Regulatory Mechanisms in Biosystems

ISSN 2519-8521 (Print)
ISSN 2520-2588 (Online)
Regul. Mech. Biosyst.

Prevalence and susceptibility profile to antibacterial drugs of diarrheagenic *Escherichia coli* isolated from children with acute intestinal infection

M. Lusta*, O. Voronkova**, T. Shevchenko**, V. Chornyi*, I. Yesaulenko*,
A. Breus*, Y. Maistrenko* A. Kovalenko*, T. Ponomarova-Herasymiuk*

**Municipal Non-Commercial Enterprise "City Clinical Hospital No. 6" of the Dnipro City Council, Dnipro, Ukraine*
***Oles Honchar Dnipro National University, Dnipro, Ukraine*

Article info

Received 08.05.2025
Received in revised form 16.06.2025
Accepted 10.07.2025

Municipal Non-Commercial Enterprise "City Clinical Hospital No. 6" of the Dnipro City Council, Manuylivskyy av., 29, Dnipro, 49023, Ukraine.
Tel.: +38-066-356-61-59.
E-mail: maksimlusta12@gmail.com

Oles Honchar Dnipro National University, Nauky av., 72, Dnipro, 49010, Ukraine.
Tel.: +38-096-225-04-63.
E-mail: voronkova.olga.04@gmail.com

Lusta, M., Voronkova, O., Shevchenko, T., Chornyi, V., Yesaulenko, I., Breus, A., Maistrenko, Y., Kovalenko, A., Ponomarova-Herasymiuk, T. (2025). Prevalence and susceptibility profile to antibacterial drugs of diarrheagenic Escherichia coli isolated from children with acute intestinal infection. Regulatory Mechanisms in Biosystems, 16(3), e25124. doi:10.15421/0225124

Escherichia coli is a common inhabitant of the gastrointestinal tract of humans and warm-blooded animals, often associated with diarrhea. Different pathotypes can be distinguished for this bacterium, depending on virulence factors and the disease it causes. To isolate and identify *E. coli*, stool samples were transferred to Endo medium, and the cultures were incubated at 37 ± 1 C for 18–24 hours under aerobic conditions. Lactose-positive and lactose-negative colonies were subcultured onto Olkenytskyi medium (trisaccharide agar) for primary biochemical identification and slant and meat-peptone agar for accumulation of pure culture. The cultures were incubated at a temperature of 37 ± 1 C for 18–24 hours under aerobic conditions. Suspected *E. coli* cultures were subjected to serotyping in agglutination reaction on a glass of pure culture with polyvalent and monovalent sera. The sensitivity of pathogenic *E. coli* of a certain serotype to antibacterial drugs was determined by the disk diffusion method in accordance with the requirements of the recommendations of the European Committee on Antimicrobial Susceptibility Testing. In 2022–2024, 3,484 stool samples from children with acute intestinal infection who were inpatients at the Municipal Non-Commercial Enterprise "City Clinical Hospital No. 6" of the Dnipro City Council were examined. 202 cultures of pathogenic *E. coli* strains were isolated, the overall efficiency (seeding rate) was 5.8%. It was found that the highest research effectiveness in 2022 was observed in the winter period of the year, in 2023 – in the summer-autumn period, and in 2024 – in the summer period. The specific gravity of isolated pathogenic *E. coli* strains among boys and girls with acute intestinal infection during the studied period was stable and amounted to 58.9% for boys and 41.1% for girls. For the period 2022–2024, among the isolated pathogenic *E. coli* strains, the most frequently encountered strains were serotype O 18 – 14.4%, serotype O 44 – 18.8%, serotype O 78 – 7.4%, serotype O 145 – 5.4%, serotype O 26 – 5.0%, serotype O 103 – 5.0%. The overall susceptibility profile to antibacterial drugs of pathogenic *E. coli* strains isolated from the stool samples of children with acute intestinal infection in 2022-2024 was 54.5% for ampicillin, 49.0% for amoxicillin-clavulanic acid, 91.6% for ceftriaxone, 96.9% for ceftazidime, 97.9% for cefepime, 89.1% for cefoxitin (screening), and 93.6% for ciprofloxacin. The aim of the study was to determine the prevalence of pathogenic *E. coli* serotypes and the antibacterial drug sensitivity profile of the isolated strains among children with acute intestinal infection.

Keywords: *Escherichia coli* pathotypes; antibacterial resistance; acute diarrhea; serotypes; children; stool; antibiotics; extended-spectrum beta-lactamase.

Introduction

Acute intestinal infection (AII) is an acute infectious disease that affects the mucous membrane of the stomach and intestines, with manifestations of general intoxication in mild, moderate or severe forms, nausea, gastritis with vomiting, acute diarrhea and dehydration. The disease affects people of different age groups, including children. AII is most dangerous for patients under 2 years of age and people with chronic pathologies of the gastrointestinal tract. Diarrheal diseases are the leading cause of death in children under 5 years of age worldwide, with an estimated 1.7 billion cases and 525,000 deaths recorded each year. The most common pathogens of AII in children are viruses and bacteria (Thystrup et al., 2024).

Escherichia coli is a genetically heterogeneous Gram-negative bacterium that survives and occupies one of the leading niches of the microbiome, especially the gastrointestinal tract of humans and warm-blooded animals, is often associated with diarrhea, and can be classified into different pathotypes depending on its virulence factors and the disease it causes. Several pathotypes of diarrheagenic *E. coli* (DEC) are distinguished: enteropathogenic *E. coli* (EPEC), enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), enteroaggregative *E. coli* (EAEC), diffusely adhesive *E. coli* (DAEC), and Shiga toxin-producing *E. coli* (STEC). Each *E. coli* pathotype includes many serotypes that may have a cross-antigenic structure, but have different pathogenic properties and mechanisms of action on the intestinal mucosa (Kralicek et al., 2022; Chercos et al., 2024; Fernández Fellenz et al., 2025). These pathotypes may have one or more specific virulence genes that are not present in commensal *E. coli*. The acquisition of virulence factors in *E. coli* can occur through various mechanisms of molecular genetic gene exchange in the bacterial cell, in particular through horizontal gene transfer from other bacterial species via plasmids, integrons, bacteriophages, pathogenicity islands, and transposons. The most common and well-characterized pathotypes causing diarrhea are considered to be EPEC, ETEC, EAEC, STEC, and EIEC. The pathogenicity and epidemiological importance of DAEC isolates in the occurrence of diarrheal diseases is a subject of ongoing debate and controversy. DEC pathotypes are responsible for approximately 30–40% of acute diarrheal episodes in children. They are widely distributed worldwide, with prevalence varying by geographic region and the frequency of different pathotypes in different age groups (Wolde et al., 2024; Martínez-Oliveros et al., 2025; Okumu et al., 2025).

These *E. coli* pathotypes cause AII due to several specific virulence factors, including toxins, lipopolysaccharides, iron absorption factors, adhesins, polysaccharide capsules, and invasins. These elements help pathogenic *E. coli* strains overcome host defense mechanisms and barriers, and infiltrate or colonize organs. *Escherichia coli* is transmitted to humans mainly through the consumption of contami-

nated foods, such as raw or undercooked meat products and raw milk. An increasing number of outbreaks are linked to the consumption of fruits and vegetables (including sprouts, spinach, lettuce, coleslaw and lettuce), with infection possibly caused by contact with faeces from domestic or wild animals at some stage of cultivation or processing. The reservoir of this pathogen is cattle, sheep, goats, deer, pigs, horses, rabbits, dogs, cats, and birds, including chickens and turkeys. Thus, the route of transmission of the pathogen can be alimentary or fecal-oral, which determines the epidemiological link to the occurrence of AII (Anueyiagu et al., 2024; Wang et al., 2024; Fernández Fellenz et al., 2025).

EPEC and STEC are two pathotypes frequently associated with AII and acute diarrhea in children. Today, EPEC infection remains the leading cause of diarrhea-related infant death in developing countries. In resource-limited countries, diarrheal diseases are a major cause of morbidity, and diarrheal *E. coli* is an important contributor to this problem. The epidemiological significance of different DEC categories in childhood diarrhea varies from geographic region to region, and there are important regional differences in the prevalence of different DEC categories over time and seasons (Olayinka et al., 2024; Sameer et al., 2024; Bizot et al., 2025). *Escherichia coli* serogroup O111 strains belong to at least three different pathotypes, including EPEC, STEC, and EAEC. EPEC O111 strains are characterized by the presence of the eae gene, which encodes the major EPEC adhesin intimin, and cause diarrhea in children worldwide. STEC O111 strains other than eae have genes encoding Shiga toxins, including stx2, or both. In addition to diarrhea, they cause life-threatening hemolytic uremic syndrome (HUS), the most common cause of acute renal failure in children. STEC O111, along with STEC O26, O103, O145, and O157, are among the 5 leading serogroups most commonly associated with human disease, including HUS, worldwide. EAEC, an additional pathotype identified among *E. coli* O111 strains, is associated with acute and persistent diarrhea in children, predominantly in developing countries but also in industrialized countries, and causes traveler's diarrhea. Their common characteristic is an aggregative pattern of "stacked bricks" adhesion to epithelial cells, which is mediated by aggregative adhesion fimbriae in five variants from AAF/I to AAF/V. EAEC virulence genes are located on the aggregative adhesion plasmid (pAA) or on the chromosome within the pathogenicity island. The expression of both chromosomal and plasmid-encoded virulence genes is controlled by the transcriptional activator AggR. EAEC that contain the aggR gene are called typical EAEC, and many studies have clearly linked them to diarrhea. EAEC that lack aggR are called atypical EAEC and are considered to be of uncertain pathogenicity, although in some studies they have been significantly associated with diarrhea (Brubaker et al., 2021; Jones et al., 2024; Schlosserová et al., 2024).

STEC are considered extremely dangerous due to their unpredictable evolution to hemolytic uremic syndrome (HUS), a life-threatening condition for which there are no clear solutions for prevention. STEC exhibit pathogenic traits encoded by a pool of virulence and fitness genes, usually located on mobile genetic elements, and assessing which of these are determinant for a given strain, causing severe disease, is still a medical challenge and public health concern. Associated with multiple *E. coli* serotypes and a diversity of reservoirs and vectors, STEC infections are routinely monitored in most European Union (EU)/European Economic Area (EEA) countries, which share surveillance data through the European Centre for Disease Prevention and Control (ECDC) for supranational surveillance and prevention of cross-border outbreaks. However, given the different ways in which health systems are organised in each country and the practical challenges associated with differences in laboratory practices and pathogen recognition, statistics may not be of the same quality. Enterohemorrhagic *Escherichia coli* (EHEC) is a subgroup of STEC serotypes that is closely associated with bloody diarrhea and HUS in industrialized countries (Glassman et al., 2021; Seliga-Gąsior et al., 2024; Usein et al., 2024).

HUS is defined as a combination of acute kidney injury, low platelet levels, and hemolytic anemia. After HUS, kidney function cannot be restored and therefore some children require long-term replacement therapy, while those who recover may develop chronic kidney disease and hypertension. Some experience residual non-renal complications, including neurological defects, insulin-dependent diabetes, pancreatic insufficiency, or gastrointestinal complications. STEC associated with diarrhea may resolve without any long-term sequelae. STEC serotypes produce high levels of various toxins in the large intestine that are closely related to the potent cytotoxins produced by Shigella dysenteriae type 1 and damage the mucosal membranes and vascular endothelium in the intestinal wall. If absorbed, they have a toxic effect on other vascular endothelium, such as the renal endothelium. The mainstay of treatment for STEC infection is supportive therapy (Usein et al., 2024; Vusirikala et al., 2024).

ETEC is the leading cause of bacterial diarrhea in children. Each year, ETEC causes an estimated 220 million reported cases and 380,000 deaths, mostly in low- and middle-income countries with poor sanitation and hygiene practices. ETEC infection contributes significantly to growth retardation in children as well as lifelong disability. Diarrhea caused by ETEC is also common among travelers to endemic areas. Infection is established when ETEC reaches the intestinal mucosa and expresses fimbriae that bind to specific cellular targets. These fimbriae are colonization factors that allow ETEC to adhere to the mucosal epithelium. Notably, over 30 different colonization factors and adhesion antigens have been identified in ETEC strains worldwide. After attachment and colonization, the bacteria multiply and produce a heat-labile enterotoxin or a heat-stable enterotoxin on the surface of the epithelium, which disrupts normal intestinal function and leads to watery diarrhea. However, the pathogenesis of ETEC involves complex interactions between the bacterium, immune responses, and the characteristics of the host's intestinal microbial tract (Akhtar et al., 2024; Tesfaw et al., 2024; Amin et al., 2025).

Enteroaggregative *E. coli* (EAEC) is an important etiological agent of acute and persistent diarrhea (≥14 days) in children worldwide. This pathogen forms a thick biofilm and a typical adhesion pattern in cell cultures, similar to stacked bricks, mediated mainly by aggregate adhesion fimbriae (AAF). There are five fimbriae variants (AAF/IV), all encoded by the plasmid pAA and dependent on the transcriptional regulator AggR as an activator. AggR has been described in EAEC as an important transcriptional activator of at least 44 virulence genes, such as those encoding AAF and dispersin (an anti-aggregation protein). This pathotype is a genetically very heterogeneous bacterial group, while recent studies have found a statistical correlation between virulence factors and disease, although the complete pathogenetic process of EAEC remains unclear (Machado Ribeiro et al., 2021).

Escherichia coli poses a significant threat to human health due to its increasing resistance to different groups of antibiotics through a variety of mechanisms. According to the World Health Organization (WHO), *E. coli* resistance to common antibiotics has reached alarming levels in many parts of the world. *E. coli* serves as a reservoir for various antibiotic resistance genes and is capable of horizontally transferring these genes to other pathogenic and commensal organisms. Therefore, understanding the antimicrobial susceptibility of *E. coli* and the genetic markers associated with resistance can provide insight into the burden of antimicrobial resistance in other Gram-negative organisms circulating in a given community (Wolde et al., 2024; Okumu et al., 2025; Martínez-Oliveros et al., 2025). In addition to the virulence profile of pathogenic *E. coli*, the mechanisms of antibiotic resistance of this bacterium are one of the most important issues in modern research. Antibiotic resistance occurs when bacteria evade the action of antibiotics either through mutations in functional genes or by acquiring genes whose products can hydrolyze antibiotics and can also be transmitted via plasmids between different strains. One of the most clinically and epidemiologically significant mechanisms of antibiotic resistance in Enterobacteriaceae is the synthesis of carbapenemases, AmpC-type β-lactamases, and extended-spectrum β-lactamases (ESBLs) (Belina et al., 2024; Bywater et al., 2024; Olayinka et al., 2024).

Treatment of AII may be ineffective due to the emergence of *E. coli* pathotypes with acquired resistance – extended-spectrum beta-lactamases (ESBL), which have hospital origin (nosocomial infec-

tions) due to the systematic prescription of antibiotics by clinicians and self-medication by patients. Among ESBLs, CTX-M-type enzymes are the most common, and their number has increased rapidly over the past 10 years. The recent global increase has been driven mainly by the bla CTX-M type gene. ESBL-producing isolates, especially CTX-M-producing *E. coli*, show a worrying trend, as there is an increase in the number of *E. coli* strains with co-resistance to other classes of antibiotics. The global spread of ESBL-producing *E. coli* in human medicine is an urgent problem that poses serious challenges to the treatment of infectious diseases (Ashenafi et al., 2024; Dikoumba et al., 2024; Morita et al., 2025).

The aim of this study was to determine the prevalence of pathogenic *E. coli* serotypes and the antibacterial drug sensitivity profile of the isolated strains among children with acute intestinal infection who received medical care at the Municipal Non-Commercial Enterprise "City Clinical Hospital No. 6" of the Dnipro City Council.

Materials and methods

Study area and data collection. Patients gave their informed consent in accordance with the primary accounting documentation No. 003-6/o "Informed voluntary consent of the patient for diagnosis, treatment and surgery and anesthesia and for the presence or participation of participants in the educational process". The study was conducted during 2022–2024. Stool samples from children with acute intestinal infection who received medical care in a hospital setting were examined by bacteriological method (culture method). The biological material was collected before the administration of ABD, after a natural act of defecation and delivered to the bacteriological laboratory within 2 hours from the moment of collection. When using transport medium or phosphate-buffered solution, the delivery time was increased to 24 hours.

Stool samples were transferred to Endo medium (Pharmaktiv, Shchaslyve, Ukraine), and the cultures were incubated at a temperature of +37 ± 1 ^{0} for 18–24 hours under aerobic conditions. Lactose-positive and lactose-negative colonies were subcultured onto Olkenytskyi medium (trisaccharide agar) (Pharmaktiv, Shchaslyve, Ukraine) for primary biochemical identification and slanted and placed on meat-peptone agar (MPA) (Pharmaktiv, Shchaslyve, Ukraine) for accumulation of pure culture.The cultures were incubated at a temperature of +37 ± 1 C for 18–24 hours under aerobic conditions. We recorded the primary biochemical identification on Olkenytskyi medium:

– cultures that oxidized lactose (yellow color of the beveled part), oxidized glucose (yellow color of the column), produced gas (presence of gas bubbles and agar rupture), did not produce hydrogen sulfide and did not hydrolyze urea were considered suspicious for *E. coli*;

– cultures that did not oxidize lactose (pink color of the beveled part), oxidized glucose (yellow color of the column), produced gas (presence of gas bubbles and agar rupture), did not produce hydrogen sulfide and did not hydrolyze urea were considered suspicious for *E. coli*.

Suspected *E. coli* cultures were subjected to serotyping in a glass agglutination reaction with polyvalent sera Anti-Coli A (Sifin, Berlin, Germany), Anti-Coli I (Sifin, Berlin, Germany), Anti-Coli II (Sifin, Berlin, Germany), Anti-Coli III (Sifin, Berlin, Germany). Cultures that showed a positive agglutination reaction with one of the polyvalent sera were further tested in a slide agglutination reaction with monospecific sera for O-antigen detection (Sifin, Berlin, Germany) corresponding to the set of polyspecific serum with which there was a positive agglutination reaction. A positive agglutination reaction with one of the monospecific sera indicated the identification of pathogenic *E. coli* of a certain serotype, which confirmed the etiology of AII in children by this pathogen.

The susceptibility to ABD of isolated strains of pathogenic *E. coli* of a certain serotype was determined by the disk diffusion method in accordance with the requirements of the recommendations of the European Committee on Antibiotic Susceptibility Testing (EUCAST). The following ABD disks were used: ampicillin (10 μg) (Farmaktiv, Shchaslyve, Ukraine), cefoxitin (30 μg) (HiMedia, Mumbai, India), ceftriaxone (30 μg) (Farmaktiv, Shchaslyve, Ukraine), amoxicillin-clavulanic acid (20–10 μg) (Farmaktiv, Shchaslyve, Ukraine), ceftazidime (10 μg) (Farmaktiv, Shchaslyve, Ukraine), cefepime (30 μg) (Farmaktiv, Shchaslyve, Ukraine), ciprofloxacin (5 μg) (Farmaktiv, Shchaslyve, Ukraine). For susceptibility testing by the disk diffusion method according to EUCAST recommendations, Mueller-Hinton agar (MHA) (Graso, Starograd Gdanski, Poland) was used. Inoculated Petri dishes with MHA and coated ABD discs were incubated at +35 ± 1 C for 18 ± 2 hours under aerobic conditions. The diameters of the growth inhibition zones around the ABD discs were measured with a calibrated ruler. Quality control of the studies was performed in accordance with the approved internal laboratory quality control program and EUCAST recommendations.

Statistical analysis. Statistical data processing was carried out using one-way analysis of variance (ANOVA) to find the dependence in the obtained data by examining the significance of differences in mean values and correlation. The ANOVA test was applied for the diameters of growth retardation zones (mm), considering $P < 0.05$ as statistically significant.

Results

In 2022–2024, 3,484 stool samples from children with AII who were inpatients at the Municipal Non-Commercial Enterprise "City Clinical Hospital No. 6" of the Dnipro City Council were examined, including 1,043 samples in 2022, 982 samples in 2023, and 1,459 samples in 2024. 202 cultures of pathogenic *Escherichia coli* strains were isolated, the overall efficiency (performance) was 5.8%.

The dynamics of the detection of pathogenic *E. coli* strains from the stool samples of children with AII for 2022–2024 are presented in Table 1.

Table 1
Trend in detection of pathogenic *E. coli* strains (n = 202) from stool samples of children with AII for 2022–2024

Reporting period	Number of samples tested (n = 3484)	Number of isolated strains (n = 202)	Detection rate (%)	χ^2	P
2022	1043	75	7.2	3.86	< 0.05
2023	982	47	4.9	1.75	> 0.05
2024	1459	80	5.5	0.1	> 0.05

For 2022–2024, the effectiveness of studies for the presence of pathogenic *E. coli* strains in the stool samples of children with AII has a weak negative correlation (correlation coefficient –0.71), which indicates a slight decrease in the detection of these strains as pathogens of AII.

The dynamics of detection of pathogenic *E. coli* strains from the stool samples of children with AII for 2022–2024, depending on the seasonality of the year, is presented in Figure 1.

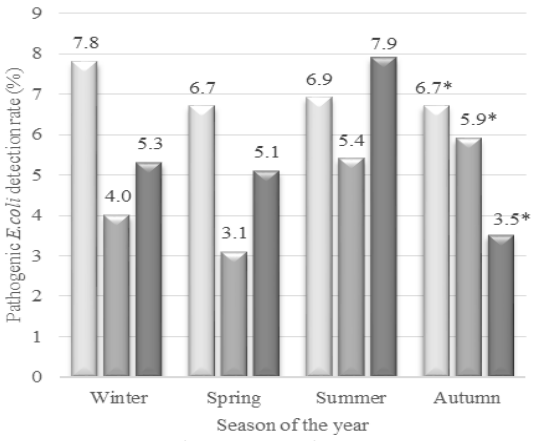

Fig. 1. Distribution of the number of pathogenic *E. coli* strains from the stool samples of children with AII depending on seasonality for 2022–2024: light gray columns – 2022, gray columns – 2023, dark gray columns – 2024; * – $P < 0.05$, the difference in the samples is not random, the assumption of the absence of a connection between the autumn periods and the number of pathogenic *E. coli* strains is rejected

The dynamics of the isolation of pathogenic *E. coli* strains depending on seasonality for 2022–2024 does not have a clear correlation (correlation coefficient in 2022 –0.76, in 2023 0.80, in 2024 –0.18, $P > 0.05$), which indicates the absence of a relationship between seasonality and the detection of pathogenic *E. coli* strains from the stool samples of children with AII. A clear negative correlation was established between the number of strains in the autumn season in the period 2022–2024 (correlation coefficient –0.96).

The distribution of the number of isolated pathogenic *E. coli* strains depending on the gender of the child with AII for 2022–2024 is presented in Table 2. The specific weight of isolated pathogenic *E. coli* strains among boys and girls with AII during the studied period is stable and amounts to 58.9% for boys and 41.1% for girls.

The distribution of the number of isolated pathogenic *E. coli* strains depending on the age category of children with AII for 2022–2024 is presented in Table 3.

A clear negative correlation was established between the specific gravity of the number of pathogenic *E. coli* strains and the age category of children with AII (correlation coefficient –0.90, $P < 0.05$) during the three reporting years, which indicates the predominant number (64.4%) of AII cases caused by pathogenic *E. coli* strains in children aged 0 to 5 years, 31.2% for children aged 6 to 12 years. The distribution of the number of isolated pathogenic *E. coli* strains depending on the age category of children with AII and seasonality for 2022–2024 is presented in Table 4.

Table 2

Specific weight of the number of isolated pathogenic *E. coli* strains (n = 202) depending on the gender of a child with AII for 2022–2024

Reporting period	Boys*		Girls*		χ^2	P
	number of isolated strains	specific weight, %	number of isolated strains	specific weight, %		
2022 (n = 75)	44	58.7	31	41.3	9.5	< 0.001
2023 (n = 47)	28	59.6	19	40.4	9.5	< 0.001
2024 (n = 80)	47	58.6	33	41.4	9.5	< 0.001
Total (n = 202)	119	58.9	83	41.1	9.5	< 0.001

Note: * – $P < 0.001$, the difference in the samples is not random, the assumption of a connection between the child's condition and the number of pathogenic *E. coli* strains is rejected.

Table 3

Specific weight of the number of isolated pathogenic *E. coli* strains (n = 202) depending on the age category of children with AII for 2022–2024

Age category, years	Reporting period						Total (n = 202)	
	2022 (n = 75)		2023 (n = 47)		2024 (n = 80)			
	number of strains	%	number of strains	%	number of strains	%	number of strains	%
0–5	48	64.0	32	68.1	50	62.5	130	64.4
6–12	23	30.7	14	29.8	26	32.5	63	31.2
13–18	4	5.3	1	2.1	4	5.0	9	4.4

Note: * – $\chi^2 = 10.2$, $P < 0.05$, the difference in the samples is not random, the assumption of no relationship between the age category of children with AII and the number of pathogenic *E. coli* strains is rejected.

Table 4

Specific weight of the number of isolated pathogenic *E. coli* strains (n = 202) depending on the age category of children with AII and seasonality for 2022–2024

Period of the year	Age category					
	0–5 years (n = 130)		6–12 years (n = 63)		13–18 years (n = 9)	
	number of strains	specific weight,%	number of strains	specific weight,%	number of strains	specific weight,%
Winter*	35	26.9	19	30.2	4	44.4
Spring**	21	16.2	10	15.8	2	22.2
Summer***	44	33.8	19	30.2	2	22.2
Autumn****	30	23.1	15	23.8	1	11.2

Note: * – $\chi^2 = 5.1$, $P < 0.05$, the difference in the samples is not random, the assumption of no relationship between the age category of children with AII, the winter period of the year and the number of pathogenic *E. coli* strains is rejected; ** – $\chi^2 = 1.4$, $P > 0.05$ no difference was found, the assumption that there is no connection between the age category of children with AII, the spring period of the year and the number of pathogenic strains of *E. coli* is not rejected; *** – $\chi^2 = 5.4$, $P < 0.05$, the difference in the samples is not random, the assumption of no relationship between the age category of children with AII, the summer period of the year and the number of pathogenic *E. coli* strains is rejected; **** – $\chi^2 = 5.1$, $P < 0.05$, the difference in the samples is not random, the assumption of no relationship between the age category of children with AII, the autumn period of the year and the number of pathogenic *E. coli* strains is rejected.

It was found that the number of pathogenic *E. coli* strains isolated from the stool samples of children with AII depends on the age group and period of the year: winter period ($\chi^2 = 5.1$, $P < 0.05$), summer period ($\chi^2 = 5.4$, $P < 0.05$), autumn period ($\chi^2 = 5.1$, $P < 0.05$). Among children aged 0 to 5 years, the largest number of strains was isolated in the summer period of the year (33.8%), the lowest – in the spring period (16.2%). Among children aged 6 to 12 years, the largest number of strains was isolated in the winter and summer periods of the year (30.2%, respectively), the lowest in the spring period (15.8%). Among children aged 13 to 18, the largest number of strains was isolated in the winter period of the year (44.4%), the lowest in the autumn period (11.2%). A direct correlation was established between the number of isolated pathogenic *E. coli* strains and the age categories of children (correlation coefficient 0.94) in the winter period of the year, which indicates an increase in the number of strains with an increase in the age category of children with AII. A negative correlation was established between the number of isolated pathogenic *E. coli* strains and the age categories of children (correlation coefficient –0.97) in the summer period of the year, which indicates a decrease in the number of strains with an increase in the age category of children with AII.

The distribution of the number of pathogenic *E. coli* strains isolated from the stool samples of children with AII by serotypes for 2022–2024 is presented in Table 5. For the period 2022–2024, among the isolated pathogenic *E. coli* strains (n = 202), the most frequently encountered strains were serotype O 18 – 14.4%, serotype O 44 – 18.8%, serotype O 78 – 7.4%, serotype O 145 – 5.4%, serotype O 26 – 5.0%, serotype O 103 – 5.0%. A slight negative correlation was found between the number of pathogenic strains of *E. coli* serotype O 1 (correlation coefficient –0.75, $P < 0.05$), a clear direct correlation between the number of pathogenic strains of serotype O 2 (correlation coefficient 0.97, $P < 0.001$), a direct correlation between the number of pathogenic strains of serotypes O 18 and O 25 (correlation coefficients 0.80 and 0.85, respectively, $P < 0.01$), strong negative correlation of the number of pathogenic strains of *E. coli* serotype O 55 (correlation coefficient –0.91, $P < 0.001$), a clear direct correlation of the number of pathogenic strains of serotypes O 86 and O 119 (correlation coefficients 0.99, respectively, $P < 0.001$), a slight negative correlation of the number of pathogenic strains of *E. coli* serotype O 114 (correlation coefficient –0.73, $P < 0.05$), a slight negative correlation between the number of pathogenic *E. coli* strains of serotypes O 142 and O 158 (correlation coefficients –0.86, respectively, $P < 0.01$) and a di-

rect correlation between the number of pathogenic strains of serotypes O 142 and O 157 (correlation coefficients 0.96 and 0.86, respectively, $P < 0.001$ and $P < 0.01$, respectively).

Table 5

Distribution by serotype of the number of isolated pathogenic *E. coli* strains (n = 202) from the stool samples of children with AII for 2022–2024

Serotype of pathogenic *E. coli*	Reporting period							
	total (n = 202)		2022 (n = 75)*		2023 (n = 47)**		2024 (n = 80)**	
	number of strains	%	number of strains	%	number of strains	%	number of strains	%
O 1	6	3.0	3	4.0	1	2.1	2	2.5
O 2	4	2.0	1	1.3	1	2.1	2	2.5
O 18	29	14.4	8	10.7	8	17.0	13	16.3
O 25	9	4.5	1	1.3	3	6.4	5	6.3
O 26	10	5.0	4	5.3	0	0.0	6	7.5
O 44	38	18.8	14	18.7	7	14.9	17	21.3
O 55	8	4.0	6	8.0	1	2.1	1	1.3
O 78	15	7.4	9	12.0	1	2.1	5	6.3
O 86	5	2.5	0	0.0	1	2.1	4	5.0
O 91	6	3.0	2	2.7	4	8.5	0	0.0
O 103	10	5.0	3	4.0	4	8.5	3	3.8
O 111	4	2.0	1	1.3	2	4.3	1	1.3
O 114	5	2.5	4	5.3	1	2.1	0	0.0
O 118	5	2.5	2	2.7	3	6.4	0	0.0
O 119	4	2.0	0	0.0	1	2.1	3	3.8
O 124	6	3.0	1	1.3	3	6.4	2	2.5
O 125	4	2.0	3	4.0	0	0.0	1	1.3
O 126	5	2.5	2	2.7	0	0.0	3	3.8
O 127	6	3.0	3	4.0	1	2.1	2	2.5
O 128	5	2.5	1	1.3	3	6.4	1	1.3
O 142	4	2.0	4	5.3	0	0.0	0	0.0
O 145	11	5.4	2	2.7	2	4.3	7	8.8
O 157	2	1.0	0	0.0	0	0.0	2	2.5
O 158	1	0.5	1	1.3	0	0.0	0	0.0

Note: * – $\chi^2 = 88.8$, $P < 0.001$, ** – $\chi^2 = 124.6$, $P < 0.001$,*** – $\chi^2 = 81.9$, $P < 0.001$, the difference in the samples is not random, the assumption of no connection between the reporting periods and serotypes of pathogenic *E. coli* strains is rejected.

Table 6

Specific weight of the number of isolated pathogenic *E. coli* strains (n = 202) from stool samples by serotypes depending on the gender of children with AII for 2022–2024

Serotype of pathogenic *E. coli* (n = 202)	Gender of the children			
	boys*		girls**	
	number of strains	%	number of strains	%
O 1	1	0.5	5	2.5
O 2	3	1.5	1	0.5
O 18	18	8.9	11	5.4
O 25	5	2.5	4	2.0
O 26	7	3.5	3	1.5
O 44	23	11.4	15	7.4
O 55	4	2.0	4	2.0
O 78	9	4.5	6	3.0
O 86	4	2.0	1	0.5
O 91	5	2.5	1	0.5
O 103	6	3.0	4	2.0
O 111	1	0.5	3	1.5
O 114	2	1.0	3	1.5
O 118	3	1.5	2	1.0
O 119	1	0.5	3	1.5
O 124	2	1.0	4	2.0
O 125	3	1.5	1	0.5
O 126	2	1.0	3	1.5
O 127	5	2.5	1	0.5
O 128	4	2.0	1	0.5
O 142	2	1.0	2	1.0
O 145	8	4.0	3	1.5
O 157	0	0.0	2	1.0
O 158	1	0.5	0	0.0

Note: * – $\chi^2 = 39.5$, $P < 0.05$, ** – $\chi^2 = 75.5$, $P < 0.001$, the difference in the samples is not random, the assumption of no relationship between the gender of the child and the serotypes of pathogenic *E. coli* strains is rejected.

The distribution of the number of pathogenic *E. coli* strains isolated from stool samples by serotypes depending on the gender of children with AII for 2022–2024 is presented in Table 6. During the period 2022–2024, among boys with AII, the most frequently isolated pathogenic strains of *E. coli* serotype O 18 – 8.9%, serotype O 44 – 11.4%, serotype O 78 – 4.5%, serotype O 145 – 4.0% were isolated from stool samples, among girls – serotype O 18 – 5.4%, serotype O 44 – 7.4%, serotype O 78 – 3.0%. A difference in the data sample was found ($P < 0.05$), which rejects the assumption of dysfunction of the relationship between the child's condition and the serotypes of pathogenic *E. coli* strains removed during AII.

The proportion of the number of isolated pathogenic *E. coli* strains from stool samples by serotypes depending on the age of children with AII for 2022–2024 is presented in Table 7.

Table 7

Distribution of the number of pathogenic *E. coli* strains (n = 202) isolated from the stool samples of children with AII by serotypes and seasonality for 2022–2024

Serotype of pathogenic *E. coli* (n = 202)	Period of the year								Correlation coefficient
	winter		spring		summer		autumn		
	number of strains	%	number of strains	%	number of strains	%	number of strains	%	
O 1	4	2.0	0	0.0	1	0.5	1	0.5	–0.60
O 2	1	0.5	0	0.0	1	0.5	2	1.0	0.63
O 18	7	3.5	5	2.5	10	5.0	7	3.5	0.31
O 25	3	1.5	2	1.0	4	2.0	0	0.0	–0.53
O 26	3	1.5	1	0.5	4	2.0	2	1.0	0.00
O 44	12	5.9	6	3.0	12	5.9	8	4.0	–0.26
O 55	3	1.5	1	0.5	2	1.0	2	1.0	–0.32
O 78	5	2.5	4	2.0	5	2.5	1	0.5	–0.75
O 86	0	0.0	1	0.5	3	1.5	1	0.5	0.51
O 91	1	0.5	1	0.5	2	1.0	2	1.0	0.89
O 103	5	2.5	1	0.5	1	0.5	3	1.5	–0.40
O 111	4	2.0	0	0.0	1	0.5	3	1.5	–0.14
O 114	3	1.5	1	0.5	0	0.0	1	0.5	–0.72
O 118	1	0.5	0	0.0	3	1.5	1	0.5	0.31
O 119	0	0.0	1	0.5	1	0.5	2	1.0	0.95
O 124	1	0.5	0	0.0	5	2.5	0	0.0	0.11
O 125	1	0.5	1	0.5	2	1.0	0	0.0	–0.32
O 126	1	0.5	1	0.5	1	0.5	2	1.0	0.77
O 127	1	0.5	0	0.0	3	1.5	2	1.0	0.60
O 128	2	1.0	1	0.5	1	0.5	1	0.5	–0.77
O 142	1	0.5	2	1.0	0	0.0	1	0.5	–0.32
O 145	3	1.5	4	2.0	1	0.5	3	1.5	–0.31
O 157	0	0.0	0	0.0	1	0.5	1	0.5	0.89
O 158	0	0.0	0	0.0	1	0.5	0	0.0	0.26
χ^2	102.4		143.5		98.7		124.1	–	–
P	< 0.001		< 0.001		< 0.001		< 0.001	–	–

For the period 2022–2024, a correlation was established between seasonality and the specific gravity of the number of isolated pathogenic strains of *E. coli* serotypes O 91, O 119 and O 157 (correlation coefficients 0.89, 0.91 and 0.89, respectively, $P < 0.001$). The difference in the samples is not accidental, the assumptions about the lack of connection between seasonality and serotypes of pathogenic *E. coli* strains are rejected.

The general profile of ABD susceptibility of pathogenic *E. coli* strains isolated from the stool samples of children with AII for 2022–2024 is presented in Table 8.

Table 8

ABD susceptibility profile of pathogenic *E. coli* strains (n = 202) isolated from stool samples of children with AII for 2022–2024

Antibacterial drug	Number of strains, %		
	S	I	R
AMP	54.5	0.0	45.5
AMO	49.0	0.0	51.0
CRO	91.6	0.5	7.9
CAZ	96.9	0.0	3.1
FEP	97.9	2.1	0.0
CX	89.1	0.0	10.9
CIP	93.6	2.0	4.5

Note: S – sensitive; I – sensitive, increased exposure; R – resistant; AMP – ampicillin, AMO – amoxicillin-clavulanic acid, CRO – ceftriaxone, CAZ – ceftazidime, FEP – cefepime, CX – cefoxitin, CIP – ciprofloxacin.

The overall susceptibility profile to ABD of pathogenic *E. coli* strains isolated from the stool samples of children with AII for 2022–2024 for ampicillin is 54.5%, for amoxicillin-clavulanic acid – 49.0%, ceftriaxone – 91.6%, ceftazidime – 96.9%, cefepime – 97.9%, cefoxitin (screening) – 89.1%, ciprofloxacin – 93.6%.

The trend in the sensitivity profile to ABD of pathogenic *E. coli* strains isolated from the stool samples of children with AII for 2022–2024 is presented in Table 9.

Table 9
Dynamics of changes in the sensitivity profile to ABD of pathogenic *E. coli* strains (n = 202) isolated from stool samples of children with AII for 2022–2024

Antibacterial drug	Number of strains, %								
	2022			2023			2024		
	S	I	R	S	I	R	S	I	R
AMP	54.6	0.0	45.4	68.1	0.0	31.9	46.3	0.0	53.7
AMO	24.0	0.0	76.0	63.8	0.0	36.2	63.8	0.0	36.2
CRO	88.0	1.3	10.7	95.7	0.0	4.3	92.5	0.0	7.5
CAZ	NT	NT	NT	100.0	0.0	0.0	95.0	0.0	5.0
FEP	NT	NT	NT	97.9	2.1	0.0	NT	NT	NT
CX	74.7	0.0	25.3	100.0	0.0	0.0	96.3	0.0	3.7
CIP	89.4	5.3	5.3	100.0	0.0	0.0	93.8	0.0	6.2
χ^2/ P	15.4 / < 0.05			9.9 / > 0.05			6.3 / > 0.05		

Note: S – sensitive; I – sensitive, increased exposure; R – resistant; AMP – ampicillin, AMO – amoxicillin-clavulanic acid, CRO – ceftriaxone, CAZ – ceftazidime, FEP – cefepime, CX – cefoxitin, CIP – ciprofloxacin; NT – not tested.

For the period 2022–2024, no correlations were recorded in the sensitivity profile to ABD of pathogenic *E. coli* strains isolated from the stool samples of children with AII and the reporting period, which indicates the absence of an increase in antibiotic resistance of these strains over the last 3 years.

The susceptibility profile to ABD of common serotypes of pathogenic *E. coli* strains isolated from the stool samples of children with AII for 2022–2024 is presented in Table 10.

Table 10
ABD susceptibility profile of common serotypes of pathogenic *E. coli* strains (n = 113) isolated from stool samples of children with AII for 2022–2024

Antibacterial drug	Number of susceptible strains, %					
	*E. coli O 18 (n=29)**	*E. coli O 26 (n=10)*	*E. coli O 44 (n=38)**	*E. coli O 78 (n=15)**	*E. coli O 103 (n=10)*	*E. coli O 145 (n=11)*
AMP	62.0	40.0	55.3	33.3	40.0	45.5
AMO	48.3	70.0	52.6	33.3	40.0	63.6
CRO	89.7	80.0	84.2	73.3	100.0	100.0
CAZ	89.7	100.0	84.2	73.3	100.0	90.0
CX	96.6	100.0	78.9	66.7	100.0	100.0
CIP	100.0	100.0	97.4	73.3	90.0	90.9

Note: AMP – ampicillin, AMO – amoxicillin-clavulanic acid, CRO – ceftriaxone, CAZ – ceftazidime, CX – cefoxitin, CIP – ciprofloxacin, * – P < 0.05, the difference in the samples is not random, the assumption of no relationship between the sensitivity profile to ABD and the serotypes of pathogenic *E. coli* strains is rejected.

It was found that the sensitivity profile to ABD of common serotypes of pathogenic *E. coli* strains isolated from the stool samples of children with AII differs (P < 0.05). It was found that the lowest sensitivity index to ampicillin was observed among pathogenic *E. coli* strains O 78 (33.3%), the highest sensitivity index was observed among pathogenic *E. coli* strains O 18 (62.0%). The lowest susceptibility to amoxicillin-clavulanic acid among pathogenic *E. coli* strains was O 78 (33.3%), the highest susceptibility was among pathogenic *E. coli* strains O 26 (70.0%). The lowest susceptibility to ceftriaxone among pathogenic *E. coli* strains was O 78 (73.3%), the highest susceptibility was among pathogenic *E. coli* strains O 103 (100.0%) and O 145 (100.0%). The lowest susceptibility to ceftazidime was observed among pathogenic *E. coli* strains O 78 (73.3%), the highest susceptibility was among pathogenic *E. coli* strains O 26 (100.0%) and O 103 (100.0%). The lowest susceptibility to cefoxitin was observed among pathogenic *E. coli* strains O 78 (66.7%), the highest susceptibility was observed among pathogenic *E. coli* strains O 26 (100.0%), O 103 (100.0%) and O 145 (100.0%). The lowest susceptibility to ciprofloxacin was observed among pathogenic *E. coli* strains O 78 (73.3%), the highest susceptibility was observed among pathogenic *E. coli* strains O 18 (100.0%) and O 26 (100.0%).

Discussion

For the period 2022–2024, we found that the rate of isolation of pathogenic *E. coli* strains from the stool samples of children with AII is 5.8% and correlates with data in Ethiopia, where the research effectiveness rate is 7.4%, with the closest rate we found in 2022 being 7.2% (Belina et al., 2024). The detection rate of pathogenic *E. coli* strains is lower than those in Kenya, Spain and Gabon – 23.5%, 16.9% and 11.4% respectively (Dikoumba et al., 2024; Martínez-Oliveros et al., 2025; Okumu et al., 2025). We have established that seasonality does not affect the increase in the number of pathogenic *E. coli* strains as an etiological factor of AII in children. It was established that the highest research efficiency in 2022 was observed in the winter period of the year, in 2023 – in the summer-autumn period, in 2024 – in the summer period. The data obtained for 2023–2024 correlate with data from researchers from Nigeria and Bahrain (Olayinka et al., 2024; Sameer et al., 2024).

A clear dependence of the number of pathogenic *E. coli* strains isolated from the stool samples of children with AII and the gender of the patients was established. For the period from 2022–2024, the proportion of strains for boys is 58.9%, for girls – 41.1%, these indicators correlate with the indicators of Olayinka et al. (2024). The number of pathogenic *E. coli* strains isolated from the stool samples of children with acute respiratory viral infections depends on the age group of the patients. The indicators we have established have stable values during 2022–2024. The majority of strains are isolated among children aged 0 to 5 years (64.0–68.1%), from 6 to 12 years the figures range from 29.8% to 32.5%, from 13 to 18 years – from 2.1% to 5.3%. The overall figures for the 3 reporting periods correlate with data from researchers from Bahrain, who found that most strains are isolated among children aged 0 to 5 years (86.0%), from 6 to 12 years the figure is 10.5%, from 13 to 18 years – 3.5% (Sameer et al., 2024).

For the period 2022–2024, among the isolated pathogenic *E. coli* strains (n = 202), the most frequently encountered strains were serotype O 18, serotype O 44, serotype O 78, serotype O 145, serotype O 26, and serotype O 103. Over the 3 reporting years, a decrease in the number of pathogenic *E. coli* strains of serotypes O 1, O 55, O 114, O 142 and O 158 and an increase in the number of pathogenic *E. coli* strains of serotypes O 2, O 18, O 25, O 86, O 119, O 142 and O 157 was recorded. During the period 2022–2024, among boys and girls with AII, pathogenic strains of *E. coli* serotypes O 18, O 44, and O 78 were most often sown from stool samples. It was found that the number of pathogenic strains of *E. coli* serotype O 1 for girls was 83.3%, and for boys – 16.7%. During the period 2022–2024, among boys and girls with AII, pathogenic strains of *E. coli* serotypes O 18, O 44, and O 78 were most often sown from stool samples. It was found that the number of pathogenic strains of *E. coli* serotype O 1 for girls was 83.3%, and for boys – 16.7%. Pathogenic strains of *E. coli* serotypes O 18, O 25, O 44, O 55, O 78, O 103, O 114, O 118, O 126, O 142 were sown among boys and girls in almost equal numbers. This relationship between the number of pathogenic *E. coli* strains and the gender of children requires further study of the prevalence of strains according to these indicators and dependencies. For the period 2022–2024, it was found that seasonality affects the seeding rate of pathogenic *E. coli* strains of serotypes O 91, O119, and O 157, which requires further study of the circulation of these strains.

A comparison with the results of researchers from other countries regarding the susceptibility profile to ABD of pathogenic *E. coli* strains isolated from the stool samples of children with AII is presented in Table 11. For the years 2022–2024, it was found that the ampicillin susceptibility profile of pathogenic *E. coli* strains isolated from the stool samples of children with AII was the highest (54.5%), compared to the indicator in Nigeria, Kenya, and Spain. The number of

pathogenic *E. coli* strains susceptible to amoxicillin-clavulanic acid is 49.0%, which is the lowest rate in Nigeria, Kenya, and Spain, however, in 2023 and 2024, the sensitivity profile was 63.8%, and in 2022, it was 24.0%, which requires further monitoring and study of the phenomenon of an increase in the number of susceptible strains. The susceptibility of pathogenic *E. coli* strains to 3rd generation cephalosporins is more than 90.0%, which correlates with data from researchers from Kenya and Spain, and is significantly different from the indicator in Nigeria. The susceptibility rate of pathogenic *E. coli* strains to cefoxitin is 10.8% higher than that in Nigeria. The susceptibility of pathogenic *E. coli* strains to ciprofloxacin correlates with data from researchers in Nigeria, Kenya and Spain. We found that the sensitivity profile to ABD of pathogenic *E. coli* strains isolated from the stool samples of children with AII differs between serotypes, which can be further investigated as markers of the prevalence of these strains. In general, the susceptibility profile to ABD of pathogenic *E. coli* strains isolated from the feces of children with AII requires further study in order to monitor the development of antibacterial resistance. Thus, we achieved our goal and confirmed the hypothesis of our research.

Table 11

Comparative characteristics of the susceptibility profile to ABD of pathogenic *E. coli* strains isolated from stool samples of children with AII with the results of researchers from other countries

Country	Number of susceptible strains, %							
	AMP	AMO	CRO	CAZ	FEP	CX	CIP	CTX
Dnipro, Ukraine	54.5	49.0	91.6	96.9	97.9	89.1	93.6	NT
Nigeria (Olayinka et al., 2024)	21.7	56.5	NT	79.7	NT	78.3	97.1	71.1
Kenya (Okumu et al., 2025)	27.6	73.2	95.3	NT	NT	NT	96.9	NT
Spain (Martínez-Oliveros et al., 2025)	41.2	52.9	NT	NT	NT	NT	95.2	97.6

Note: AMP – ampicillin, AMO – amoxicillin-clavulanic acid, CRO – ceftriaxone, CAZ – ceftazidime, FEP – cefepime, CX – cefoxitin, CIP – ciprofloxacin; NT – not tested.

Conclusions

The rate of isolation of pathogenic *E. coli* strains in stool studies of children with AII is 5.8%. The dynamics of detection of pathogenic *E. coli* strains depending on seasonality for 2022–2024 does not have a clear correlation. The number of isolated pathogenic *E. coli* strains among boys and girls with AII did not change over the 3 reporting years. There is a clear relationship between the specific gravity of the number of pathogenic *E. coli* strains and the age category of children with AII. The number of pathogenic *E. coli* strains isolated from the stool samples of children with AII depends on the age group and seasonality of the year. For the period 2022–2024, among the isolated pathogenic strains of *E. coli* from the stool samples of children with AII, the most frequently encountered strains were serotype O 18, serotype O 44, serotype O 78, serotype O 145, serotype O 26, and serotype O 103. Ampicillin may be the drug of choice for empirical antibacterial therapy in 54.5% of cases, 3rd generation cephalosporins and fluoroquinolones – in more than 90.0% of cases. The results of the studies correlate with the data of researchers from other countries, which indicates compliance with the methods and high-quality conduct of bacteriological studies of stool samples. This study did not receive any specific grant from financial institutions in the public, commercial, or non-profit sectors. The authors declare that they have no known competing financial interests or personal relationships that could influence the work reported in this article.

Special thanks to Valerii Chornyi, the general director of the Municipal Non-Commercial Enterprise “City Clinical Hospital No. 6” of the Dnipro City Council, for understanding the importance of conducting the above-mentioned bacteriological studies and allocating the necessary funding to ensure the smooth operation of the bacteriological laboratory. We also express our sincere thanks to the medical directors Artem Breus, Inna Yesaulenko, the head of the Infection Control Department Yevhen Maystrenko, the head of the bacteriological laboratory Maksym Lusta for the organization of the work of the laboratory and to all the staff of the bacteriological laboratory for organizing the work of the laboratory and performing bacteriological research qualitatively.

References

Akhtar, M., Begum, Y. A., Isfat Ara Rahman, S., Afrad, M. H., Parvin, N., Akter, A., Tauheed, I., Amin, M. A., Ryan, E. T., Khan, A. I., Chowdhury, F., Bhuiyan, T. R., & Qadri, F. (2024). Age-dependent pathogenic profiles of enterotoxigenic *Escherichia coli* diarrhea in Bangladesh. Frontiers in Public Health, 12, 1484162.

Amin, M. A., Akhtar, M., Khan, Z. H., Islam, M. T., Firoj, M. G., Begum, Y. A., Rahman, S. I. A., Afrad, M. H., Bhuiyan, T. R., Chowdhury, F., Faruque, A. S. G., Ryan, E. T., Qadri, F., & Khan, A. I. (2025). Coinfection and clinical impact of enterotoxigenic *Escherichia coli* harboring diverse toxin variants and colonization factors: 2017–2022. International Journal of Infectious Diseases, 151, 107365.

Anueyiagu, K. N., Agu, C. G., Umar, U., & Lopes, B. S. (2024). Antimicrobial resistance in diverse *Escherichia coli* pathotypes from Nigeria. Antibiotics, 13(10), 922.

Ashenafi, G., Tilahun, D., Aliyo, A., & Sisay, B. (2024). Magnitude of enteric pathogens associated with diarrhea and antibiotic resistance of enteric bacterial pathogens isolated among children under 5 years of age in Bule Hora town, West Guji, Ethiopia. Front Public Health, 12, 1398264.

Belina, D., Gobena, T., Kebede, A., Chimdessa, M., & Hald, T. (2024). Genotypic antimicrobial resistance profiles of diarrheagenic *Escherichia coli* and nontyphoidal *Salmonella* strains isolated from children with diarrhea and their exposure environments in Ethiopia. Infection and Drug Resistance, 17, 4955–4972.

Bizot, E., Bonacorsi, S., Labé, P., Pinhas, Y., Cointe, A., Ferroni, A., Cohen, J. F., Lécuyer, H., & Toubiana, J. (2025). Use of gastrointestinal syndromic multiplex molecular assays and detection of *Escherichia coli* pathotypes in pediatric wards. Journal of Clinical Microbiology, 63(4), e0107324.

Brubaker, J., Zhang, X., Bourgeois, A.L., Harro, C., Sack, D.A., & Chakraborty, S. (2021). Intestinal and systemic inflammation induced by symptomatic and asymptomatic enterotoxigenic *E. coli* infection and impact on intestinal colonization and ETEC specific immune responses in an experimental human challenge model. Gut Microbes, 13(1), 1891852.

Bywater, A., Dintwe, G., Alexander, K. A., & Ponder, M. A. (2024). Characterization of diarrheagenic *Escherichia coli* and *Salmonella enterica* from produce in the Chobe District of Botswana. Journal of Food Protection, 87(10), 100351.

Chercos, D. H., Wafula, S. T., Lusingu, J. P. A., Minja, D. T. R., Gesase, S., Mbwana, J. R., Schotte, U., May, J., Mardeis, L., Jaeger, A., Rojak, S., Lamshöft, M., Kaseka, J., Lorenz, E., Frickmann, H., & Dekker, D. (2024). Epidemiology and multiple colonization of gastrointestinal pathogens in rural Tanzanian children with and without diarrhea: A case-control study. PLoS One, 19(6), e0305469.

Dikoumba, A. C., Mbehang Nguema, P. P., Oyaba Yinda, L. E. D., Lendamba, R. W., Obague Mbeang, J. C., Ndong Atome, G. R., Zinga Koumba, C. R., Godreuil, S., & Onanga, R. (2024). Characterization of extended-spectrum beta-lactamase-producing *Escherichia coli* in diarrhoeal faeces from 0 to 5-year-old children attending public hospitals in Franceville, Gabon. Antibiotics, 13(11), 1059.

Fernández Fellenz, D., Ruiz, J. M., Etcheverría, A. I., Colello, R., Velez, M. V., Sanz, M. E., Sparo, M. D., Lissarrague, S., Pereyra, J., Zanelli, G., & Padola, N. L. (2025). Detection of EPEC and STEC strains isolated from children with diarrhea in Argentina. Revista Argentina de Microbiología, 57(1), 59–62.

Glassman, H., Suttorp, V., White, T., Ziebell, K., Kearney, A., Bessonov, K., Li, V., & Chui, L. (2021). Clinical outcomes and virulence factors of Shiga toxin-producing *Escherichia coli* (STEC) from Southern Alberta, Canada, from 2020 to 2022. Pathogens, 13(10), 822.

Jones, A., Ahmed, S. M., Platts-Mills, J. A., Kotloff, K. L., Levine, A. C., Nelson, E. J., Pavia, A. T., Khan, A. I., & Leung, D. T. (2024). Etiology of severely dehydrating diarrheal illness in infants and young children residing in low- and middle-income countries. Open Forum Infectious Diseases, 11(11), ofae619.

Kralicek, S. E., Sitaraman, L. M., Kuprys, P. V., Harrington, A. T., Ramakrishna, B., Osman, M., & Hecht, G. A. (2022). Clinical manifestations and

stool load of atypical enteropathogenic *Escherichia coli* infections in United States children and adults. Gastroenterology, 163(5), 1321–1333.

Machado Ribeiro, T. R., Salgaço, M. K., Adorno, M. A. T., da Silva, M. A., Piazza, R. M. F., Sivieri, K., & Moreira, C. G. (2021). Human microbiota modulation via QseC sensor kinase mediated in the *Escherichia coli* O104:H4 outbreak strain infection in microbiome model. BMC Microbiology, 21(1), 163.

Martínez-Oliveros, Y. P., Rita-Iotti, L., Sánchez, B. F., Eiros, J. M., & de Frutos, M. (2025). Distribución de patotipos de *Escherichia coli* diarreagénica en población pediátrica y perfil de sensibilidad antibiótica en el área de salud de Valladolid Oeste (ASVAO) [Distribution of diarrheagenic *Escherichia coli* pathotypes in the pediatric population and antibiotic susceptibility profile in the Valladolid Oeste health area (ASVAO)]. Revista Española de Quimioterapia, 38(2), 129–132.

Morita, D., & Kuroda, T. (2025). Recent antimicrobial resistance situation and mechanisms of resistance to key antimicrobials in enterotoxigenic *Escherichia coli*. Biological and Pharmaceutical Bulletin, 48(3), 222–229.

Okumu, N. O., Muloi, D. M., Moodley, A., Ochien'g, L., Watson, J., Kiarie, A., Ngeranwa, J. J. N., Cumming, O., & Cook, E. A. J. (2025). Epidemiology of antimicrobial-resistant diarrheagenic *Escherichia coli* pathotypes from children, livestock and food in Dagoretti South, Nairobi Kenya. International Journal of Antimicrobial Agents, 65(3), 107419.

Olayinka, A. A., Oginni-Falajiki, I. O., Okeke, I. N., & Aboderin, A. O. (2024). Diarrhoeagenic *Escherichia coli* associated with childhood diarrhoea in Osun State, Nigeria. BMC Infectious Diseases, 24(1), 928.

Sameer, M., Masood, A., Almutawea, L., Fox, G., Loni, R., Ahmed, A., Ben Turkia, H., Abdulsamad, M., & Mary, I. (2024). Gastrointestinal panel performance for the diagnosis of acute gastroenteritis in pediatric patients. Cureus, 16(6), e61979.

Schlosserová, K., Daniel, O., Labská, K., Jakubů, V., Stárková, T., Bílý, J., Dresler, J., Lang, C., Fruth, A., Flieger, A., Žemličková, H., Bielaszewska, M., & Havlíčková, M. (2024). Enteroaggregative *Escherichia coli*: Frequent, yet underdiagnosed pathotype among *E. coli* O111 strains isolated from children with gastrointestinal disorders in the Czech Republic. International Journal of Medical Microbiology, 316, 151628.

Seliga-Gąsior, D., Sokól-Leszczyńska, B., Krzysztoń-Russjan, J., Wierzbicka, D., Stępień-Hołubczat, K., Lewandowska, P., Frankiewicz, E., Cacko, A., Leszczyńska, B., Demkow, U., & Podsiadły, E. (2024). Epidemiological characteristics of Shiga toxin-producing *Escherichia coli* responsible for infections in the Polish pediatric population. Polish Journal of Microbiology, 73(2), 177–187.

Tesfaw, G., Siraj, D. S., Abdissa, A., Jakobsen, R. R., Johansen, Ø. H., Zangenberg, M., Hanevik, K., Mekonnen, Z., Langeland, N., Bjørang, O., Safdar, N., Mapes, A. C., Kates, A., Krych, L., Castro-Mejía, J. L., & Nielsen, D. S. (2024). Gut microbiota patterns associated with duration of diarrhea in children under five years of age in Ethiopia. Nature Communications, 15(1), 7532.

Thystrup, C., Majowicz, S. E., Kitila, D. B., Desta, B. N., Fayemi, O. E., Ayolabi, C. I., Hugho, E., Buys, E. M., Akanni, G. B., Machava, N. E., Monjane, C., Hald, T., & Pires, S. M. (2024). Etiology-specific incidence and mortality of diarrheal diseases in the African region: A systematic review and meta-analysis. BMC Public Health, 24(1), 1864.

Usein, C. R., Oprea, M., Dinu, S., Popa, L. I., Cristea, D., Militaru, C. M., Ghiță, A., Costin, M., Popa, I. L., Croitoru, A., Bologa, C., & Rusu, L. C. (2024). Shiga toxin-producing *Escherichia coli* strains from Romania: A whole genome-based description. Microorganisms, 12(7), 1469.

Vusirikala, A., Yanshi, Robin, C., Rowell, S., Dabke, G., Fox, G., Bell, J., Manuel, R., Jenkins, C., Love, N. K., McCarthy, N., Sumilo, D., & Balasegaram, S. (2024). Facilitators and barriers to implementing successful exclusion among children with shiga toxin-producing *Escherichia coli*: A qualitative analysis of public health case management records. BMC Public Health, 24(1), 2272.

Wang, Z., Sun, M., Guo, S., Wang, Y., Meng, L., Shi, J., Geng, C., Han, D., Fu, X., Xue, J., Ma, H., & Liu, K. (2024). Detection of drug resistance in *Escherichia coli* from calves with diarrhea in the Tongliao Region: An analysis of multidrug-resistant strains. Frontiers in Veterinary Science, 11, 1466690.

Wolde, D., Eguale, T., Medhin, G., Haile, A.F., Alemayehu, H., Mihret, A., Pirs, M., Strašek Smrdel, K., Avberšek, J., Kušar, D., Cerar Kišek, T., Janko, T., Steyer, A., & Starčič Erjavec, M. (2024). Diarrheagenic *Escherichia coli* in stool specimens collected from patients attending primary healthcare facilities in Ethiopia: Whole-genome sequencing-based molecular characterization. International Journal of Molecular Sciences, 25(19), 10251.