Resistance to Antibacterial Agents in *Escherichia coli* Isolated from Domestic Cats and Dogs in the Northern Region of the Republic of Kazakhstan

Anara Yeleussizova, Yuliya Aleshina, Anara Mendybayeva, Madina Khassanova and Raushan Rychshanova

1Department of Veterinary Sanitation, A. Baitursynov Kostanay Regional University, Kazakhstan
2Research Institute of Applied Biotechnology, A. Baitursynov Kostanay Regional University, Kazakhstan
3Department of Veterinary Medicine, A. Baitursynov Kostanay Regional University, Kazakhstan

**Abstract:** The widespread use of antimicrobial agents for pets in veterinary practice has led to the emergence and spread of drug resistance not only in pathogenic but also in opportunistic bacteria. The study aims to evaluate the profile of resistance to antibacterial agents in *Escherichia coli* strains isolated from domestic cats and dogs, as well as to look into the determinants of resistance responsible for the ability of microorganisms to resist the effects of antimicrobial agents. During 2021-2022, biological material from cats and dogs, taken in veterinary clinics of Kostanay, Republic of Kazakhstan, was analyzed. Identification of genes encoding antimicrobial resistance was carried out by Polymerase Chain Reaction (PCR). As a result, it was found that all isolated strains of microorganisms showed sensitivity to the action of meropenem included in the group of beta-lactam antibiotics and showed resistance to tetracycline, doxycycline, ofloxacin, ampicillin, and amoxicillin. Resistance genes were identified for all the studied groups of antibiotics in the DNA of *E. coli* isolated from cats and no genes encoding resistance to fluoroquinolones were detected in the DNA of strains isolated from dogs. The most common genes were genes encoding resistance to aminoglycosides (43.8%), tetracyclines (35%), beta-lactams (33.5%), sulfonamides (16.1%), and fluoroquinolones (1.24%). In general, domestic cats and dogs have a high prevalence of *E. coli* strains resistant to beta-lactam drugs (ampicillin: 40%, amoxicillin: 36%) and tetracyclines (tetracycline: 71%, doxycycline: 47%). Resistance in most cases was explained by the presence of such resistance genes as blaTEM, OXA, tetA, and tetB.

**Keywords:** Strain, Bacterium, Antibiotic, Antibiotic Sensitivity, Resistance Genes

**Introduction**

Previously, it was assumed that only animals consumed by humans were the main source of antibiotic-resistant strains of microorganisms, through the transmission of resistant bacteria or genes along the food chain (McEwen and Fedorka-Cray, 2002; Smith et al., 2002; Angulo et al., 2000). However, it was later found that the transmission of resistance by non-food route should be investigated equally (Barber et al., 2003).

Every year, an increasing number of antimicrobial agents are used to treat small pets, including medications used in human medicine (in particular cephalosporins and fluoroquinolones). There is evidence that, among the bacteria that cause infection in pets, the growth of antimicrobial resistance increases (Vasaikar et al., 2017; Karkaba et al., 2019; Umeda et al., 2019).

Studies conducted in the UK and Portugal show that resistance to the tetracycline group is widespread among *E. coli* microorganisms isolated from pets, reaching up to 40% (Costa et al., 2008; Wedley et al., 2017). Other recent clinical studies conducted in Belgium report that the resistance of *E. coli* strains was 12% higher to the beta-lactam group and 17% higher to tetracyclines, but a very low or undetectable level of resistance was detected to fluoroquinolones (De Graef et al., 2004).
conducted in Australia also report increased resistance of *E. coli* isolates to β-lactams, as well as the absence of resistance to carbapenems (Saputra et al., 2017).

The transfer of antibiotic-resistant strains from animals to humans is still being studied globally (Guardabassi et al., 2004; Lloyd, 2007). To date, there is no data on the prevalence of both resistant strains and resistance genes among domestic cats and dogs living in the Republic of Kazakhstan.

The study of the determinants of resistance to antibacterial agents in small pets (cats and dogs) will allow us to assess the existing picture of the prevalence of resistance at the genetic level.

The study aims to evaluate the profile of resistance to antibacterial agents in *E. coli* strains isolated from domestic cats and dogs, as well as to look into the determinants of resistance responsible for the ability of microorganisms to resist the effects of antimicrobial agents.

**Materials and Methods**

No ethical permission was required to conduct this study. In this study, the following biological material (n = 944) was analyzed: Urine, feces, and swabs from the nasal and oral cavities, rectum, and vagina from cats (n = 582) and dogs (n = 362) (clinically healthy and with various pathologies) taken in veterinary clinics of Kostanay in the period from January 2021 to June 2022. The laboratory studies were conducted at the Department of microbiological analysis of the research institute of applied biotechnology of the Kostanay Regional University (KRU) named after A. Baitursynov.

When the owners brought their animals to the veterinary clinic, they were asked to provide data concerning biological information about the animal (age, gender), diseases, and antimicrobial treatment received. The study of the determinants of resistance to antibacterial agents in small pets (cats and dogs) is determined by the change in the color of the medium and the appearance of gas bubbles in the Kligler agar. The change in the medium was taken into account after 24 h incubation at a temperature of +37°C.

The enzymatic properties of bacteria were studied on Hiss media with lactose and mannitol. The utilization of sodium citrate during culture growth was studied by changing the color of the Simmons medium and the formation of indole was studied by the appearance of a red ring of the medium after the addition of Kovacs reagent (4-dimethylaminobenzaldehyde, amyl alcohol and hydrochloric acid). The mobility of the isolates in question was studied by their growth when seeded with an injection into semi-liquid agar. The change of media during growth was taken into account after 2 days of incubation.

The Voges-Proskauer test was performed based on the detection of acetoin by adding α-naphthol and potassium hydroxide (KOH) to a 2-day culture of microorganisms on Clark's medium.

The methyl red test was used for a certain concentration of ions (pH) in the medium of glucose-fermenting microorganisms by adding 5 drops of the methyl red indicator to the culture of the microorganism and observing the color change.

To detect indole, a reaction was carried out using Kovacs reagent, by adding it to the culture of the microorganism on Beef Extract Broth (BEB). With a positive reaction, the formation of a red ring was observed.

**Antibiotic Sensitivity**

The sensitivity to antibacterial agents in the obtained isolates was investigated by applying standard antibiotic discs to the freshly sown bacterial lawn using Mueller-Hinton agar. The results were considered by the presence of microbe growth inhibition zones around the discs, which, according to the instructions, indicates either the sensitivity of the pathogen to the medication or its resistance to this antibiotic.

All isolated cultures of microorganisms were tested to determine sensitivity to beta-lactams (ampicillin, amoxicillin, cefoperazone, cefoxitin, cefpodoxime, meropenem), aminoglycosides (streptomycin, kanamycin, gentamicin), amphenicols (levomycetin), tetracyclines (tetracycline and doxycycline), fluoroquinolones (enrofloxacin, ciprofloxacin, norfloxacin, ofloxacin, gemifloxacin), quinolones (nalidixic acid), sulfonamides (trimethoprim/sulfamethoxazole) and nitrofurans (furazolidone and furadonin). Sensitivity was determined following the recommendations of the EUCAST version 11.0, CLSI and according to Methodical Instructions (MI) 4.2.1890-04 (CLSI, 2019; Kahlmeter et al., 2019).

The ability of bacteria to ferment lactose and glucose, as well as to form gas and hydrogen sulfide was determined by the change in the color of the medium and the appearance of gas bubbles in the Kligler agar. The change in the medium was taken into account after 24 h incubation at a temperature of +37°C.
Identification of Resistance Genes of Opportunistic Microorganisms

For molecular research, DNA material was obtained by bacterial lysis according to the recommendations of the European Union Reference Laboratory for Antimicrobial Resistance (SVA, 2021). Identification of genes encoding antimicrobial resistance was carried out by Polymerase Chain Reaction (PCR).

To determine the bacterial resistance profiles, primers were used and 242 samples of E. coli DNA were tested by PCR for the presence of genes encoding resistance.

Data Analysis

Data analysis was carried out using the MS Excel 2017 package.

Results

In total, biological material from 944 animals was examined, including 362 (38.3%) dogs and 582 (61.7%) cats. In 25.6% of the subjects (242 animals), the presence of E. coli was isolated and identified, where 10.6% (100 isolates) were isolated from dogs and 15% (142 isolates) from cats (Fig. 1).

Morphological, tinctorial, and cultural properties of the obtained isolates were characteristic of their family and genus.

Biological information, data on admission to the clinic, and previous use of antibacterial agents of all animals participating in the study are shown in Table 1.

From the data presented in Table 1, it can be seen that the average age of dogs participating in the study was 3.6 years, the age of cats was 3.3 years, the predominant majority were females (54.9% of dogs and 59.1% of cats) and E. coli was isolated in 58% of female dogs and 59.8% of female cats. Among all the animals participating in the study, 79.5% (81.2% of dogs and 78.5% of cats) had diseases of various body systems and the rest of the animals were healthy. E. coli was detected in 24.9% of sick animals and 28.5% of healthy ones. Antimicrobial treatment before admission to the clinic had been received by 26.5% of all dogs and 17.7% of cats, of which E. coli was found in 40.6% of dogs and 18.4% of cats.

The ratio of the number of isolated E. coli isolates from cats and dogs, depending on the disease, is shown in Fig. 2.

Analysis of the frequency of isolation of E. coli microorganisms obtained from cats with various pathologies showed that 58.3% of E. coli was isolated from cats with surgical conditions, 13.8% from cats with orthopedic-traumatic diseases, 11.1% from cats with diseases of the gastrointestinal tract, 9.26% from cats with diseases of the genitourinary system, 3.7% from cats with infectious diseases, 1.85% from cats with neoplasms and the smallest number of microorganisms (0.95%) were isolated from cats with dermatological and invasive diseases.

Of 79 E. coli isolates obtained from dogs with various diseases, 26.6% were found in animals with surgical pathologies, 22.8% in dogs with infectious diseases, 12.6% in dogs with diseases of the genitourinary system, 10.13% in dogs with orthopedic-traumatic diseases and neoplasms, 8.9% in dogs with invasive diseases, 7.6% in dogs with gastrointestinal diseases and the smallest number of microorganisms (1.3%) was isolated from dogs with dermatological diseases.

Of the 142 studied E. coli strains isolated from cats, 70.4% (100 strains) were resistant to tetracycline, 47.2% (67 strains) to doxycycline, 42.3% (60 strains) to ofloxacin, 38.7% (55 strains) to ampicillin, 36.6% (52 strains) to amoxicillin, 33% (47 strains) to cefpodoxime, 30.3% (43 strains) to norfloxacin, 25.4% (36 strains) to ciprofloxacin, 24.6% (35 strains) to enrofloxacin, 22.5% (32 strains each) to trimethoprim/sulfamethoxazole and nalidixic acid, 18.3% (26 strains) to cefoperazone and levomycetin, 13.4% (19 strains) to gemifloxacin, 11.9% (17 strains) to cefotixin, 10.6% (15 strains) to gentamicin, 8.5% (12 strains) to kanamycin, 2.8% (4 strains) to furadonin and 1.4% (2 strains each) to streptomycin and furazolidone. No strains resistant to meropenem were identified (Fig. 3).
A study of 100 E. coli microorganisms isolated from dogs for antibiotic resistance showed that 71% of the strains were resistant to tetracycline, 47% to doxycycline, 46% to ofloxacin, 40% to ampicillin, 36% to amoxicillin, 32% to norfloxacin, 30% to cefpodoxime, 29% to ciprofloxacin, 27% to nalidixic acid, 23% to enrofloxacin, 22% to trimethoprim/sulfamethoxazole, 18% were resistant to cefoxitin, 15% to cefoperazone and levomycetin, 14% to gemifloxacin, 6% to gentamicin and 3% to kanamycin. The smallest number of microorganisms (2%) were resistant to furazolidone and furadonin and (1%) to streptomycin. No resistant strains were identified for meropenem (Fig. 4).

All E. coli isolates showing phenotypic resistance to antibacterial agents were tested by PCR for the presence of genes encoding resistance. The results are presented in Table 2.

Based on the data presented in Table 2, it can be seen that resistance genes were observed for all the studied groups of antibiotics in the DNA of E. coli isolated from cats and no genes encoding resistance to fluoroquinolones were detected in the DNA of strains isolated from dogs. The genes encoding resistance to aminoglycosides were most often isolated in 43.8% of strains (StrA: 46 samples, StrB: 48 samples, aadB: 2 samples, aphA1: 10 samples).

A study of 100 E. coli microorganisms isolated from dogs

Table 1: Data on animals included in the study

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Dogs</th>
<th>Cats</th>
</tr>
</thead>
<tbody>
<tr>
<td>Average age (years)</td>
<td>Total (n = 362)</td>
<td>E. coli was found (n = 100)</td>
</tr>
<tr>
<td>Gender</td>
<td>3.6</td>
<td>3.5</td>
</tr>
<tr>
<td>Female</td>
<td>199.0</td>
<td>58.0</td>
</tr>
<tr>
<td>Male</td>
<td>163.0</td>
<td>42.0</td>
</tr>
<tr>
<td>Diagnosis</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Surgical operations</td>
<td>74.0</td>
<td>21.0</td>
</tr>
<tr>
<td>Orthopedic-traumatic diseases</td>
<td>41.0</td>
<td>8.0</td>
</tr>
<tr>
<td>Gastrointestinal diseases</td>
<td>23.0</td>
<td>6.0</td>
</tr>
<tr>
<td>Diseases of the genitourinary system</td>
<td>55.0</td>
<td>10.0</td>
</tr>
<tr>
<td>Dermatological diseases</td>
<td>7.0</td>
<td>1.0</td>
</tr>
<tr>
<td>Infectious diseases</td>
<td>54.0</td>
<td>18.0</td>
</tr>
<tr>
<td>Invasive diseases</td>
<td>20.0</td>
<td>7.0</td>
</tr>
<tr>
<td>Neoplasms</td>
<td>18.0</td>
<td>8.0</td>
</tr>
<tr>
<td>Other diseases</td>
<td>2.0</td>
<td>-</td>
</tr>
<tr>
<td>Healthy animals</td>
<td>68.0</td>
<td>21.0</td>
</tr>
<tr>
<td>Antibiotic therapy before admission to the clinic</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ceftriaxone</td>
<td>43.0</td>
<td>19.0</td>
</tr>
<tr>
<td>Lincomycin</td>
<td>8.0</td>
<td>5.0</td>
</tr>
<tr>
<td>Amoxicillin</td>
<td>38.0</td>
<td>14.0</td>
</tr>
<tr>
<td>Enrofloxacin</td>
<td>5.0</td>
<td>1.0</td>
</tr>
<tr>
<td>Trimethoprim</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>Penicillin</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>Gentamicin</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>Cefazolin</td>
<td>2.0</td>
<td>0.0</td>
</tr>
<tr>
<td>Levomycetin</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>Tetracycline</td>
<td>0.0</td>
<td>0.0</td>
</tr>
</tbody>
</table>

A study of 100 E. coli microorganisms isolated from dogs for antibiotic resistance showed that 71% of the strains were resistant to tetracycline, 47% to doxycycline, 46% to ofloxacin, 40% to ampicillin, 36% to amoxicillin, 32% to norfloxacin, 30% to cefpodoxime, 29% to ciprofloxacin, 27% to nalidixic acid, 23% to enrofloxacin, 22% to trimethoprim/sulfamethoxazole, 18% were resistant to cefoxitin, 15% to cefoperazone and levomycetin, 14% to gemifloxacin, 6% to gentamicin and 3% to kanamycin. The smallest number of microorganisms (2%) were resistant to furazolidone and furadonin and (1%) to streptomycin. No resistant strains were identified for meropenem (Fig. 4).

Table 2: Resistance genes of microorganisms

<table>
<thead>
<tr>
<th>Group of antibiotics</th>
<th>From cats</th>
<th>From dogs</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Beta-lactams</td>
<td>BlaTEM</td>
<td>BlaTEM</td>
<td>81</td>
</tr>
<tr>
<td></td>
<td>20</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td></td>
<td>28</td>
<td>16</td>
<td></td>
</tr>
<tr>
<td>Aminoglycosides</td>
<td>StrA</td>
<td>StrA</td>
<td>106</td>
</tr>
<tr>
<td></td>
<td>25</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td></td>
<td>27</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Tetracyclines</td>
<td>tetA</td>
<td>tetA</td>
<td>85</td>
</tr>
<tr>
<td></td>
<td>39</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td></td>
<td>27</td>
<td>21</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>Sulfonamides</td>
<td>SUL1</td>
<td>SUL1</td>
<td>39</td>
</tr>
<tr>
<td></td>
<td>12</td>
<td>5</td>
<td></td>
</tr>
<tr>
<td></td>
<td>11</td>
<td>11</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Fluoroquinolones</td>
<td>qepA</td>
<td>qepA</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>
Genes encoding resistance to tetracyclines were detected in 35% of cases (tetA: 60 samples, tetB: 25 samples). Beta-lactam resistance genes were found in 33.5% of isolates (blaTEM: 37 samples, OXA: 44 samples). Genes encoding resistance to sulfonamides were also identified in 16.1% of cases (SUL1: 17 samples, SUL3: 22 samples). The number of samples having genes causing resistance to fluoroquinolones (1.24%) was the smallest of all obtained values (qepA: 2 samples, qnr: 1 sample).

Discussion

As a result of the conducted studies, 25.6% (242 animals) of them were found to carry the E. coli strains, including 41.3% (100 isolates) obtained from dogs and 58.7% (142 isolates) from cats. These data correlate with the results of several studies conducted in the Netherlands, where the prevalence of colonization by enterobacteria in dogs and cats (including healthy and sick animals) ranged from 3.1-55% (Baebe et al., 2015; Vandenburg et al., 2020). In studies conducted in Thailand and the US, a higher percentage of E. coli excretion was observed, where it was 66 and 52%, respectively (Thungrat et al., 2015; Soonthornsit et al., 2022).

The average age of dogs participating in the study was 3.6 years, the age of cats was 3.3 years, the majority of them were females (dogs: 54.9%, cats: 59.1%) and E. coli was isolated in 58% of female dogs and 59.8% of female cats. E. coli was more often isolated in female dogs than in males, which is consistent with previous studies. Perhaps this is due to the anatomical difference between the urinary tract in females and males: In particular, the female's urethra is shorter and wider than that of the male, and E. coli, as the causative agent of urinary tract infection, will be detected more often in females than in males (Hall et al., 2013).

Among all the animals participating in the study, 79.5% (81.2% of dogs and 78.5% of cats) had diseases of various body systems and the rest of the animals were healthy. E. coli was detected in 24.9% of sick animals and 28.5% of healthy ones. The data obtained by us have average indicators since in studies conducted in the Netherlands intestinal carrier state was detected in 45% of healthy dogs and in Korea, E. coli was detected in 23.8% of isolates from admitted dogs (So et al., 2012; Hordijk et al., 2013).

Antimicrobial treatment before admission to the clinic had been received by 26.5% of all dogs and 17.7% of cats, of which E. coli was found in 40.6% of dogs and 18.4% of cats. These data are consistent with previous observations carried out in different countries, in which bacterial carrier was observed after a certain period after the use of antibiotics and prove the spread of antibiotic-resistant strains among humans and pets (Espinosa-Gongora et al., 2015; Zhao et al., 2016; Karkaba et al., 2019).

In general, all isolated E. coli strains showed the highest percentage of resistance (71%) to the action of tetracycline, which is consistent with studies conducted in several countries (Great Britain, Portugal), where, of all the selected antibiotics, the maximum resistance was found to the action of tetracycline (Costa et al., 2008; Wedley et al., 2017). Besides, in studies of previous years (2007-2014), a low level of sensitivity to the action of antimicrobial agents of the tetracycline group was demonstrated (Pedersen et al., 2007; Ball et al., 2008; Kroemer et al., 2014).

The study found a low percentage of isolates resistant to fluoroquinolones. These antimicrobial agents are often used to treat dogs and cats (Lloyd, 2007; Pedersen et al., 2007; Murphy et al., 2012). We evaluated the sensitivity of bacteria to second-generation fluoroquinolones (enrofloxacin, ciprofloxacin, norfloxacin, ofloxacin, and gemifloxacin). The percentage of strains resistant to ofloxacin and norfloxacin was slightly higher, by 22.7% and 10.3%, respectively than to other antibiotics of this group. In studies conducted in Australia and Poland, a decrease in the effectiveness of fluoroquinolones against enterobacteria was also observed (Gibson et al., 2010; Rzewuska et al., 2015).

Other recent studies conducted in Australia confirm our data that E. coli isolates have increased resistance to the beta-lactam group (ampicillin, amoxicillin, cefpodoxime), as well as a lack of resistance to carbapenems (meropenem) (Saputra et al., 2017). Probably, this may be due to the prolonged and more intensive use of ampicillin and amoxicillin in pets, compared with meropenem. In a study conducted in Spain, beta-lactams were the antimicrobial agent most commonly prescribed to dogs (Gomez-Poveda and Moreno, 2018). This antimicrobial agent should be used with caution for the treatment of infections caused by E. coli due to the rapid development of resistance caused by the production of beta-lactamases (Boehmer et al., 2018).

Resistance to other groups of antimicrobial agents (aminoglycosides and nitrofurans) tested against E. coli isolates from dogs and cats was absent or at a very low level. However, studies conducted in European countries show the opposite results, speaking of high resistance to
these antibiotics (Bywater et al., 2004; Hendriksen et al., 2008). In general, there are differences in the prevalence of resistance in isolates of opportunistic enterobacteria in different countries (Harada et al., 2012). Perhaps the reason for this is the differences in the strains and resistance genes circulating in different territories.

As a result of the conducted studies, it was found that in 88 E. coli DNA samples that had phenotypic resistance to antibacterial agents, there was a link with genotypic resistance. However, in 21 samples, resistance genes to antibacterial agents of the aminoglycoside group (StrA, strB, aadB, aphA1) were found and in 8 samples we found resistance genes to the beta-lactam group (blaTEM), while phenotypic resistance in these microorganisms to these groups of medications was not detected. Probably, we are dealing with the so-called “silent” genes, which have been found in studies conducted in the UK and China but have been little studied so far (Xu et al., 2014; Wang et al., 2017; Zhang et al., 2018).

In 124 E. coli strains, phenotypic resistance to the group of fluoroquinolones (enrofloxacin, ciprofloxacin, norfloxacin, ofloxacin, gemifloxacin) was detected, but genotypic resistance, i.e., the presence of qepA and qnrA genes was not observed. This is probably due to differences in the mechanisms of resistance, such as a decrease in membrane permeability and the overactivity of the efflux pump, a similar situation occurs in studies by other scientists (Bardasheva et al., 2021; Galal et al., 2019).

**Conclusion**

In the Northern region of Kazakhstan, domestic cats and dogs have a high prevalence of E. coli strains. The study of antibiotic resistance of the isolated strains showed high resistance to medications of the beta-lactam group and tetracyclines. Resistance in most cases was explained by the presence of such resistance genes as blaTEM, OXA, tetA, and tetB.

Uncontrolled and frequent use of antibacterial agents of the beta-lactam group and tetracyclines leads to the spread of not only phenotypic but also genotypic resistance among microorganisms.

Further studies of antimicrobial resistance mechanisms in the E. coli population of dogs and cats in Kazakhstan are needed. Given the growing resistance of bacteria to medications widely used in the veterinary practice of small animals, it seems extremely important that the treatment of bacterial infections should take into account the testing of sensitivity to antibacterial agents. Thus, it is necessary to constantly monitor the sensitivity to E. coli antimicrobial agents in dogs and cats and develop recommendations for the use of antibiotics in the practice of small animals. Also, further research is needed on zoonotic strains of bacteria in other parts of the country, as the close bond between humans and their companion animals provides opportunities for exchange of microorganisms, including multidrug resistance pathogens.

**Acknowledgment**

The authors thank the reviewers for their contribution to the peer evaluation of this study.

**Funding Information**

This study was carried out within the framework of the AP09058122 project “Prevalence of determinants of antibacterial drug resistance” grant provided by the Ministry of Education and Science of the Republic of Kazakhstan for 2021-2023.

**Author’s Contributions**

All authors equally contributed to this study.

**Ethics**

This article is original and contains unpublished material. The corresponding author confirms that all of the other authors have read and approved the manuscript and no ethical issues are involved.

**References**


https://doi.org/10.1016/j.cimid.2013.10.001

https://doi.org/10.1086/519254

https://doi.org/10.1086/340246

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3280785/

https://doi.org/10.1093/jac/dkm269

https://doi.org/10.1155/2015/408205


https://doi.org/10.1016/j.vetmic.2017.09.014

http://dx.doi.org/10.1073/pnas.082188899

https://doi.org/10.1016/j.diagmicrobio.2012.03.010

https://digital.car.chula.ac.th/ijvm/vol52/iss1/22/

https://doi.org/10.1016/j.vetmic.2015.06.012

http://dx.doi.org/10.1099/jmm.0.000933

https://doi.org/10.1093/jac/dkz462

https://doi.org/10.1155/2017/8486742

http://dx.doi.org/10.1038/nmicrobiol.2016.260

https://doi.org/10.1016/j.vetmic.2016.11.017
