepted: 27 May 2025

Introduction

E. coli holds a unique position in microbiology, functioning as both a commensal bacterium and a potential pathogen (1). Most *E. coli* strains are non-pathogenic in mammals and poultry, constituting part of the normal intestinal flora (2). However, pathogenic strains can affect different organs and systems in diseased poultry, leading to conditions such as omphalitis, coligranulomatosis, air sac disease, avian cellulitis, swollen head syndrome, peritonitis, salpingitis, osteomyelitis, and panophthalmitis (2). Unlike in mammals, where *E. coli* may cause intestinal diseases, in poultry, it primarily leads to secondary localized or systemic infections due to a weakened or insufficiently functional immune system (2). Additionally, *E. coli* infections can contribute to significant economic losses in the poultry industry (2). Young birds, typically between 2 and 12 weeks old, are most susceptible, with the highest mortality rates occurring around 4 to 9 weeks of age (3). The earliest indications of illness include reduced appetite, lethargy, and a dejected posture

with ruffled feathers. Infected birds may retract their heads and necks into their bodies, and as the condition progresses, they exhibit labored, rapid breathing, gasping, or other signs of respiratory distress (3).

Colibacillosis is a globally prevalent bacterial infection in poultry, with its incidence varying by region due to differences in management, climate, and biosecurity practices (4). It affects broilers, layers, breeders, and other species such as pigs, rabbits, and pet animals (4). Seasonal patterns influence its occurrence, with cold and wet conditions promoting *E. coli* survival and increasing disease outbreaks (4). Within poultry farms, factors like farm size, biosecurity, and stocking density play a crucial role in disease dynamics, with largescale farms being more vulnerable to outbreaks (4).

A significant concern associated with *E. coli* is the potential transmission through numerous pathways of virulent and/or antimicrobial-resistant strains, as these bacteria contribute to the global challenge of antimicrobial resistance and the transfer of resistance genes (1).

Antimicrobial resistance continues to pose a major threat to human and veterinary medicine (5). Although many AMR genes originate from the environment and resistance is a natural phenomenon, the intensive use of antibiotics in recent decades has been one of the main causes of the emergence and rapid spread of AMR (6, 7, 8). Another challenge in combating the spread of AMR is that it is evolving faster than the development and market introduction of new antimicrobial drugs (9). The use of antibiotics is widespread in commercial poultry production, one of the most widespread branches of animal production with an annual global production of over 90 billion tons of chicken meat in 2018 (10). An important milestone in the fight against the spread of AMR was the Regulation (EC) No 1831/2003 of the European Commission, which introduced an EU-wide ban on the use of antibiotics as growth promoters in the EU (11). In the United States of America (USA), similar legislation came into force in 2017 (12). Despite these efforts, the occurrence of resistant bacteria and antibiotic residues in poultry and poultry products remains a cause for concern (10). The digestive tract of poultry and other animals can serve as a reservoir for resistant bacteria such as *E. coli*, *Salmonella* and *Campylobacter* (13).

In Bosnia and Herzegovina, the "Law on Medicinal Products Used in Veterinary Medicine" (14) regulates the production, trade, testing and control of medicinal products used in veterinary medicine to protect animal health. It also defines the manner of prescribing and dispensing medicinal products and the conditions for trade of veterinary medicinal products (15, 16). However, the current regulations in BiH does not specify how and under what conditions antibiotics may be used in animal husbandry.

Of concern is that commensal *E. coli* strains can contribute to the spread of certain beta-(β)lactamases encoding genes known as extended spectrum β-lactamases (ESBL) encoding genes (13), as well as plasmid-mediated β-lactamases (pAmpC) (1). These enzymes are able to hydrolyze penicillins and cephalosporins up to the 3rd generation. ESBLs are often inhibited by clavulanic acid (18).

Poultry can be a potential source of ESBL-producing bacteria that can be transmitted to humans and lead to infections (19). Several EU Member States reported a high prevalence of ESBL-producing enterobacteria in European broiler production (20, 21, 22, 23, 24). In a study by Blaak et al. (23), ESBL-producing *E. coli* isolates were found to be highly prevalent in Dutch poultry production, especially in broiler flocks (81%), which could be related to AMU in broilers, which are more common than in layers. On the other hand, Mo et al. (22) state that the first ESBL-producing *E. coli* strain was isolated from the feces of a healthy broiler in 2006 and that broiler production in Norway could be a reservoir for ESBL-producing *E. coli* (24). Furthermore, Gao et al. (25) point out that ESBL-carrying *E. coli* can be spread from animals via the food chain and water. The ESBL-producing *E. coli* isolates were detected in the meconium of 1-day-old chicks, indicating that ESBL-encoding genes can be transmitted vertically (26).

In addition to ESBL-producing bacteria in livestock, carbapenem resistance in enterobacteria is also of increasing concern (27). In recent years, several studies have detected bacteria with carbapenemase-encoding genes in livestock and wild birds (28, 29, 30, 31, 32, 33, 34). The concern is justified by the importance of carbapenems as important antimicrobial agents (35) and their use in severe life-threatening infections with multidrugresistant bacteria in humans (36, 37, 38). Due to their importance in human therapy, carbapenems are not authorized for use in food-producing animals in the EU (29).

Considering the sparse data on AMR in commensal *E. coli* isolates from commercial broiler production in BiH, the aim of this study was to isolate and identify *E. coli* from specific broiler farms and test their in vitro susceptibility to specific antibiotics from the group of βlactams, cephalosporins, carbapenems, tetracyclines and fluoroquinolones. In addition, a screening with multiplex real-time PCR was performed to identify the potential presence of potential ESBL- and carbapenemase-encoding genes.

Materials and methods

Sampling of diagnostic material was conducted between March 2019 and October 2020 on 48 broiler farms in BiH. The selection of these 48 flocks was based on a stratified random sampling method, ensuring representation from various regions within the country and accounting for factors such as farm size, production system, and biosecurity

practices. This approach aimed to capture a diverse range of conditions and practices that could influence the prevalence of *E. coli* infections. Broiler flocks consisted of at least 10 000 animals per farm. The sampled broiler flocks, all of COBB 500 provenance, were between 27 and 35 days old. Sampling was performed using two pairs of boot swabs per flock in the production area of each farm. The shoe covers were required to have adequate moisture absorption capacity and were pre-soaked with sterile 0.8% saline solution 0.8% saline (Centrohem d.o.o., Serbia). To ensure representative sampling, the designated area was walked through whole area. Upon completion, the boot swabs were carefully removed, turned inside out to retain the collected material, and properly packaged and labeled. Samples were transported to the laboratory as soon as possible in airtight, sealed containers under cold chain conditions. The time frame between sample collection and laboratory processing did not exceed 24 hours, ensuring sample integrity and minimizing potential changes in microbial composition.

Isolation of E. coli

The boot swabs were incubated for 18 ± 2 hours at 37 °C in 225 ml buffered peptone water (Condalab, Madrid, Spain). After incubation, the contents were inoculated onto MacConkey agar (Condalab, Madrid, Spain) to isolate *E. coli*, meanwhile another loopful was streaked onto MacConkey agar containing 1 mg/l cefotaxime (MC+CTX) (Acros Organics, China) to screen for *E. coli* resistant to third generation cephalosporins and incubated overnight at 37 °C. A presumptive *E. coli* colony was inoculated onto eosin methylene blue agar (Liofilchem s.r.l., Italy) and incubated overnight at 37 °C. API 20 E biochemical strips (BioMerieux, France) were used to confirm *E. coli* according to the manufacturer's instructions. Confirmed *E. coli* isolates were stored as stab cultures in nutrient agar for further antibiotic susceptibility testing and real-time PCR.

Antibiotic susceptibility testing (AST)

To test the antibiotic susceptibility of *E. coli* isolates, the disc diffusion method was performed according to the recommendations of the Clinical and Laboratory Standards Institute (CLSI) and the European Committee for Antimicrobial Susceptibility Testing (EUCAST) (39, 40). In addition, the Combination Disc Test (CDT) was performed to detect ESBL-producing *E. coli* isolates.

a) Disc diffusion method

For the disc diffusion method, isolates were suspended in sterile 0.8% saline solution and adjusted to a turbidity of 0.5 McFarland (BioMerieux, France) and inoculated uniformly onto Mueller-Hinton agar (Condalab, Madrid, Spain). After drying of the plate surface, antibiotic discs [ampicillin (10 µg), amoxicillin + clavulanic acid (20 µg + 10 µg), cefepime (30 µg), cefoxitin (30 µg), cefotaxime (30 µg), ceftazidime (30 µg), meropenem (10 µg), imipenem (10 µg), ertapenem (10 µg), ciprofloxacin (5 µg), azithromycin (15 µg), tetracycline (30 µg), tigecycline (15 µg)] (Liofilchem s.r.l, Italy) were added and the plates were incubated overnight at 37 °C (39). Growth inhibition around the discs was measured the next day. The results were interpreted in accordance with the CLSI recommendations (39), with the exception of tigecycline, for which the interpretation was according to EUCAST (40). Depending on the diameter of the zone of inhibition, the *E. coli* isolates tested were classified as sensitive (S), intermediate (I), resistant (R) and susceptibility dosedependent (SDD). *E. coli* isolates were classified as SDD if the zone diameter for cefepime was 19-24 mm, as CLSI (39) does not have a breakpoint value for classifying isolates as "intermediate" for the above antibiotic. The interpretation categories and zone diameter breakpoints are listed in Table 1

Table 1; Interpretative categories and zone diameter in mm 600 breakpoints for selected antibiotics

Antibiotics	Interpretative categories and zone diameter breakpoints			
	S	I	R	SDD
Ampicillin	≥17	14-16	≤13	-
Amoxicillin + clavulanic acid	≥18	14-17	≤13	-
Cefepime	≥25	-	≤18	19-24
Cefoxitin	≥18	15-17	≤14	-
Cefotaxime	≥26	23-25	≤22	-
Ceftazidime	≥21	18-20	≤17	-
Meropenem	≥23	20-22	≤19	-
Ertapenem	≥22	19-21	≤18	-
Imipenem	≥23	20-22	≤19	-
Ciprofloxacin	≥26	22-25	≤21	-
Azithromycin	≥13	-	≤12	-
Tetracycline	≥15	12-14	≤11	-

b) Combination Disc Test (CDT)

E. coli isolates grown on MacConkey with 1 mg/l cefotaxime (Acros Organics, China) were subjected to CDT. For CDT, the *E. coli* isolates were adjusted to a turbidity of 0.5 McFarland (BioMerieux, France) and inoculated onto Mueller-Hinton agar (Condalab, Madrid, Spain). After drying the plate surface for 15 min, cefotaxime (30 µg), cefotaximeclavulanic acid (30 µg and 10 µg), ceftazidime (30 µg) and ceftazidime-clavulanic acid (30 plus 10 µg) (Liofilchem

s.r.l., Italy) were applied at least 25 mm apart from another (39). The test was positive if the zone of inhibition with clavulanic acid was ≥ 5 mm compared to that without clavulanic acid (e.g. ceftazidime = 16, ceftazidime + clavulanic acid = 21) (39). The *E. coli* strain ATCC 25922 was used as quality control.

Detection of potential AMR-associated genes

a) Bacterial DNA extraction by thermal lysis

The DNA template was prepared by the adapted boiling method according to Roschanski et al. (44). Thermal lysis was performed with 1 ml of an overnight culture of *E. coli* in BPW (Condalab, Madrid, Spain). The culture was centrifuged at 14 000 rpm for five minutes, the supernatant was discarded and the remaining pellet was resuspended in 300 µl of sterile TE buffer (10 mM Tris, 0.1 mM EDTA, pH 8). To lyse the cells, this was heated to 99 °C for 10 minutes. The suspension was cooled on ice for three minutes, vortexed centrifuged at 14000 rpm for two minutes. Finally, 100 µl of the supernatant was stored at -20 °C for subsequent real-time PCR (44).

b) Real-time PCR for potential ESBL and carbapenemase-encoding AMR genes

The bacterial DNA of the isolates was subjected to a screening method by multiplex realtime PCR for the detection of AMR genes, using the specific primer pairs and fluorescent probes from previous studies (41, 42, 43). PCR cycling conditions for the detection of ESBL and carbapenemase-encoding genes were performed according to the protocol of Roschanski et al. (44) and van der Zee et al. (43).

Results

Isolation and identification of E. coli

Of a total of 48 broiler flocks examined, *E. coli* was detected in booth swabs from all broiler farms (n=48). All 48 isolates showed pink colour, shiny and smooth colony on the surface of MacConkey agar and characteristic metallic green sheen on EMB agar. By using CDT for ESBL identification, the presence of both ESBL-producing and non-producing *E. coli* isolates were confirmed. The results showed that 10 (20.83%) isolates were ESBL producers.

Antimicrobial susceptibility testing

The results of the antimicrobial susceptibility testing revealed variations in the susceptibility of *E. coli* isolates, as presented in Table 2. *E. coli* isolates derived from broiler farms showed the highest resistance rates, particularly to tetracycline (75%), ampicillin (72.92%), ceftazidime (66.67%), ciprofloxacin (31.25%), cefotaxime (20.83%), amoxicillin-clavulanic acid (18.75%), cefepime (14.58%), azithromycin (4.17%), and cefoxitin (2.08%). Notably, the resistance was towards tigecycline or carbapenems (meropenem, ertapenem, and imipenem) was not detected.

Table 2: Results of antibiotic susceptibility testing using the disc diffusion method

Antibiotics	Interpretative categories and zone diameter breakpoints			
	S	I	R	SDD
Ampicillin	3 (6.25%)	10 (20.83%)	35 (72.92%)	-
Amoxicillin/ clavulanic acid	38 (79.17%)	1 (2.08%)	9 (18.75%)	-
Cefepime	22 (45.83%)	0%	7 (14.58%)	19 (39.58%)
Cefoxitin	46 (95.83%)	1 (2.08%)	1 (2.08%)	-
Cefotaxime	38 (79.17%)	0%	10 (20.83%)	-
Ceftazidime	14 (29.17%)	2 (4.16%)	32 (66.67%)	-
Meropenem	48 (100%)	0%	0%	-
Ertapenem	48 (100%)	0%	0%	-
Imipenem	48 (100%)	0%	0%	-
Ciprofloxacin	7 (14.58%)	26 (54.17%)	15 (31.25%)	-
Azithromycin	46 (95.83%)	0%	2 (4.17%)	-
Tetracycline	12 (25%)	0%	36 (75%)	-
Tigecycline	48 (100%)	0%	0%	-

Screening of potential ESBL-associated and carbapenemase-encoding AMR genes

Among the 48 *E. coli* isolates obtained from broiler farms, resistance genes encoding ESBL/pAmpC were identified—either individually or in combination—in 24 (50%) isolates as shown in Figure 1. Among these, the most prevalent resistance genes were bla_{TEM} (35.42%), bla_{CTX-M} (6.25%), and bla_{CMY} (2.08%). Some isolates carried combinations of resistance genes, including $bla_{TEM+blaCMY}$ (4.17%) and $bla_{TEM+blaCTX-M}$ (2.08%). Neither bla_{SHV} nor carbapenemase-encoding genes (bla_{KPC}, bla_{NDM}, bla_{OXA-48}, bla_{VIM} and bla_{GES}) were detected.

Discussion

Antimicrobial resistance has become a major threat to public health, leading to problems in the prevention and treatment of persistent infections (44). Despite scientific efforts

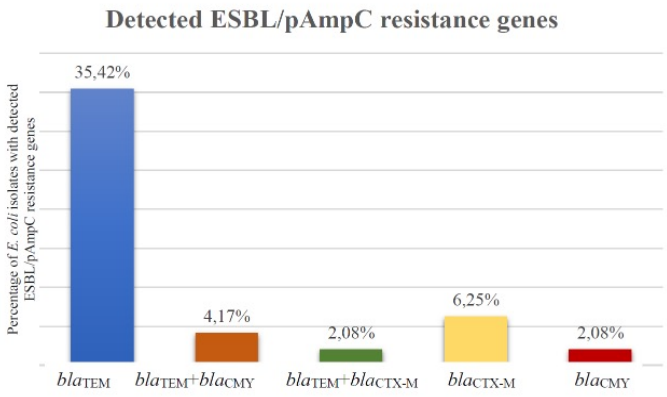

Figure 1: Detected ESBL/pAMPC resistance genes

to address this problem in recent decades, the spread of antimicrobial resistance remains a problem (44). The main reason for the emergence of AMR is considered to be AMU in veterinary, human medicine and in agricultural production (45). Antimicrobial resistance is influenced by spontaneous evolution, bacterial mutation and the transfer of resistant genes by horizontal gene transfer (44). It is particularly important to emphasize the role of Gramnegative bacteria such as *E. coli*, which are ubiquitous in humans and animals (1). *E. coli* can serve as a reservoir for AMR-encoding genes that can be transferred between different bacterial species, including zoonotic bacteria (1, 46, 47).

Among the *E. coli* isolates examined in this study, the highest resistance rate was found for tetracycline (75%), ampicillin (72.92%) and ceftazidime (66.67%), followed by ciprofloxacin (31.25%), cefotaxime (20.83%), amoxicillin + clavulanic acid (18.75%), cefepime (14.58%), azithromycin (4.17%) and cefoxitin (2.08%) (Table 2). A similar observation was made by Persoons et al. (51), where high resistance to ampicillin, nalidixic acid, streptomycin, tetracycline and a combination of trimethoprim and sulfonamides was found in *E. coli* isolates from cloacal swabs and carcasses of broilers. Furthermore, the high levels of resistance to tetracyclines and ampicillin may be associated with the frequent use of these antibiotics in poultry production in our country. On the other hand, Much et al. (52) reported a high resistance rate to ciprofloxacin (69.1%) in *E. coli* isolated from appendix samples of conventionally reared broilers in Austria. In addition, Gholami-Ahangaran et al (50) reported a high rate of resistance to β-lactam antibiotics, macrolides, tetracyclines, fluoroquinolones, nitrofurans, aminoglycosides, folate pathway antagonists and phenicols in ESBL-producing *E. coli* isolates from turkey meat samples. According to these findings, it is hypothesized that the high resistance to β-lactams and other antibiotic classes may be due to the co-transfer of a plasmid carrying MDR-encoding genes (50).

In our study, 10 isolates showed resistance to cefotaxime. In a study by Hadžić-Hasanović et al (51), resistance to penicillins, nalidixic acid, cephalexin and ceftriaxone was found in *E. coli* isolates from chicken skin samples, including fresh and frozen meat samples, while Fetahagić et al. (52) reported resistance to amoxicillin, cefazolin, cefotaxime and ceftriaxone in cefotaxime-resistant *E. coli* isolates from poultry in BiH.

In addition, Gholami-Ahangaran et al. (50) state that AMR could be influenced by geographical location. Even though the resistance rate of *E. coli* varies in different European countries such as Poland, Germany, France and the United Kingdom, the resistance rate to penicillins is high in all countries (70%) (47). In addition, Blaak et al. (23) pointed out that ESBL-producing *E. coli* are widespread in poultry production in the Netherlands, especially in broiler flocks.

In the studies by Hadžić-Hasanović et al. (51) and Fetahagić et al. (52), phenotypically confirmed ESBL-producing *E. coli* isolates were sensitive to carbapenems. This was also confirmed in our study, as selected *E. coli* isolates were sensitive to meropenem, ertapenem and imipenem. According to the EFSA report 2021/2022 (53), resistance of *E. coli* to carbapenems was less common. In this regard, resistance to meropenem was detected in one isolate from broilers in 2021/2022. The less resistance to selected carbapenems can be explained by the fact that these antibiotics are not approved for use in food-producing animals (54, 55). According to Silva et al (56), the detection of carbapenemases in enterobacteria is less pronounced in *E. coli* and *Salmonella* spp. than in *Klebsiella (K.) pneumoniae*. This is confirmed by several studies from Europe in which sporadic carbapenem resistance was found in *E. coli* from pigs and their environment (33, 57, 58, 59). Resistance to tigecycline was found only in three isolates from broilers and pigs from Belgium and three isolates from pigs from Malta (53). No resistance to tigecycline was detected in our study.

Since β-lactams are used in veterinary and human medicine (60), the most common βlactamases in Gram-negative bacteria contain genes encoding resistance to these antibiotics, represented by different genes belonging to *bla*$_{TEM}$, *bla*$_{SHV}$, *bla*$_{OXA}$, *bla*$_{CMY}$ and *bla*$_{CTX-M}$ (60, 61). In our study, the *bla*$_{TEM}$ gene was the most represented (41.6%) (n=17) (Figure 1), but further molecular subtyping of this gene was not performed, so it is not possible to specify which subtype of *bla*$_{TEM}$ it is and whether or not it is associated with ESBL production. A similar observation about the presence of the *bla*$_{TEM}$ gene in *E. coli* isolates from poultry was made in a study from Thailand (65). The *bla*$_{CTX-M}$ gene was found in three isolates that were also phenotypically resistant to cefotaxime. GholamiAhangaran et al (50) state that the presence of high resistance as well as the frequency of the *bla*$_{CTX-M}$ gene can be associated with the presence of the ESBL gene and resistance to cefotaxime. It is important to point out that the combination of *bla*$_{TEM/blaCMY}$ (n=2) and *bla*$_{TEM/blaCTX-M}$ (n=1) genes was detected in some isolates. The *bla*$_{CMY}$ gene was detected in one *E. coli* isolate. Previous studies have observed that combinations of different AMR genes are present in *E. coli* isolates (50, 63). Jafari et al.

(66) detected a combination of two or three ESBL genes in 15 (10 %) *E. coli* isolates from broiler chickens. The most frequent gene combinations in *E. coli* isolates were bla_{TEM} + $bla_{CTX-M-15}$, bla_{TEM} + bla_{SHV}, bla_{SHV} + $bla_{CTX-M-15}$ and as bla_{TEM} + bla_{SHV} + $bla_{CTX-M-15}$ type (66). In Iran, Gholami-Ahangaran et al (50) detected a combination of two ESBL genes in *E. coli* isolates from meat and intestinal contents of turkeys, with the most common gene combination being bla_{TEM} + bla_{CTX-M}. Molecular analysis in our study revealed that 7 out of 10 phenotypically confirmed ESBLproducing *E. coli* isolates carried at least one of the potential ESBL-associated genes: bla_{CMY} (n=1), bla_{CTX-M} (n=3), bla_{TEM} + bla_{CMY} (n=2), and bla_{TEM} + bla_{CTX-M} (n=1). On the other hand, in 3 out of 10 phenotypically confirmed ESBL-producing *E. coli* isolates, no AMR genes were detected using the molecular screening method. The lack of a genotypephenotype association could be explained by other resistance genes (67) or factors that were not investigated in this study.

In addition, a larger panel of genes encoding β-lactamases could help determine the genetic determinants of resistance in these isolates (65). Furthermore, despite the presence of blaTEM genes (n=17), no phenotypic resistance was observed. In this context, we did not characterize the subtypes of AMR genes detected, which would provide valuable information for a better understanding of the molecular AMR epidemiology. Discrepancies in genotype–phenotype association have been demonstrated in previous studies with clinical isolates of *E. coli* and K. pneumoniae (66, 67). Zhang et al. (66) investigated whether ESBL genes are present in clinical, non-ESBL-producing, antibiotic-susceptible K. pneumoniae isolates. A total of 8.9% (18/202) of the isolates carried only one ESBL gene, including the bla_{SHV} and bla_{CTX-M} genes. Nine of the isolates carrying ESBL genes did not exhibit phenotypic resistance (66). In their study, Kazemian et al. (67) observed the phenotypic and genotypic characteristics of ESBL-, AmpC- and carbapenemase-producing *K. pneumoniae* and *E. coli* recovered from clinical isolates. With the exception of one *E. coli* isolate, the genotypic method confirmed the phenotypic results (67). It is likely that the antibiotic regulates the antimicrobial resistance genes so that they are only slightly expressed *in vitro*, or that the phenomenon of heteroresistance associated with unstable tandem gene amplification, rare mutation and environmental modulation of the resistant genes may explain the different susceptibilities (64). Moreover, in a previous study, $bla_{CTX-M-1}$, bla_{TEM-52} and bla_{SHV-12} genes were observed as the most represented types of ESBLencoding genes in poultry (26). An increase in the prevalence of the CTX-M type was previously described in the United Kingdom, the Netherlands and Germany (26). In the study by Hadžić-Hasanović (51), ESBL-producing *E. coli* isolates from BiH obtained from chicken skin contained different ESBL-encoding genes, including bla_{CTX-M} type genes, as well as mutations in TEM and SHV, encoding ESBL enzymes.

In different studies from African, American, Asian and European countries (43, 68, 59, 70, 71, 72, 73, 74, 75), carbapenemase-encoding genes were detected in bacteria from farm animals (cattle, pigs, poultry), domestic animals (dogs, cats, ornamental birds) and wild animals. In Europe, carbapenemase-encoding genes are only sporadically detected in poultry. In our study, no carbapenemase-encoding resistance genes (bla_{KPC}, bla_{NDM}, bla_{OXA48}, bla_{VIM} and bla_{GES} genes) were detected. It should be noted that the route of transmission of carbapenemase-resistant enterobacteria from food-producing animals, pets and food is not yet fully understood (54). Although the origin of most carbapenemase-encoding genes is not fully understood, it is believed that carbapenemase-encoding genes are most likely acquired from environmental bacteria (76) or from the human field, where carbapenems are used to treat serious life-threatening human infections (77).

Recent studies highlight the ongoing challenges in managing antimicrobial resistance in veterinary pathogens. Gioushy et al. (78) emphasize the difficulty in treating *Mycoplasma bovis* mastitis due to variable resistance patterns, underlining the necessity of susceptibilityguided therapy. Given the increasing difficulties in treating resistant bacterial infections, alternative strategies are being explored. Phage therapy, in particular, is regaining attention. Stilec et al. (79) highlighted the potential of bacteriophages as precision tools that specifically target pathogenic bacteria, thus minimizing collateral damage to beneficial microbiota. Šumonja and Kotnik (80) further demonstrated the utility of phages in managing skin dysbiosis in atopic dogs, presenting a case for phage therapy as a viable alternative to antibiotics in veterinary medicine (80). These findings support the notion that alongside efforts to monitor antimicrobial gene spread, the veterinary field must begin integrating alternative treatment approaches.

To the best of our knowledge, this is among the few studies in Bosnia and Herzegovina that have identified ESBL and/or pAmpC resistance genes in *E. coli* isolates from broilers. Nevertheless, the study has certain limitations. The sample size was relatively small, and a more comprehensive investigation involving a larger number of samples and more detailed genetic characterization of the resistant isolates would have provided deeper insights. Antimicrobial resistance is a global challenge for veterinary and human medicine. Coordinated multidisciplinary initiatives focusing on antibiotic alternatives and reducing overall antibiotic consumption are being used to reduce antimicrobial resistance on chicken farms. It is necessary to develop and implement programs to monitor and control antibiotic resistance. In this regard, as in other countries, it is very important that the current legislation in BiH introduces a framework for the control of antibiotic use in the veterinary sector.

Acknowledgements

This paper is part of the project "*Escherichia coli*: Biodiversity and antibiotic resistance with public health implication",

funded by the Ministry of Education, Science and Youth of Sarajevo Canton (Contract number: 11/05-14-27888-1/19).

Declaration of conflicting interests. The author(s) declared no potential conflicts of interest with respect to the research, author-ship, and/or publication of this article. The project ,,Escherichia coli: Biodiversity and antibiotic resistance with public health im-plication'' funded the authors as follows: Amira Koro-Spahić, Emina Rešidbegović, Teufik Goletić, Aida Kustura and Adis Softić.

References

1. Poirel L, Madec JY, Lupo A, et al. Antimicrobial resistance in Escherichia coli. Microbiol Spectr 2018; 6(4): 10.1128/microbiolspec.arba-0026-2017. doi: 10.1128/microbiolspec.ARBA-0026-2017
2. Nolan LK, Barnes HJ, Vaillancourt JP, Abdul-Azit T, Louge CM. Colibacillosis. In: Swayne DE, ed. Diseases of poultry. 13th ed. Ames: John Wiley & Sons, 2013: 751–808.
3. Pattison M, Paul M, Janet MB, Dennis A. Poultry diseases. 6th ed. Edinburgh: Elsevier, 2007: 145–73.
4. Kika TS, Cocoli S, Pelić DL, Puvača N, Lika E, Pelić M. Colibacillosis in modern poultry production. J Agron Technol Eng Manag 2023; 6(6): 975–87. doi: 10.55817/YZFA3391
5. Palma E, Tilocca B, Roncada P. Antimicrobial resistance in veterinary medicine: an overview. Int J Mol Sci 2020; 21(6): 1914. doi: 10.3390/ijms21061914
6. Davies J, Davies D. Origins and evolution of antibiotic resistance. Microbiol Mol Biol Rev 2010; 74(3): 417–33. doi: 10.1128/MMBR.00016-10
7. Wright GD. Q&A: antibiotic resistance: where does it come from and what can we do about it?. BMC Biol 2010; 8: 123. doi: 10.1186/1741-7007-8-123
8. Davey P, Wilcox MH, Irving W, Thwaites G. Antimicrobial chemotherapy. 7th ed. Oxford: Oxford University Press, 2015: 91–100.
9. Vangchhia BL. Genetic structure and antimicrobial resistance of food-borne Escherichia coli in Australia. The Australian National University, Research School of Biology, 2017. Doctoral thesis.
10. Agyare C, Boamah VE, Zumbi CN, Osei FB. Antibiotic use in poultry production and its effects on bacterial resistance. In: Antimicrob resistance: a global threat. London: IntechOpen, 2018: 33–50.
11. European Commission. Ban on antibiotics as growth promoters in animal feed enters into effect. Brussels: Europen Commission, 2005. https://ec.europa.eu/commission/presscorner/detail/en/IP_05_1687 (20. 1. 2025).
12. AASV. FDA Announces Implementation of GFI #213, Outlines Continuing Efforts to Address Antimicrobial Resistance. Perry: American Association of Swine Veterinarians, 2017. https://www.aasv.org/2017/01/fda-announces-implementation-of-gfi-213-outlines-continuing-efforts-to-address-antimicrobial-resistance/ (20. 1. 2025).
13. Heredia N, García S. Animals as sources of food-borne pathogens: a review. Anim Nutr 2018; 4(3): 250–5. doi: 10.1016/j.aninu.2018.04.006
14. The veterinary law in Bosnia and Herzegovina. Off J B&H 2022; 34(2): 1–65. https://www.vet.gov.ba/pdffiles/Zakon_O_Vetrinarstvu/Veterinary%20Law.pdf (20. 1. 2025).
15. [Rulebook on the manner of prescribing and dispensing medicines used in veterinary medicine ("Official Gazette of FBiH" No.: 54/99)]. In Bosnian. 1999.
16. [Rulebook on Conditions for Trade in Medicinal Products Used in Veterinary Medicine (''Official Gazette of the FBiH'' No.: 5/10)]. In Bosnian. 2010.
17. Ramos S, Silva V, Dapkevicius MLE, et al. Escherichia coli as commensal and pathogenic bacteria among food-producing animals: health implications of extended spectrum β-lactamase (ESBL) production. Animals (Basel) 2020; 10(12): 2239. doi: 10.3390/ani10122239
18. Ghafourian S, Sadeghifard N, Soheili S, Sekawi Z. Extended spectrum betalactamases: definition, classification and epidemiology. Curr Issues Mol Biol 2015; 17: 11–21. doi: 10.21775/cimb.017.011
19. Falgenhauer L, Imirzalioglu C, Oppong K, et al. Detection and characterization of ESBL-producing Escherichia coli from humans and poultry in Ghana. Front Microbiol 2019; 9: 3358. doi: 10.3389/fmicb.2018.03358
20. Randall LP, Clouting C, Horton RA, et al. Prevalence of Escherichia coli carrying extended-spectrum β-lactamases (CTX-M and TEM-52) from broiler chickens and turkeys in Great Britain between 2006 and 2009. J Antimicrob Chemother 2011; 66(1): 86–95. doi: 10.1093/jac/dkq396
21. Laube H, Friese A, Von Salviati C, et al. Longitudinal monitoring of extendedspectrum-beta-lactamase/AmpC-producing Escherichia coli at German broiler chicken fattening farms. Appl Environ Microbiol 2013; 79(16): 4815–20. doi: 10.1128/AEM.00856-13
22. Mo SS, Norström M, Slettemeås JS, Løvland A, Urdahl AM, Sunde M. Emergence of AmpC-producing Escherichia coli in the broiler production chain in a country with a low antimicrobial usage profile. Vet Microbiol 2014; 171(3/4): 315–20. doi: 10.1016/j.vetmic.2014.02.002
23. Blaak H, van Hoek AH, Hamidjaja RA, et al. Distribution, numbers, and diversity of ESBL-producing *E. coli* in the poultry farm environment. PLoS One 2015; 10(8): e0135402. doi: 10.1371/journal.pone.0135402
24. Thomas C, Idler C, Ammon C, Amon T. Effects of the C/N ratio and moisture content on the survival of ESBL-producing Escherichia coli during chicken manure composting. Waste Manag 2020; 105: 110–8. doi: 10.1016/j.wasman.2020.01.031
25. Gao L, Hu J, Zhang X, et al. Dissemination of ESBL-producing Escherichia coli of chicken origin to the nearby river water. J Mol Microbiol Biotechnol 2014; 24(4): 279–85. doi: 10.1159/000365786
26. Saliu EM, Vahjen W, Zentek J. Types and prevalence of extended–spectrum beta– lactamase producing Enterobacteriaceae in poultry. Anim Health Res Rev 2017; 18(1): 46–57. doi: 10.1017/S1466252317000020
27. Muktan B, Shrestha UT, Dhungel B, et al. Plasmid mediated colistin resistant mcr-1 and co-existence of OXA-48 among Escherichia coli from clinical and poultry isolates: first report from Nepal. Gut Pathog 2020; 12: 44. doi: 10.1186/s13099-020-00382-5
28. Guerra B, Fischer J, Helmuth R. An emerging public health problem: acquired carbapenemase-producing microorganisms are present in food-producing animals, their environment, companion animals and wild birds. Vet Microbiol 2014; 171(3/4): 290–7. doi: 10.1016/j.vetmic.2014.02.001
29. Madec JY, Haenni M, Nordmann P, Poirel L. Extended-spectrum βlactamase/AmpC-and carbapenemase-producing Enterobacteriaceae in animals: a threat for humans? Clin Microbiol Infect 2017; 23(11): 826–33. doi: 10.1016/j.cmi.2017.01.013
30. Fischer J, Schmoger S, Jahn S, Helmuth R, Guerra B. NDM-1 carbapenemaseproducing Salmonella enterica subsp. enterica serovar Corvallis isolated from a wild bird in Germany. J Antimicrob Chemother 2013; 68(12): 2954–6. doi: 10.1093/jac/dkt260

31. Fischer J, Rodríguez I, Schmoger S, et al. Salmonella enterica subsp. enterica producing VIM-1 carbapenemase isolated from livestock farms. J Antimicrob Chemother 2013; 68(2): 478–80. doi: 10.1093/jac/dks393

32. Borowiak M, Szabo I, Baumann B, et al. VIM-1-producing Salmonella Infantis isolated from swine and minced pork meat in Germany. J Antimicrob Chemother 2017; 72(7): 2131–3. doi: 10.1093/jac/dkx101

33. Roschanski N, Friese A, von Salviati-Claudius C, et al. Prevalence of carbapenemase producing Enterobacteriaceae isolated from German pig-fattening farms during the years 2011–2013. Vet Microbiol 2017; 200: 124–9. doi: 10.1016/j.vetmic.2015.11.030

34. Roschanski N, Hadziabdic S, Borowiak M, et al. Detection of VIM-1-producing enterobacter cloacae and Salmonella enterica serovars Infantis and Goldcoast at a breeding pig farm in Germany in 2017 and their molecular relationship to former VIM-1-Producing S. infantis isolates in german livestock production. mSphere 2019; 4(3): e00089-19. doi: 10.1128/mSphere.00089-19

35. WHO. Critically important antimicrobials for human medicine. 6th ed. Geneva: World Health Organization, 2019. https://apps.who.int/iris/bitstream/handle/10665/312266/9789241515528-eng.pdf (20. 1. 2025).

36. Almugadam BS, Ali NO, Ahmed AB, Ahmed EB, Wang L. Prevalence and antibiotics susceptibility patterns of carbapenem resistant Enterobacteriaceae. J Bacteriol Mycol 2018; 6(3):187–90. doi: 10.15406/jbmoa.2018.06.00201

37. Bonardi S, Pitino R. Carbapenemase-producing bacteria in food-producing animals, wildlife and environment: A challenge for human health. Ital J Food Saf 2019; 8(2): 7956. doi: 10.4081/ijfs.2019.7956

38. Peyclit L, Baron SA, Rolain JM. Drug repurposing to fight colistin and carbapenem-resistant bacteria. Front Cell Infect Microbiol 2019; 9: 193. doi: 10.3389/fcimb.2019.00193

39. CLSI M100. Performance standards for antimicrobial susceptibility testing. 35th ed. Wayne: Clinical and Laboratory Standards Institute; 2025.

40. EUCAST. Breakpoint tables for interpretation of MICs and zone diameters. Version 11.0. Växjö: The European Committee on Antimicrobial Susceptibility Testing, 2021. https://megumed.de/wp-content/uploads/2021/06/v_11.0_Breakpoint_Tables.pdf (20. 1. 2025).

41. Roschanski N, Fischer J, Guerra B, Roesler U. Development of a multiplex realtime PCR for the rapid detection of the predominant beta-lactamase genes CTX-M, SHV, TEM and CIT-type AmpCs in Enterobacteriaceae. PLoS One 2014; 9(7): e100956. doi: 10.1371/journal.pone.0100956

42. van der Zee A, Roorda L, Bosman G, et al. Multi-centre evaluation of real-time multiplex PCR for detection of carbapenemase genes OXA-48, VIM, IMP, NDM and KPC. BMC Infect Dis 2014; 14: 27. doi: 10.1186/1471-2334-14-27

43. Swayne RL, Ludlam HA, Shet VG, Woodford N, Curran MD. Real-time TaqMan PCR for rapid detection of genes encoding five types of non-metallo-(class A and D) carbapenemases in Enterobacteriaceae. Int J Antimicrob Agents 2011; 38(1): 35–8. doi: 10.1016/j.ijantimicag.2011.03.010

44. Dadgostar P: Antimicrobial resistance: implications and costs. Infect Drug Resist 2019; 12: 3903. doi: 10.2147/IDR.S234610

45. Wall BA, Mateus AL, Marshall L, Pfeiffer DU. Drivers, dynamics and epidemiology of antimicrobial resistance in animal production. Rome: Food and Agriculture Organization of the United Nations, 2016. https://openknowledge.fao.org/server/api/core/bitstreams/95efae06-4da2-4689-b12a-1b33fffc2244/content (20. 1. 2025).

46. European Food Safety Authority. Report from the Task Force on Zoonoses Data Collection including guidance for harmonized monitoring and reporting of antimicrobial resistance in commensal Escherichia coli and Enterococcus spp. from food animals. EFSA J 2008; 141: 1–44. doi: 10.2903/j.efsa.2008.141r

47. Roth N, Käsbohrer A, Mayrhofer S, Zitz U, Hofacre C, Domig KJ. The application of antibiotics in broiler production and the resulting antibiotic resistance in Escherichia coli: a global overview. Poult Sci 2019; 98(4): 1791–804. doi: 10.3382/ps/pey539

48. Persoons D, Dewulf J, Smet A, et al. Prevalence and persistence of antimicrobial resistance in broiler indicator bacteria. Microb Drug Resist 2010; 16(1): 67–74. doi: 10.1089/mdr.2009.0062

49. Much P, Sun H, Lassnig H, Koeberl-Jelovcan S, Schliessnig H, Stueger HP. Differences in antimicrobial resistance of commensal Escherichia coli isolated from caecal contents of organically and conventionally raised broilers in Austria, 2010– 2014 and 2016. Prev Vet Med 2019; 171: 104755. doi: 10.1016/j.prevetmed.2019.104755

50. Gholami-Ahangaran M, Moravvej AH, Safizadeh Z, Nogoorani VS, Zokaei M, Ghasemian SO. The evaluation of ESBL genes and antibiotic resistance rate in Escherichia coli strains isolated from meat and intestinal contents of turkey in Isfahan, Iran. Iran J Vet Res 2021; 22(4): 318–25. doi: 10.22099/ijvr.2021.39493.5737

51. Hadžić-Hasanović V, Jerković-Mujkić A, Hasanović E, Bačić A, Hukić M. Phenotypic and genotypic detection of ESBL-producing *E. coli* isolates from chicken skin in Bosnia and Herzegovina. Med Glas (Zenica) 2020; 17(2): 308–15. doi: 10.17392/1206-20

52. Fetahagić M, Ibrahimagić A, Uzunović S, et al. Detection and characterisation of extended-spectrum and plasmid-mediated AmpC β-lactamase produced by Escherichia coli isolates found at poultry farms in Bosnia and Herzegovina. Arh Hig Rada Toksikol 2021; 72(4): 305–14. doi: 10.2478/aiht-2021-72-3560

53. European Food Safety Authority. The European Union Summary Report on Antimicrobial Resistance in zoonotic and indicator bacteria from humans, animals and food in 2021-2022. EFSA J 2024; 22(2): 8583. doi: 10.2903/j.efsa.2024.8583

54. Köck R, Daniels-Haardt I, Becker K, et al. Carbapenem-resistant Enterobacteriaceae in wildlife, food-producing, and companion animals: a systematic review. Clin Microbiol Infect 2018; 24(12): 1241–50. doi: 10.1016/j.cmi.2018.04.004

55. Montoro-Dasí L, Villagrá A, Sevilla-Navarro S, Pérez-Gracia MT, Vega S, Marin C. The dynamic of antibiotic resistance in commensal Escherichia coli throughout the growing period in broiler chickens: fast-growing vs. slow-growing breeds. Poult Sci 2020; 99(3): 1591–7. doi: 10.1016/j.psj.2019.10.080

56. Silva N, Carvalho I, Currie C, Sousa M, Igrejas G, Poeta P. Extended-spectrum-β-lactamase and carbapenemase-producing Enterobacteriaceae in food-producing animals in Europe: an impact on public health? In: Capelo-Martinez JL, eds. Antibiotic drug resistance. Hoboken: John Wiley & Sonc, 2019: 261–73. doi: 10.1002/9781119282549.ch12

57. Fischer J, Rodríguez I, Schmoger S, et al. Escherichia coli producing VIM-1 carbapenemase isolated on a pig farm. J Antimicrob Chemother 2012; 67(7): 1793–5. doi: 10.1093/jac/dks108

58. Fischer J, San José M, Roschanski N, et al. Spread and persistence of VIM-1 carbapenemase-producing Enterobacteriaceae in three German swine farms in 2011 and 2012. Vet Microbiol 2017; 200: 118–23. doi: 10.1016/j.vetmic.2016.04.026

59. Pulss S, Semmler T, Prenger-Berninghoff E, Bauerfeind R, Ewers C. First report of an Escherichia coli strain from swine carrying an OXA-181 carbapenemase and the colistin resistance determinant MCR-1. Int J Antimicrob Agents 2017; 50(2): 232–6. doi: 10.1016/j.ijantimicag.2017.03.014

60. Pourhossein Z, Asadpour L, Habibollahi H, Shafighi ST. Antimicrobial resistance in fecal Escherichia coli isolated from poultry chicks in northern Iran. Gene Rep 2020; 21(20): 100926. doi: 10.1016/j.genrep.2020.100926

61. Ahmed AM, Shimamoto T, Shimamoto T. Molecular characterization of multidrugresistant avian pathogenic Escherichia coli isolated from septicemic broilers. Int J Med Microbiol 2013; 303(8): 475–83. doi: 10.1016/j.ijmm.2013.06.009

62. Thomrongsuwannakij T, Narinthorn R, Mahawan T, Blackall PJ. Molecular and phenotypic characterization of avian pathogenic Escherichia coli isolated from commercial broilers and native chickens. Poult Sci 2022; 101(1): 101527. doi: 10.1016/j.psj.2021.101527

63. Jafari RA, Motamedi H, Maleki E, Ghanbarpour R, Mayahi M. Phylogenetic typing and detection of extended-spectrum β-lactamases in Escherichia coli isolates from broiler chickens in Ahvaz, Iran. Vet Res Forum 2016; 7(3): 227–33.

64. Urmi UL, Nahar S, Rana M, et al. Genotypic to phenotypic resistance discrepancies identified involving β-lactamase genes, blaKPC, blaIMP, blaNDM-1, and blaVIM in uropathogenic Klebsiella pneumoniae. Infect Drug Resist 2020; 13: 2863. doi: 10.2147/IDR.S262493

65. Vinueza-Burgos C, Ortega-Paredes D, Narváez C, De Zutter L, Zurita J. Characterization of cefotaxime resistant Escherichia coli isolated from broiler farms in Ecuador. PLoS One 2019; 14(4): e0207567. doi: 10.1371/journal.pone.0207567

66. Zhang Z, Zhai Y, Guo Y, et al. Characterization of Unexpressed ExtendedSpectrum Beta-Lactamase Genes in Antibiotic–Sensitive Klebsiella pneumoniae Isolates. Microb Drug Resist 2018; 24(6): 799–806. doi: 10.1089/mdr.2017.0018

67. Kazemian H, Heidari H, Ghanavati R, et al. Phenotypic and genotypic characterization of ESBL-, AmpC-, and carbapenemase-producing Klebsiella pneumoniae and Escherichia coli isolates. Med Princ Prac 2019; 28(6): 547–51. doi: 10.1159/000500311

68. Bachiri T, Bakour S, Lalaoui R, et al. Occurrence of carbapenemase-producing Enterobacteriaceae isolates in the wildlife: first report of OXA-48 in wild boars in Algeria. Microb Drug Resist 2018; 24(3): 337–45. doi: 10.1089/mdr.2016.0323

69. Braun SD, Ahmed MF, El-Adawy H, et al. Surveillance of extended-spectrum betalactamase-producing Escherichia coli in dairy cattle farms in the Nile Delta, Egypt. Front Microbiol 2016; 7: 1020. doi: 10.3389/fmicb.2016.01020

70. Liu X, Liu H, Li Y, Hao C. High prevalence of β-lactamase and plasmid-mediated quinolone resistance genes in extended-spectrum cephalosporin-resistant Escherichia coli from dogs in Shaanxi, China. Front Microbiol 2016; 7: 1843. doi: 10.3389/fmicb.2016.01843

71. Liu BT, Song FJ, Zou M, Zhang QD, Shan H. High incidence of Escherichia coli strains coharboring mcr-1 and bla NDM from chickens. Antimicrob Agents Chemother 2017; 61(3): e02347–16. doi: 10.1128/AAC.02347-16

72. Liu Z, Wang Y, Walsh TR, et al. Plasmid-mediated novel bla NDM-17 gene encoding a carbapenemase with enhanced activity in a sequence type 48 Escherichia coli strain. Antimicrob Agents Chemother 2017; 61(5): e02233–16. doi: 10.1128/AAC.02233-16

73. Mollenkopf DF, Stull JW, Mathys DA, et al. Carbapenemase-producing Enterobacteriaceae recovered from the environment of a swine farrow-to-finish operation in the United States. Antimicrob Agents Chemother 2017; 61(2): e01298–16. doi: 10.1128/AAC.01298-16

74. Melo LC, Boisson MN, Saras E, et al. OXA-48-producing ST372 Escherichia coli in a French dog. J Antimicrob Chemother 2017; 72(4): 1256–8. doi: 10.1093/jac/dkw531

75. Yousfi M, Touati A, Mairi A, et al. Emergence of carbapenemase-producing Escherichia coli isolated from companion animals in Algeria. Microb Drug Resist 2016; 22(4): 342–6. doi: 10.1089/mdr.2015.0196

76. Hamza E, Dorgham SM, Hamza DA. Carbapenemase-producing Klebsiella pneumoniae in broiler poultry farming in Egypt. J Glob Antimicrob Resist 2016; 7: 8–10. doi: 10.1016/j.jgar.2016.06.004

77. Poirel L, Stephan R, Perreten V, Nordmann P. The carbapenemase threat in the animal world: the wrong culprit. J Antimicrob Chemother 2014; 69(7): 2007–8. doi: 10.1093/jac/dku054

78. Gioushy M, Abdelaziz Soliman EE, Elkenany RM, et al. Molecular characterization, virulence, and antimicrobial susceptibility of Mycoplasma bovis associated with chronic mastitis in dairy cows. Slov Vet Res 2024; 61(4): 271–9. doi: 10.26873/SVR-1882-2024

79. Stilec V, Durcik M, Peterka M. Rediscovering phage therapy: promising approach for combating antimicrobial resistance. Slov Vet Res 2024; 61(2): 77–80. doi: 10.26873/SVR-2063-2024

80. Šumonja I, Kotnik T. Skin dysbiosis in atopic dogs: is phage therapy an alternative to antibiotics? Slov Vet Res 2024; 61(2): 85–96. doi: 10.26873/SVR-1880-2024

Profiliranje protimikrobne odpornosti izbranih izolatov *E. coli* in odkrivanje genov, ki kodirajo ESBL/pAmpC, v jatah brojlerjev v Bosni in Hercegovini z uporabo PCR v realnem času

A. Koro-Spahić, S. Hadžiabdić, T. Goletić, A. Alić, A. Kustura, A. Softić, E. Rešidbegović

Izvleček: Protimikrobna odpornost (AMR) je vse večji globalni problem, ki ga povzroča neciljna uporaba protimikrobnih sredstev pri živini. Perutnina, zlasti brojlerji, lahko predstavlja pomemben rezervoar odpornih sevov *Escherichia (E.) coli*. Namen študije je bil izolirati *E. coli* iz jat brojlerjev in oceniti njihovo in vitro občutljivost za β-laktame, cefalosporine, karbapeneme, tetracikline in fluorokinolone. Poleg tega je bil za odkrivanje genov, ki kodirajo β-laktamaze z razširjenim spektrom (ESBL) in karbapenemaze, uporabljen hkratni PCR v realnem času. Analizirali smo skupno 48 izolatov komenzalne *E. coli* iz jat brojlerjev v Bosni in Hercegovini (BiH). Fenotipska odpornost, določena z metodo difuzije z diski, je bila opažena pri ampicilinu (87,5 %), amoksicilinu/klavulanski kislini (62,5 %), cefepimu (41,7 %), cefoksitinu (45,8 %), cefotaksimu (50,0 %), ceftazidimu (47,9 %), azitromicinu (58,3 %), ciprofloksacinu (66,7 %) in tetraciklinu (72,9 %). Analiza PCR je potrdila gene bla_{TEM}, $bla_{CTX\text{-}M}$ in bla_{CMY} v 24 izolatih (50 %), medtem ko genov bla_{SHV} in genov, ki kodirajo karbapenemaze (bla_{KPC}, bla_{NDM}, $bla_{OXA\text{-}48}$, bla_{VIM} in bla_{GES}), nismo odkrili. Visoka prevalenca večkratno odpornih sevov *E. coli* poudarja potrebo po izboljšanem upravljanju s protimikrobnimi sredstvi v perutninski proizvodnji. Zmanjšanje uporabe antibiotikov, spodbujanje alternativnih ukrepov za nadzor bolezni in izvajanje sistematičnih programov spremljanja odpornosti so ključni za zmanjšanje AMR na farmah brojlerjev in potencialnega prenosa na ljudi.

Ključne besede: protimikrobna odpornost; *E. coli*; brojlerji; Bosna in Hercegovina