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Antimicrobial Resistance Patterns and Risk Factors Associated with ESBL-Producing and MDR *Escherichia coli* in Hospital and Environmental Settings in Lusaka, Zambia: Implications for One Health, Antimicrobial Stewardship and Surveillance Systems

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Abstract: Antimicrobial resistance (AMR) is a public health problem threatening human, animal, and environmental safety. This study assessed the AMR profiles and risk factors associated with *Escherichia coli* in hospital and environmental settings in Lusaka, Zambia. This cross-sectional study was conducted from April 2022 to August 2022 using 980 samples collected from clinical and environmental settings. Antimicrobial susceptibility testing was conducted using BD Phoenix™ 100. The data were analysed using SPSS version 26.0. Of the 980 samples, 51% were from environmental sources. Overall, 64.5% of the samples tested positive for *E. coli*, of which 52.5% were from clinical sources. Additionally, 31.8% were ESBL, of which 70.1% were clinical isolates. Of the 632 isolates, 48.3% were MDR. Most clinical isolates were resistant to ampicillin (83.4%), sulfamethoxazole/trimethoprim (73.8%), and ciprofloxacin (65.7%) while all environmental isolates were resistant to sulfamethoxazole/trimethoprim (100%) and some were resistant to levofloxacin (30.6%). The drivers of MDR in the tested isolates included pus (AOR = 4.6, CI: 1.9–11.3), male sex (AOR = 2.1, CI: 1.2–3.9), and water (AOR = 2.6, CI: 1.2–5.8). This study found that *E. coli* isolates were resistant to common antibiotics used in humans. The presence of MDR isolates is a public health concern and calls for vigorous infection prevention measures and surveillance to reduce AMR and its burdens.

Keywords: *Escherichia coli*; ESBL; One Health; antibiotics; multidrug resistance; antimicrobial stewardship; Zambia

1. Introduction

Antimicrobial resistance (AMR) is a growing public health crisis that affects both human and animal health and has a strong relationship with the environment [1–5]. The

concerns regarding AMR have been steadily increasing worldwide, endangering a wide variety of effective medical interventions (e.g., surgery, chemotherapy, intensive care), and the ability to effectively prevent and cure infectious diseases [6,7]. It has been established by numerous studies that the overuse and misuse of antibiotics in the agricultural, veterinary, and human medical sectors promote the development and spread of multidrug-resistant (MDR) pathogens and allow for the emergence of novel resistance mechanisms [8–11]. Additionally, antimicrobial-resistant bacteria and their resistomes spread between humans, animals, and their environment [12–14]. In real-world settings, infections caused by MDR bacteria are associated with increased morbidity and mortality [4,6,7,15]. The significance of MDR infections has been estimated by the Global Burden of Disease (GBD) study, where it was shown that ~1.27 million (95% UI: 0.91–1.71 million) deaths were directly attributable to bacterial MDR globally in the year 2019 alone [6,16]. Among these MDR bacteria, *Escherichia coli* (*E. coli*), *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Streptococcus pneumoniae*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa* were the most significant and associated with ~0.93 million (95% UI: 0.66–1.27 million) directly attributable deaths [6,7,16]. Alongside these consequences, other AMR implications include increased medical costs with a negative impact on the economy (both due to direct and indirect costs), and limited options to treat infections, endangering sustainable development globally [15,17–21].

E. coli, a gram-negative rod belonging to the Enterobacterales order, is a lactose and non-lactose fermenting microbe [22–24]. It is among the microorganisms that have developed considerable levels of resistance to most antimicrobials used in humans, animals, and agriculture, and has the potential to spread effectively in the environment [1,25–31]. The injudicious handling of antimicrobials in the One Health ecology further exacerbates the resistance situation [32–37]. *E. coli* is considered a major cause of pediatric infections that result in adverse outcomes [37,38]. It has been reported as one of the most common pathogens responsible for infections, particularly in countries with unstable healthcare and surveillance systems [6,39–42]. Despite being a common member of the intestinal microbiota in humans and animals, *E. coli* is also found in water, soil, and around plants, and is the leading cause of several common bacterial infections, including gastroenteritis, urinary tract infections (UTIs), septicemia, and neonatal meningitis [2,43–49]. In recent years, the rise of MDR *E. coli* has been documented in almost all countries worldwide [43,46,50–53]. The spread of extended-spectrum β -lactamase (ESBL)-producing bacteria (including ESBL-*E. coli*; ESBL-EC) through the environment—a major cause of healthcare problems (i.e., in healthcare-associated infections) and community-acquired infections—is caused by the increasing global dependence and use of β -lactam antibiotics (i.e., penicillins, cephalosporins, carbapenems, and monobactams), which necessitates urgent action [54–57].

ESBL-EC possesses various β -lactamase enzymes that rapidly evolve through the ability to hydrolyze antimicrobials and cause increased resistance to β -lactam antibiotics [57,58]. Extended-spectrum cephalosporins—such as cefotaxime, ceftriaxone, and ceftazidime—and monobactams (such as aztreonam) are susceptible to hydrolysis by ESBLs [59,60]. Resistance to other antimicrobial classes, such as aminoglycosides, macrolides, tetracyclines, quinolones, and sulfonamides, may be acquired by plasmid-encoded resistance determinants—coexisting in bacteria-harboring ESBLs—rapidly reaching the phenotype of MDR, which further limits therapeutic options and poses a therapeutic conundrum [2,16,60,61]. β -lactam antibiotics are among the most commonly administered drugs globally, as they have an advantageous side effect profile and in many patient populations (i.e., children, the elderly, and pregnant women), they are the only suitable antimicrobials [62–65]. However, the development of resistance to these agents in recent years has become a serious public health concern [66–68]; this is especially true in low-income countries, such as Zambia, where β -lactam antibiotics are overused and misused and are often readily available without a medical prescription [63,64,69]. In addition to β -lactamases, the modification of penicillin-binding proteins (PBPs), the decreased permeability of the bacterial outer membrane, and the co-existence of several resistance mechanisms contributed to this phenomenon [57]. One of the direct causes of the development of ESBL strains in

resource-constrained healthcare settings includes the empirical and symptomatic (without a diagnosis) use of antibiotics [70]. Despite multiple cases of nosocomial outbreaks attributed to these pathogens, there is limited information regarding the frequency of ESBL-producing bacteria in most Zambian hospitals.

Due to the isolation of MDR bacteria—such as *E. coli*—from humans, animals, and the environment, it is being increasingly understood that a One Health approach is required to address this problem [45,71,72]. This is because there is a clear interaction between humans and animals in the environment that can facilitate the transmission of *E. coli* from humans to animals or the environment and vice-versa [73]. Moreover, the presence of antimicrobial-resistant *E. coli* and other pathogens in humans, animals, and the environment calls for a holistic, multi-disciplinary collaborative action guided by the World Health Organization Global Action Plan (GAP) on AMR [74]. The One Health approach aims to address AMR across all the abovementioned domains (i.e., humans, animals, and the environment), as there is a higher transmission potential at the human and animal interface in the environment [1,5,75,76]. Therefore, a One Health approach (i.e., the systems thinking within ecological systems) promotes, and is an integral part of, antimicrobial stewardship (AMS) programmes for the prudent of antimicrobials in humans, animals, and the environment [77–81]. Most AMR data comes from high-income countries (HICs), while the AMR burden of sub-Saharan Africa (SSA)—including Zambia—is inadequately documented. In Zambia, the National Action Plan (NAP) on AMR was developed in 2017 in line with the GAP on AMR to tackle this problem using a One Health approach [82,83]. Alongside this, there have been some studies published to promote AMS in human and animal health in this geographical region [27,28,63,64,84–91]. However, there is still very little information on the isolation, resistance patterns, and risk factors associated with ESBL-producing and/or MDR *E. coli* originating in humans, food-producing animals, other food products, and the environment. With this in mind, this study aimed to comprehensively assess the AMR patterns and risk factors associated with ESBL-producing and MDR *E. coli* in hospital and environmental settings in Lusaka, Zambia.

2. Materials and Methods

2.1. Study Design and Site Location

The present cross-sectional study was conducted between April and August 2022 at the main referral University Teaching Hospital (UTH) and townships (administrative sub-districts) in the capital city of Zambia, Lusaka. The samples collected and included in the data analysis were (i) clinical samples (i.e., urine, stool, blood, cerebrospinal fluid) from inpatients and outpatients and (ii) environmental samples (i.e., meat, fruits and vegetables, water, and those isolated from hospital equipment). The UTH has a bed capacity of 1665 beds, acting as a national and the largest tertiary referral hospital in Lusaka that provides specialised patient care for patients from all over Zambia. Lusaka (360 km²) is the capital city of Zambia, with an estimated 687,923 households [92], and a human population of approximately 3,079,964 [93].

2.2. Data Collection

Data collection for clinical samples included the date and time of sample collection, sample type, anonymised identification code, and the age and sex of the patients. Information corresponding to the environmental samples included the source, type and area sampled. Only the samples kept at an ambient temperature for no longer than two hours were included in the study.

2.3. Specimen Collection and Processing

The environmental samples were first swabbed and enriched in buffered peptone water (BPW) (Oxoid Ltd., Basingstoke, Hampshire, UK) and incubated for 3 h at 37 °C. A sterile loop was dipped into the enriched BPW, where the sample was incubated. Afterwards, a 0.5 mL sample of incubated BPW was inoculated on CHROMagar™ ECC (*E. coli*

and coliforms; HiMedia Laboratories Pvt. Ltd., Mumbai MS, India) agar plates at 37 °C for 18 to 24 h for the isolation of *E. coli*. Presumptive *E. coli* colonies were streaked on Eosin Methylene Blue (EMB) agar (Oxoid™, Basingstoke, Hampshire, UK) for the identification of *E. coli*.

For clinical specimens, the presumptive identification of *E. coli* colonies was defined as the growth of lactose-fermenting, donut-shaped colonies on Xylose Lysine Deoxycholate (XLD) agar (Oxoid Ltd., Basingstoke, Hampshire, UK), MacConkey agar (Oxoid Ltd., Basingstoke, Hampshire, UK), and Hichrome chromogenic UTI agar (HiMedia Laboratories Pvt. Ltd., Mumbai MS, India). Therefore, urine samples were inoculated directly onto Hichrome chromogenic UTI agar and incubated at 37 °C for 18 to 24 h. Presumptive *E. coli* colonies were characterised by the appearance of dark blue to violet colonies. The stool was inoculated and incubated on XLD for 24 h at 37 °C, and *E. coli* colonies were defined after the appearance of yellow colonies. Clinical specimens were inoculated directly on MacConkey agar (Oxoid Ltd., Basingstoke, Hampshire, UK) and incubated for 24 h at 37 °C. On MacConkey agar, lactose-fermenting colonies appeared pink in colour while non-lactose-fermenting colonies appeared off-white opaque. On EMB, greenish metallic colonies were presumed to be *E. coli* and were sub-cultured on nutrient agar (Oxoid Ltd., Basingstoke, Hampshire, UK), where they appeared large, thin, circular, and greyish-white after 24 h of aerobic incubation at 37 °C. To differentiate *E. coli* from other lactose-fermenting bacteria, phenotypic confirmation was performed on all pure colonies using a battery of biochemical tests, including triple sugar iron (TSI) agar, lysine iron agar (LIA), simmons citrate agar (SCA), and sulfide indole motility (SIM) agar, respectively. Only colonies that passed the biochemical tests were identified as *E. coli*. The identified presumptive colonies of *E. coli* were selected and cultured on nutrient agar for purification purposes and further analysis. For further confirmation, *E. coli* isolates were subjected to identification using the Becton Dickinson BD Phoenix™ 100 system (BD Diagnostic Systems, Sparks, MD, USA).

2.4. Antibiotic Susceptibility Testing

Antimicrobial susceptibility testing (AST) for the respective *E. coli* isolates was performed using disk diffusion and the BD Phoenix™ 100 Automated Microbiology System (BD Diagnostic Systems, Sparks, MD; based on minimum inhibitory concentrations). The following antibiotics were used for AST: ampicillin 10 µg (AMP), amoxicillin/clavulanic acid 10 µg (AMC), cefepime 30 µg (FEP), ceftazidime 30 µg (CAZ), cephazolin 30 µg (KZ), ceftriaxone 30 µg (CRO), cefuroxime 30 µg (CXM), ciprofloxacin 5 µg (CIP), ertapenem 30 µg (ETP), gentamicin 10 µg (CN), imipenem 10 µg (IPM), levofloxacin 5 µg (LEV), nitrofurantoin 30 µg (NIT), and sulfamethoxazole/trimethoprim 23 µg (SXT). Interpretation of the AST results (i.e., defined as susceptible, intermediate or resistant) was based on the standards and breakpoints as defined by the Clinical and Laboratory Standard Institute (CLSI) [94]. Furthermore, ESBL-producing isolates were confirmed by the combined double-disk test (with cefotaxime and ceftazidime alone, and in combination with cefotaxime/clavulanic acid) and the Becton Dickinson BD Phoenix™ 100 system (Becton, Dickinson Company, Sparks, MD, USA) as defined by CLSI guidelines [94]. Each batch incorporated a control strain of *E. coli* ATCC 25922 to ensure the validity and reliability of AST. Isolates were classified as MDR (resistance to at least one agent in ≥3 different antibiotic classes), extensive drug resistance (XDR; susceptibility to 1 or 2 remaining antibiotics), and pan-drug resistance (non-susceptibility to all classes of antibiotics) (PDR) [95].

2.5. Data Analysis

The raw data of the isolates was summarised, cleaned, and coded in Microsoft Excel 2013 (Microsoft Corp., Redmond, WA, USA). Descriptive analysis was conducted to characterise the data using means, medians, ranges, and percentages. Various statistical tests were employed to determine the factors associated with ESBL and MDR *E. coli* isolates, including Chi-square tests, univariate and multiple logistic regression (ESBL), and multinomial (MDR) analyses. The backward elimination method (MDR: based on the likelihood ratio

test) was utilised to select the most relevant variables, accounting for confounding factors. Adherence to the assumptions of the Chi-square tests was ensured, and if not met, Fisher's exact test with Monte Carlo simulation ($n = 1000$) was used. The analyses were performed using the Statistical Package for Social Sciences (SPSS), version 26.0 (IBM Corp, Armonk, NY, USA). The normality of the data was assessed through the Kolmogorov-Smirnov test. All statistical tests were performed at a 95% confidence level with a $p < 0.05$ indicating statistical significance.

3. Results

3.1. Descriptive Characteristics of Clinical and Environmental *E. coli* Strains

A total of $n = 980$ samples were collected and subjected to microbial culture for *E. coli* using phenotypic methods. Of the $n = 980$ samples, $n = 480$ were from clinical sources, while $n = 500$ were from environmental sources (Figure 1); out of the total sample number, *E. coli* was isolated from $n = 632$ (64.5%) of samples, where the distribution was $n = 332$ (69.2%) and $n = 300$ (60.0%) from clinical and environmental sources, respectively.

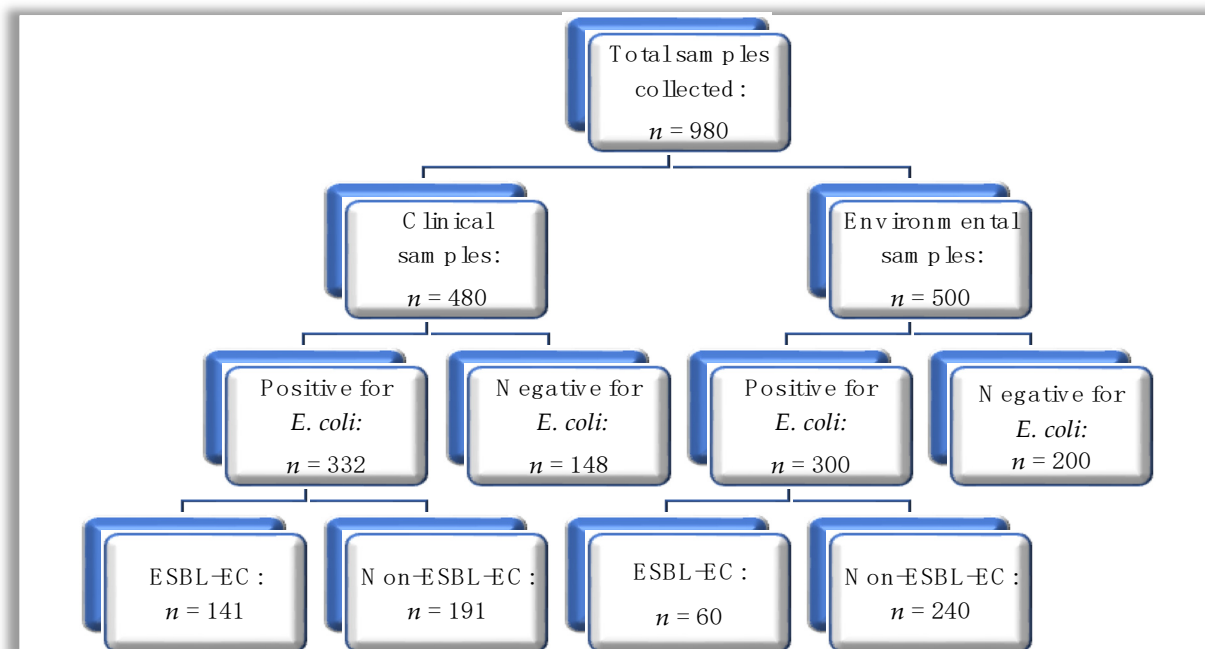


Figure 1. A hierarchical diagram showing the summary of clinical and environmental samples processed for *E. coli*; ESBL-EC: ESBL-producing *E. coli*.

The characteristics of patients and specimens corresponding to positive clinical samples ($n = 332$) are summarised in Table 1. Most of the samples were from female participants (58.7%), patients aged 0 to 14 years, urine (74.4%), and outpatient department (35.5%) (Table 1).

The origins of the $n = 300$ environmental *E. coli* specimens are summarised in Table 2. The majority of the samples were from medical equipment, meat and fruits/vegetables (Table 2).

3.2. Antibiotic Susceptibility Patterns of *E. coli* Isolated from Clinical Samples

The majority of the clinical *E. coli* isolates were highly resistant to AMP, SXT, CIP, KZ, and LEV (Table 3). However, the isolates were highly susceptible to ETP, IPM, NIT, and CN. Higher rates of resistance in clinical *E. coli* strains were shown against penicillin-derivatives, fluoroquinolones, cephalosporins, and SXT in specimens such as blood cultures, CSF, and urine; additionally, only two that were resistant to carbapenems were from pus samples (Supplementary Table S1). Most of the *E. coli* isolates with extensive resistance originated

from general adults' wards, the ICU (both adult and neonatal), surgical wards, and the pediatric unit; the isolates that were resistant to CL were from the adult medical ward ($n = 1$), the outpatient department ($n = 1$), and from paediatrics ($n = 2$); while the isolates that were resistant to carbapenems were from the outpatient department ($n = 1$) and surgical unit ($n = 1$), respectively (Supplementary Table S2).

Table 1. Descriptive characteristics of clinical samples positive for *E. coli*.

Variables	Frequency (n)	Percentages (%)
Sex		
Female	195	58.7
Male	137	41.3
Age (years)		
0–14	69	20.8
15–24	54	16.3
25–34	74	22.3
35–44	34	10.2
45–54	34	10.2
55 and above	67	20.2
Specimen Type		
Blood	12	3.6
Cerebrospinal fluid (CSF)	11	3.3
Pus	60	18.1
Stool	2	0.6
Urine	247	74.4
Origin of the sample (hospital department)		
Admission	8	2.4
General adult	52	15.7
Intensive care unit (ICU)	21	6.3
Obstetrics and Gynaecology	38	11.4
Outpatient Department (OPD)	118	35.5
Paediatrics and Neonatology	45	13.6
Surgery	50	15.1

Table 2. Descriptive characteristics of samples positive for *E. coli* from environmental sources.

Environmental Samples	Frequency (n)	Percentages (%)
Chicken and eggs	9	3.0
Fish	29	9.7
Water	35	11.7
Meat	56	18.7
Fruits and Vegetables	65	21.7
Medical Equipment	106	35.3

3.3. Antibiotic Susceptibility Patterns of *E. coli* Isolated from Environmental Samples

Isolates of *E. coli* from environmental samples were highly resistant to SXT, followed by LEV and KZ. However, the isolates were highly susceptible to ETP, IPM, CN, AMP, and CRO (Table 4). Environmental *E. coli* showing higher rates of non-susceptibility was isolated from water, fruits/vegetables and medical equipment (Supplementary Table S3).

3.4. Prevalence of ESBL-Producing, and MDR/XDR *E. coli* from Clinical and Environmental Sources

Overall, 48.3% ($n = 304/632$) of *E. coli* were MDR (clinical: 67.4% [$n = 205/304$], environmental 32.5% [$n = 99/304$]), while 13.2% ($n = 40/304$) were XDR (clinical: 32.5%

[$n = 13/40$], environmental 67.5% [$n = 27/40$]); MDR isolates were more common among *E. coli* from clinical sources ($p = 0.021$), while this association was not found for XDR isolates ($p = 0.729$). The detailed distribution of MDR and XDR *E. coli* among environmental and clinical samples is presented in Supplementary Figures S1–S3. The overall prevalence of ESBL-EC was 31.8% ($n = 201$), out of which, 70.1% ($n = 141$) were of clinical, while 29.9% ($n = 60$) were of environmental origin; ESBL-EC were significantly more common in clinical than environmental samples ($p = 0.0328$).

Table 3. Antibiotic susceptibility patterns of *E. coli* isolated from clinical samples.

Antibiotic Categories	Antibiotics	n (%)		
		Susceptible	Intermediate	Resistant
Aminoglycosides	CN	281 (84.6%)	7 (2.1%)	44 (13.3%)
Carbapenems	ETP	326 (98.2%)	4 (1.2%)	2 (0.6%)
	IPM	328 (98.8%)	2 (0.6%)	2 (0.6%)
	KZ	113 (34%)	4 (1.2%)	215 (64.8%)
Cephalosporins	CXM	117 (35.2%)	8 (2.4%)	207 (62.4%)
	CAZ	157 (47.3%)	9 (2.7%)	166 (50%)
	CRO	123 (37%)	-	209 (63%)
Penicillin-derivatives	FEP	159 (47.9%)	-	173 (52.1%)
	AMP	55 (16.6%)	-	277 (83.4%)
Sulphonamides	AMC	118 (35.5%)	98 (29.6%)	116 (34.9%)
	SXT	87 (26.2%)	-	245 (73.8%)
Furans	NIT	298 (89.8%)	18 (5.4%)	16 (4.8%)
Fluoroquinolones	CIP	113 (34%)	1 (0.3%)	218 (65.7%)
	LEV	119 (35.8%)	-	213 (64.2%)

Abbreviations: AMC-Amoxicillin/clavulanic acid; FEP-Cefepime; CN-Gentamicin; AMP-Ampicillin; IMP-Imipenem; CAZ-Ceftazidime; KZ-Cephazolin; CIP-Ciprofloxacin; LEV-Levofloxacin; NIT-Nitrofurantoin; CRO-Ceftriaxone; CXM-Cefuroxime; SXT-Sulfamethoxazole/trimethoprim; ETP-Ertapenem.

Table 4. Antibiotic susceptibility patterns of *E. coli* isolated from environmental samples.

Antibiotic Categories	Antibiotics	n (%)		
		Susceptible	Intermediate	Resistant
Penicillin	AMP	241 (80.3%)	-	59 (19.7%)
	AMC	238 (79.3%)	9 (3%)	53 (17.7%)
	KZ	215 (71.7%)	-	85 (28.3%)
	CXM	235 (78.3%)	4 (1.3%)	61 (20.4%)
Cephalosporins	CAZ	243 (81%)	-	57 (19%)
	CRO	241 (80.3%)	-	59 (19.7%)
	FEP	246 (82%)	-	54 (18%)
Carbapenems	ETP	300 (100%)	-	-
	IPM	300 (100%)	-	-
Aminoglycosides	CN	244 (81.3%)	2 (0.7%)	54 (18%)
Fluoroquinolones	CIP	225 (75%)	-	75 (25%)
	LEV	200 (66.7%)	8 (2.7%)	92 (30.6%)
Furans	NIT	237 (79%)	4 (1.3%)	59 (19.7%)
Sulphonamides	SXT	-	-	300 (100%)

The largest number of ESBL-EC were from samples of patients aged between 0 and 14 years, females (54.6%), urine (56.7%), pus (34%), outpatient department (27.7%), and medical equipment (43.4%) (Table 5). Statistical significance was found among isolates from CSF, urine, surgical ward, and meat (Table 5).

Table 5. Epidemiological characteristics of ESBL-positive and negative *E. coli* among clinical and environmental isolates.

Variables	ESBL Positive		Total (n)	OR	95%CI	p-Value
	Negative n (%)	Positive n (%)				
Clinical Samples						
Age (Years)						
0–14	33 (17.3%)	36 (25.5%)	69	-	-	-
15–24	35 (18.3%)	19 (13.5%)	54	0.498	0.239–1.034	0.0615
25–34	41 (21.5%)	33 (23.4%)	74	0.738	0.382–1.425	0.3652
35–44	20 (10.5%)	14 (9.9%)	34	0.642	0.280–1.472	0.2950
45–54	22 (11.5%)	12 (8.5%)	34	0.500	0.214–1.167	0.1088
55 and above	40 (20.9%)	27 (19.1%)	67	0.619	0.314–1.220	0.1660
Sex						
Female	118 (61.8%)	77 (54.6%)	195	-	-	-
Male	73 (38.2%)	64 (45.4%)	137	0.744	0.479–1.158	0.1901
Specimen Type						
Blood	2 (1%)	10 (7.1%)	12	-	-	-
Cerebrospinal fluid (CSF)	8 (4.2%)	3 (2.1%)	11	0.075	0.010–0.563	0.0118
Pus	12 (6.3%)	48 (34%)	60	0.800	0.154–4.144	0.7904
Urine	169 (88.5%)	80 (56.7%)	249	0.095	0.021–0.448	0.0027
Origin of the sample (hospital department)						
Admission/ Adult	40 (20.9%)	20 (14.2%)	60	-	-	-
Intensive care unit (ICU)	9 (4.7%)	12 (8.5%)	21	2.667	0.964–7.375	0.0588
Obstetrics and Gynecology	22 (11.5%)	16 (11.3%)	38	0.987	0.510–1.910	0.9698
Outpatient Department (OPD)	79 (41.4%)	39 (27.7%)	118	1.454	0.629–3.364	0.3811
Paediatrics and Neonatology	23 (12%)	22 (15.6%)	45	1.913	0.865–4.230	0.1091
Surgery	18 (9.4%)	32 (22.7%)	50	3.555	1.616–7.821	0.0061
Environmental Samples						
Fish	23 (8.1%)	6 (8.7%)	29	-	-	-
Water	22 (7.7%)	13 (18.8%)	35	2.265	0.732–7.014	0.156
Meat	62 (21.8%)	3 (4.3%)	65	0.185	0.043–0.804	0.024
Fruits and Vegetables	48 (16.8%)	17 (24.6%)	65	1.358	0.473–3.900	0.570
Medical Equipment	130 (45.6%)	30 (43.5%)	160	0.885	0.331–2.362	0.807

Note: SE = Standard error; OR = Odds ratio; B = Beta Estimate; CI = Confidence interval.

This study found that isolates from samples of individuals aged between 45 and 54 years (AOR = 0.175, CI: 0.047–0.651) were less likely to be ESBL-EC compared to those aged between 0 and 14 years. Additionally, isolates from CSF were less likely to be ESBL-EC (AOR = 0.050, CI: 0.005–0.363) compared to those from blood. Finally, isolates from urine were less likely to be ESBL-EC (AOR = 0.093, CI: 0.014–0.388) compared to those from blood (Table 6).

Most MDR *E. coli* were isolated from samples of patients aged between 0 and 14 years (24.9%), males (52.7%), urine (66.3%), outpatient department (29.3%), and fruits/vegetables (44.4%). This study revealed that MDR *E. coli* isolates were significantly associated with age, sex, specimen type, hospital department, and environmental samples (Table 7).

Table 6. Risk factors associated with ESBL-producing *E. coli*.

Variables		B (SE)	p-Value	AOR	95% CI for AOR	
					Lower	Upper
Sex	Male	−0.6270 (0.5805)	0.280	0.534	0.171	1.666
Age	15–24	−0.4757 (0.7081)	0.5017	0.621	0.155	2.489
	25–35	1.2354 (0.7572)	0.1028	3.440	0.780	15.173
	35–44	0.2458 (0.7653)	0.7481	1.279	0.285	5.730
	45–54	−1.7412 (0.6694)	0.0093	0.175	0.047	0.651
	>55	−0.9926 (0.5248)	0.0586	0.371	0.132	1.037
Sample	CSF	−2.9888 (1.0846)	0.0059	0.050	0.005	0.363
	Pus	−0.0740 (0.880)	0.9336	0.929	0.123	0.4631
	Urine	−2.3720 (0.8148)	0.0036	0.093	0.014	0.388

Note: AOR = Adjusted Odds Ratio.

Table 7. Distribution of MDR *E. coli* isolates among clinical and environmental samples.

Variables	Total (n)	MDR			Chi-Square	p-Value
		Negative n (%)	MDR n (%)	XDR n (%)		
Clinical Samples						
Age (Years)					22.900	0.004
0–14	69 (20.3%)	17 (14.9%)	51 (24.9%)	1 (7.7%)		
15–24	54 (16.3%)	25 (21.9%)	26 (12.7%)	3 (23.1%)		
25–34	74 (22.3%)	26 (22.8%)	47 (22.9%)	1 (7.7%)		
35–44	34 (10.2%)	17 (14.9%)	14 (6.8%)	3 (23.1%)		
45–54	34 (10.2%)	14 (12.3%)	18 (8.8%)	2 (15.4%)		
55 and above	67 (20.2%)	15 (13.2%)	49 (23.9%)	3 (23.1%)		
Sex					11.083	0.004
Female	137 (41.3%)	33 (28.9%)	97 (47.3%)	7 (53.8%)		
Male	195 (58.7%)	81 (71.1%)	108 (52.7%)	6 (46.2%)		
Specimen Type					41.905	<0.001
Blood	12 (3.6%)	0 (0.0%)	10 (4.9%)	2 (15.4%)		
Cerebrospinal fluid (CSF)	11 (3.3%)	0 (0.0%)	10 (4.9%)	1 (7.7%)		
Pus	60 (18.1%)	8 (7.0%)	49 (23.9%)	3 (23.1%)		
Stool	2 (0.6%)	2 (1.8%)	0 (0.0%)	0 (0.0%)		
Urine	247 (74.4%)	104 (91.2%)	136 (66.3%)	7 (53.8%)		
Hospital Department					25.464	0.005
Admission	8 (2.4%)	6 (5.3%)	2 (1.0%)	0 (0.0%)		
General adult	52 (15.7%)	13 (11.4%)	35 (17.1%)	4 (30.8%)		
Intensive care unit (ICU)	21 (6.3%)	3 (2.6%)	18 (8.8%)	0 (0.0%)		
Obstetrics and Gynecology	38 (11.4%)	15 (13.2%)	22 (10.7%)	1 (7.7%)		
Outpatient Department (OPD)	118 (35.5%)	54 (47.4%)	60 (29.3%)	4 (30.8%)		
Paediatrics and Neonatology	45 (13.6%)	12 (10.5%)	32 (15.6%)	1 (7.7%)		
Surgery	50 (15.1%)	11 (9.6%)	36 (17.6%)	3 (23.1%)		
Environmental Samples						
Fish	18 (8.8%)	7 (5.7%)	4 (14.8%)	29 (8.2%)	18.037	0.001
Water	12 (5.9%)	17 (13.9%)	6 (22.2%)	35 (9.9%)		
Meat	46 (22.4%)	16 (13.1%)	3 (11.1%)	65 (18.4%)		
Fruits and Vegetables	37 (18.0%)	16 (13.1%)	12 (44.4%)	65 (18.4%)		
Medical Equipment	92 (44.9%)	66 (54.1%)	2 (7.4%)	160 (45.2%)		

Table 8 summarises the results of the logistic regression analysis for the factors significantly associated with MDR in *E. coli* isolates: notably, clinical isolates originating from pus and male patients were significantly associated with the MDR phenotype; in the case of environmental sources, isolates from water were significantly associated with the MDR phenotype (Table 8).

Table 8. Risk factors for MDR *E. coli* isolates from both clinical and environmental sources.

Variables	p-Value	AOR	95% CI for AOR	
			Lower	Upper
Clinical				
Pus	0.001	4.6	1.9	11.3
Male sex	0.010	2.1	1.2	3.9
Environment				
Water	0.019	2.6	1.2	5.8

AOR: adjusted odds ratio; CI: confidence intervals.

4. Discussion

AMR has become a rising global burden, endangering global public health and sustainable healthcare for both developing and developed countries [6,7]. According to the O'Neill report, AMR may become the second leading cause of death by 2050, responsible for over 10 million deaths worldwide [96]. To establish effective regional, national, and global strategies to curb AMR, it is essential to investigate the prevalence of this problem and to develop empirical treatment strategies (local antibiograms). The objective of the present study was to examine ESBL-producing *E. coli* and the antimicrobial susceptibility patterns of isolates from various clinical and environmental sources to a wide range of antibiotic groups. Production of β -lactamase enzymes—especially ESBLs, owing to their rapid and successful spread across the globe, is one of the most significant mediators conferring resistance to a wide range of β -lactams in *E. coli* [43,97]. These enzymes form a large class of resistance determinants that are frequently encoded on plasmids and are a major driver in the emergence of MDR that confers resistance to penicillins and cephalosporins. Due to their considerable prevalence, clinicians are now often forced to use carbapenems (the last of the β -lactams), or other antibiotics with more disadvantageous adverse effects [98].

This present study investigated the AMR profiles and risk factors associated with ESBL-producing *E. coli* in hospital and environmental settings in Zambia. This study found that the prevalence of *E. coli* was 64.5%, of which 52.5% were from clinical sources. Additionally, 31.8% were ESBL, of which 70.1% were clinical isolates. Of the 632 isolates, 48.3% were MDR. Most clinical isolates were resistant to AMP (83.4%), SXT (73.8%), and CIP (65.7%) while most environmental isolates were resistant to SXT (100%). The risk factors associated with MDR of the tested *E. coli* isolates included pus, male sex, and water. Finally, *E. coli* isolates from samples of patients aged from 45 to 54 years and urine were less likely to be ESBL-producers.

The present study found the prevalence of *E. coli* to be 64.5%, of which 52.5% were isolated from clinical samples and 47.5% from environmental samples. Our low prevalence of *E. coli* isolated from the environment compared to the hospital setting could be due to the challenges in isolation methods of *E. coli* from environmental samples [99]. The prevalence of *E. coli* found in our study is higher than that reported in Pakistan where 23.75% of *E. coli* were isolated from urine samples [100]. A study in Poland reported a higher *E. coli* isolation rate of 78% (identified using 16S rRNA sequencing) and 82% (identified using MALDI Biotype) from river water and wastewater [100]. However, our isolation rate of *E. coli* from water samples was lower compared to that reported in Pakistan where the researchers found an isolation rate of 26.7% [100]. These differences in isolation rates could be due to technical differences and slight variability in methods. Interestingly, the isolation of *E. coli* from environmental and clinical samples demonstrates the need for a One Health approach

in the surveillance of infections and AMR [73,101]. Additionally, genomic surveillance of priority pathogens should be promoted [102].

The current study found that most clinical *E. coli* isolates were highly resistant to AMP. Our findings corroborate findings from other studies where *E. coli* isolates from clinical and environmental samples were highly resistant to penicillins such as AMP [85,103–109]. The high resistance of *E. coli* to ampicillin can be attributed to its potential to develop intrinsic resistance against penicillins. Additionally, exposure to antibiotics such as penicillins also contributes to the high resistance of *E. coli* reported in many studies [47,48,50,85,89,91,110]. Conversely, a lower resistance rate of *E. coli* to ampicillin has been reported in other studies' findings. The lower resistance can be due to the low use of antibiotics in other settings. Other studies found a high resistance of *E. coli* isolated from clinical and environmental samples to SXT [103,109,111–113]. The high resistance of *E. coli* to SXT could be due to its overuse and misuse in humans and animals [85,114–116]. However, a low resistance rate of *E. coli* to SXT was reported in a study that was conducted in Turkey among outpatients [117]. Similarly, low resistance of *E. coli* to SXT was reported in Australia due to the restriction of antibiotic use [118]. Hence, restricting the use of antibiotics may help curb AMR [119,120].

Our study also found high resistance of *E. coli* to quinolones such as CIP and LEV. The high resistance of *E. coli* to quinolones has been reported in other studies [114,121–126]. This high resistance could be due to the overuse and misuse of quinolones in human and animal health systems [114]. This is a huge problem because quinolones are largely used to treat urinary tract infections, respiratory tract infections, and other infections. However, lower resistance rates of *E. coli* to quinolones have been reported in similar settings [103,127]. This low use could be due to the effective implementation of AMS programmes in healthcare facilities. High resistance of *E. coli* to cephalosporins such as cefuroxime was found in our study. This is similar to a study that was conducted in Uganda and Nigeria, where *E. coli* isolates were 100% resistant to cefuroxime [109,125], and in South Africa where high resistance of *E. coli* to cephalothin was reported [128]. High resistance to Ceftriaxone [129,130], Ceftazidime [125], and Nalidixic acid [125] has also been reported. In Zambia, there is an overuse and misuse of antibiotics such as cephalosporins, which could be a driver of the high resistance [63,64,90,131].

The present study found that *E. coli* isolates were highly susceptible to CN, ETP, IPM, and NIT. This was observed for both clinical and environmental isolates. These findings corroborate reports from a meta-analysis where *E. coli* was highly susceptible to antibiotics such as amikacin, IPM, and NIT [103]. High susceptibility of *E. coli* to gentamicin was also reported in South Africa [128] and other similar studies [106,132]. The high susceptibility of *E. coli* isolates to IPM was also reported in other studies [129,133,134]. The high susceptibility of *E. coli* to these antibiotics suggests that they are the most effective drugs for the treatment of infections caused by *E. coli*, such as UTIs [132].

The current study found that 48.3% of *E. coli* isolates were MDR. A comparable *E. coli* MDR prevalence of 49.48% was reported in Ghana [135]. However, the finding in our study is lower than the 52% MDR reported in South Africa [128], 63.3% in Mexico [136], 68.3% in Ethiopia [43], 80% in Brazil [137], 91.4% in the United Kingdom [133], 97% in another Mexican study [138], and 98% in Bangladesh [139]. It is well known that susceptibility patterns can change over time and can differ between geographical locations [140]. Further, the high MDR among the *E. coli* isolates in hospital and environmental settings is partially due to the misuse and overuse of antibiotics both in humans and the environment [141]. It is also critical to note that MDR pathogens limit antibiotic treatment options, contributing to increased morbidity and mortality globally [141]. Therefore, the study of bacterial resistance to multiple antibiotics is essential for determining the most effective therapy for the subsequent infection, as the rise of MDR bacterial strains poses a significant threat to the health of people of all ages.

ESBL-producing *E. coli* may arise from interactions between ESBL type, strain genetic background, and selective pressures in various ecologic niches [54,142–145]. ESBL-producing *E. coli* is an important cause of both nosocomial and community-onset infections

globally [146]. Additionally, ESBL-producing *E. coli* often shows resistance to multiple drugs, which limits treatment options [56,147–149]. Commonly used treatments for severely ill patients, such as fluoroquinolones, aminoglycosides, and trimethoprim, are often associated with co-resistance, resulting in higher rates of morbidity and mortality [150].

In this present study, the prevalence of ESBL-producing *E. coli* was found to be 31.8%. A low prevalence of ESBL-producing *E. coli* was reported in other studies [58,151,152]. Consequently, a higher prevalence of ESBL-producing *E. coli* was reported in other studies, including 38% in Sudan [124], 38.07% in China [153], 42.5% in Thailand [154], 50% in Brazil [137], 55.5% in India [134], 57.7% in Ethiopia [43], 62% in Jordan [155], and 88.8% in the United Kingdom [133]. The overuse and misuse of antibiotics, especially cephalosporins and fluoroquinolones in humans, animals, and the environment, have contributed to the emergence of ESBL-producing *E. coli* [153]. The increased ESBL-producing *E. coli* indicates a greater extent of resistance to antibiotics. Consequently, increased rates of ESBL producers limit treatment options [156].

The present study found that most ESBL producers were isolated from urine (56.7%). This finding is different from a study that was conducted in India that found that most of the ESBL-producing strains were isolated from blood (66.67%) [134]. Further, our study revealed that most ESBL producers were isolated from the outpatient department, in contrast with findings from a similar study where most ESBL producers were isolated from in-patients [134]. A study in the United Arab Emirates (UAE) reported that ESBL-producing *E. coli* were responsible for 75% of UTIs in communities, indicating their high prevalence in outpatients [157]. Our study revealed that *E. coli* isolates from samples of patients aged between 45 and 54 years, CSF, and urine were less likely to be ESBL-producers. Older age was found to be a risk factor for ESBL-producing *E. coli* [158]. Similar studies have reported other risk factors of ESBL-producing *E. coli*, including previous hospitalisations, and use of urinary catheters [155].

In this study, most MDR *E. coli* isolates were isolated from samples of patients aged between 0 and 14 years, males, urine, outpatient department, and fruits/vegetables. The isolation of MDR *E. coli* from similar samples has been reported in other studies [159]. Additionally, *E. coli* isolates from males were more likely to be MDR than those from female patients. This is in line with other studies that reported similar results of males having higher odds of harbouring MDR *E. coli* isolates than females [160,161]. The impact of sex on the pattern of resistance was solely dependent on the clinical factors and location of the samples within the clinical isolates. Further, the risk of isolating MDR *E. coli* in our study was noted from pus samples. Our findings are similar to reports from previous studies which reported a larger fraction of MDR *E. coli* from pus [162,163]. However, some studies revealed that urine had a high prevalence of MDR *E. coli* [164–168]. Additionally, the present study found that water (drinking water from the community taps, boreholes, and wells) was significantly associated with MDR. This may be due to contaminated water sources within the communities or poor water quality. This is similar to a study in Zambia that reported that shallow water in peri-urban areas was significantly more contaminated with *E. coli* [169]. Our findings conform to other studies that have demonstrated the presence of high rates of MDR *E. coli* in water samples [170–175]. These findings indicate the presence of MDR *E. coli* in various samples.

We are aware of the limitations of our study: This study was conducted in the Lusaka province of Zambia; therefore, generalisation of the findings should be performed with caution. Additionally, we did not collect equal numbers of clinical and environmental samples, which may affect the comparison of results. However, we believe that the obtained results on the AMR patterns of *E. coli* isolated from clinical and environmental settings require heightened surveillance programs. Additionally, the identified risk factors, including isolates from pus, male sex, and water samples, emphasise the need for a One Health approach, which is critical to the surveillance of AMR across the human, animal, and environmental sectors.

5. Conclusions

This study reported a high prevalence rate of ESBL-producing *E. coli* among clinical and environmental samples. Most of these *E. coli* strains showed multiple AMR patterns to commonly used antibiotics, most of which were MDR and potential XDR strains. Significantly, risk factors in ESBL strains were associated with pus and blood specimens, with most isolates showing high resistance to cephalosporins, fluoroquinolones, ampicillin, and colistin, and only a few isolates being sensitive to aminoglycosides and carbapenems. The importance of these findings was the identification of ESBL-producing *E. coli* in humans, animals, and the environment. This suggests that surveillance and routine screening for MDR and ESBL-producing *E. coli* is important to control the spread of resistant strains as part of a One Health approach.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/microorganisms11081951/s1>, Table S1. Antimicrobial Susceptibility of Clinical *E. coli* categorised according to sample types; Table S2. Antimicrobial Susceptibility of Clinical *E. coli* categorised according to hospital departments; Table S3. Antimicrobial Susceptibility of Environmental *E. coli* categorised according to sample types; Figure S1. Distribution of MDR and XDR environmental *E. coli* isolates categorised according to sample types; Figure S2. Distribution of MDR and XDR clinical *E. coli* isolates categorised according to sample types; Figure S3. Distribution of MDR and XDR clinical *E. coli* isolates categorised according to hospital departments.

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References

1. Iramiot, J.S.; Kajumbula, H.; Bazira, J.; Kansime, C.; Asiimwe, B.B. Antimicrobial resistance at the human-animal interface in the Pastoralist Communities of Kasese District, South Western Uganda. *Sci. Rep.* **2020**, *10*, 14737. [[CrossRef](#)] [[PubMed](#)]
2. Wu, D.; Ding, Y.; Yao, K.; Gao, W.; Wang, Y. Antimicrobial Resistance Analysis of Clinical Escherichia coli Isolates in Neonatal Ward. *Front. Pediatr.* **2021**, *9*, 670470. [[CrossRef](#)] [[PubMed](#)]
3. Peterson, E.; Kaur, P. Antibiotic resistance mechanisms in bacteria: Relationships between resistance determinants of antibiotic producers, environmental bacteria, and clinical pathogens. *Front. Microbiol.* **2018**, *9*, 2928. [[CrossRef](#)]
4. Prestinaci, F.; Pezzotti, P.; Pantosti, A. Antimicrobial resistance: A global multifaceted phenomenon. *Pathog. Glob. Health* **2015**, *109*, 309. [[CrossRef](#)] [[PubMed](#)]

5. Woolhouse, M.; Ward, M.; Van Bunnik, B.; Farrar, J. Antimicrobial resistance in humans, livestock and the wider environment. *Philos. Trans. R. Soc. B Biol. Sci.* **2015**, *370*, 20140083. [[CrossRef](#)]
6. Murray, C.J.; Ikuta, K.S.; Sharara, F.; Swetschinski, L.; Robles Aguilar, G.; Gray, A.; Han, C.; Bisignano, C.; Rao, P.; Wool, E.; et al. Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *Lancet* **2022**, *399*, 629–655. [[CrossRef](#)]
7. Ikuta, K.S.; Swetschinski, L.R.; Robles Aguilar, G.; Sharara, F.; Mestrovic, T.; Gray, A.P.; Davis Weaver, N.; Wool, E.E.; Han, C.; Gershberg Hayoon, A.; et al. Global mortality associated with 33 bacterial pathogens in 2019: A systematic analysis for the Global Burden of Disease Study 2019. *Lancet* **2022**, *400*, 2221–2248. [[CrossRef](#)]
8. Berendonk, T.U.; Manaia, C.M.; Merlin, C.; Fatta-Kassinos, D.; Cytryn, E.; Walsh, F.; Bürgmann, H.; Sørum, H.; Norström, M.; Pons, M.-N.; et al. Tackling antibiotic resistance: The environmental framework. *Nat. Rev. Microbiol.* **2015**, *13*, 310–317. [[CrossRef](#)]
9. Chang, D.; Sharma, L.; Dela Cruz, C.S.; Zhang, D. Clinical Epidemiology, Risk Factors, and Control Strategies of Klebsiella pneumoniae Infection. *Front. Microbiol.* **2021**, *12*, 750662. [[CrossRef](#)]
10. Denissen, J.; Reyneke, B.; Waso-Reyneke, M.; Havenga, B.; Barnard, T.; Khan, S.; Khan, W. Prevalence of ESKAPE pathogens in the environment: Antibiotic resistance status, community-acquired infection and risk to human health. *Int. J. Hyg. Environ. Health* **2022**, *244*, 114006. [[CrossRef](#)]
11. Abass, A.; Ahmed, M.; Ibrahim, I.; Yahia, S. Bacterial Resistance to Antibiotics: Current Situation in Sudan. *J. Adv. Microbiol.* **2017**, *6*, 1–7. [[CrossRef](#)]
12. Khalifa, H.O.; Soliman, A.M.; Ahmed, A.M.; Shimamoto, T.; Nariya, H.; Matsumoto, T.; Shimamoto, T. High Prevalence of Antimicrobial Resistance in Gram-Negative Bacteria Isolated from Clinical Settings in Egypt: Recalling for Judicious Use of Conventional Antimicrobials in Developing Nations. *Microb. Drug Resist.* **2019**, *25*, 371–385. [[CrossRef](#)] [[PubMed](#)]
13. Nossair, M.A.; Abd El Baqy, F.A.; Rizk, M.S.Y.; Elaadli, H.; Mansour, A.M.; El-Aziz, A.H.A.; Alkhedaide, A.; Soliman, M.M.; Ramadan, H.; Shukry, M.; et al. Prevalence and Molecular Characterization of Extended-Spectrum β -Lactamases and AmpC β -lactamase-Producing Enterobacteriaceae among Human, Cattle, and Poultry. *Pathogens* **2022**, *11*, 852. [[CrossRef](#)] [[PubMed](#)]
14. Ali, M.M.M.; Ahmed, S.F.; Klena, J.D.; Mohamed, Z.K.; Moussa, T.A.A.; Ghenghesh, K.S. Enterococcal Escherichia coli in diarrheic children in Egypt: Molecular characterization and antimicrobial susceptibility. *J. Infect. Dev. Ctries.* **2014**, *8*, 589–596. [[CrossRef](#)] [[PubMed](#)]
15. Dadgostar, P. Antimicrobial resistance: Implications and costs. *Infect. Drug Resist.* **2019**, *12*, 3903–3910. [[CrossRef](#)]
16. Azab, K.S.M.; Abdel-Rahman, M.A.; El-Sheikh, H.H.; Azab, E.; Gobouri, A.A.; Farag, M.M.S. Distribution of extended-spectrum β -lactamase (EsbI)-encoding genes among multidrug-resistant gram-negative pathogens collected from three different countries. *Antibiotics* **2021**, *10*, 247. [[CrossRef](#)] [[PubMed](#)]
17. Wozniak, T.M.; Dyda, A.; Merlo, G.; Hall, L. Disease burden, associated mortality and economic impact of antimicrobial resistant infections in Australia. *Lancet Reg. Health-West. Pacific* **2022**, *27*, 100521. [[CrossRef](#)]
18. Innes, G.K.; Randad, P.R.; Korinek, A.; Davis, M.F.; Price, L.B.; So, A.D.; Heaney, C.D. External societal costs of antimicrobial resistance in humans attributable to antimicrobial use in livestock. *Annu. Rev. Public Health* **2019**, *41*, 141–157. [[CrossRef](#)]
19. Jonas, O.B.; Irwin, A.; Berthe, F.C.J.; Le Gall, F.G.; Marquez, P. Drug-resistant infections: A Threat to Our Economic Future. *World Bank Rep.* **2017**, *2*, 1–132.
20. Naylor, N.R.; Atun, R.; Zhu, N.; Kulasabanathan, K.; Silva, S.; Chatterjee, A.; Knight, G.M.; Robotham, J.V. Estimating the burden of antimicrobial resistance: A systematic literature review. *Antimicrob. Resist. Infect. Control* **2018**, *7*, 58. [[CrossRef](#)]
21. Tacconelli, E.; Pezzani, M.D. Public health burden of antimicrobial resistance in Europe. *Lancet Infect. Dis.* **2019**, *19*, 4–6. [[CrossRef](#)]
22. Mazumder, R.; Hussain, A.; Phelan, J.E.; Campino, S.; Haider, S.M.A.; Mahmud, A.; Ahmed, D.; Asadulghani, M.; Clark, T.G.; Mondal, D. Non-lactose fermenting Escherichia coli: Following in the footsteps of lactose fermenting E. coli high-risk clones. *Front. Microbiol.* **2022**, *13*, 1027494. [[CrossRef](#)]
23. Braz, V.S.; Melchior, K.; Moreira, C.G. Escherichia coli as a Multifaceted Pathogenic and Versatile Bacterium. *Front. Cell. Infect. Microbiol.* **2020**, *10*, 548492. [[CrossRef](#)] [[PubMed](#)]
24. Yaratha, G.; Perloff, S.; Changala, K. Lactose vs Non-Lactose Fermenting E. coli: Epidemiology, Clinical Outcomes, and Resistance. *Open Forum Infect. Dis.* **2017**, *4*, S589–S590. [[CrossRef](#)]
25. Shrestha, P.; Cooper, B.S.; Coast, J.; Oppong, R.; Do Thi Thuy, N.; Phodha, T.; Celhay, O.; Guerin, P.J.; Wertheim, H.; Lubell, Y. Enumerating the economic cost of antimicrobial resistance per antibiotic consumed to inform the evaluation of interventions affecting their use. *Antimicrob. Resist. Infect. Control* **2018**, *7*, 98. [[CrossRef](#)]
26. Muloi, D.; Kiiru, J.; Ward, M.J.; Hassell, J.M.; Bettridge, J.M.; Robinson, T.P.; van Bunnik, B.A.D.; Chase-Topping, M.; Robertson, G.; Pedersen, A.B.; et al. Epidemiology of antimicrobial-resistant Escherichia coli carriage in sympatric humans and livestock in a rapidly urbanizing city. *Int. J. Antimicrob. Agents* **2019**, *54*, 531–537. [[CrossRef](#)]
27. Phiri, N.; Mainda, G.; Mukuma, M.; Sinyangwe, N.N.; Banda, L.J.; Kwenda, G.; Muonga, E.M.; Flavien, B.N.; Mwansa, M.; Yamba, K.; et al. Antibiotic-resistant Salmonella species and Escherichia coli in broiler chickens from farms, abattoirs, and open markets in selected districts of Zambia. *J. Epidemiol. Res.* **2020**, *6*, 13–21. [[CrossRef](#)]
28. Muligisa-Muonga, E.; Mainda, G.; Mukuma, M.; Kwenda, G.; Hang’ombe, B.; Flavien, B.N.; Phiri, N.; Mwansa, M.; Munyeme, M.; Muma, J.B. Antimicrobial resistance of Escherichia coli and Salmonella isolated from retail broiler chicken carcasses in Zambia. *J. Epidemiol. Res.* **2021**, *6*, 35–43. [[CrossRef](#)]

29. Kabali, E.; Pandey, G.S.; Munyeme, M.; Kapila, P.; Mukubesa, A.N.; Ndebe, J.; Muma, J.B.; Mubita, C.; Muleya, W.; Muonga, E.M.; et al. Identification of *Escherichia coli* and related enterobacteriaceae and examination of their phenotypic antimicrobial resistance patterns: A pilot study at a wildlife-livestock interface in Lusaka, Zambia. *Antibiotics* **2021**, *10*, 238. [[CrossRef](#)] [[PubMed](#)]
30. Nomamiukor, B.O.; Horner, C.; Kirby, A.; Hughes, G.J. Living conditions are associated with increased antibiotic resistance in community isolates of *Escherichia coli*. *J. Antimicrob. Chemother.* **2015**, *70*, 3154–3158. [[CrossRef](#)]
31. Leski, T.A.; Taitt, C.R.; Bangura, U.; Stockelman, M.G.; Ansumana, R.; Cooper, W.H.; Stenger, D.A.; Vora, G.J. High prevalence of multidrug-resistant Enterobacteriaceae isolated from outpatient urine samples but not the hospital environment in Bo, Sierra Leone. *BMC Infect. Dis.* **2016**, *16*, 167. [[CrossRef](#)] [[PubMed](#)]
32. Chem, E.D.; Anong, D.N.; Akoachere, J.F.K.T. Prescribing patterns and associated factors of antibiotic prescription in primary health care facilities of Kumbo East and Kumbo West Health Districts, North West Cameroon. *PLoS ONE* **2018**, *13*, e0193353. [[CrossRef](#)] [[PubMed](#)]
33. Kasimanickam, V.; Kasimanickam, M.; Kasimanickam, R. Antibiotics Use in Food Animal Production: Escalation of Antimicrobial Resistance: Where Are We Now in Combating AMR? *Med. Sci.* **2021**, *9*, 14. [[CrossRef](#)] [[PubMed](#)]
34. Chang, Y.; Chusri, S.; Sangthong, R.; McNeil, E.; Hu, J.; Du, W.; Li, D.; Fan, X.; Zhou, H.; Chongsuvivatwong, V.; et al. Clinical pattern of antibiotic overuse and misuse in primary healthcare hospitals in the southwest of China. *PLoS ONE* **2018**, *14*, e0214779. [[CrossRef](#)]
35. Watts, J.E.M.; Schreier, H.J.; Lanska, L.; Hale, M.S. The rising tide of antimicrobial resistance in aquaculture: Sources, sinks and solutions. *Mar. Drugs* **2017**, *15*, 158. [[CrossRef](#)]
36. Ahmad, I.; Malak, H.A.; Abulreesh, H.H. Environmental antimicrobial resistance and its drivers: A potential threat to public health. *J. Glob. Antimicrob. Resist.* **2021**, *27*, 101–111. [[CrossRef](#)]
37. Tola, M.A.; Abera, N.A.; Gebeyehu, Y.M.; Dinku, S.F.; Tullu, K.D. High prevalence of extended-spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae* fecal carriage among children under five years in Addis Ababa, Ethiopia. *PLoS ONE* **2021**, *16*, e0258117. [[CrossRef](#)]
38. MacKinnon, M.C.; McEwen, S.A.; Pearl, D.L.; Lyytikäinen, O.; Jacobsson, G.; Collignon, P.; Gregson, D.B.; Valiquette, L.; Laupland, K.B. Increasing incidence and antimicrobial resistance in *Escherichia coli* bloodstream infections: A multinational population-based cohort study. *Antimicrob. Resist. Infect. Control* **2021**, *10*, 131. [[CrossRef](#)]
39. Tadesse, S.; Mulu, W.; Genet, C.; Kibret, M.; Belete, M.A. Emergence of High Prevalence of Extended-Spectrum Beta-Lactamase and Carbapenemase-Producing Enterobacteriaceae Species among Patients in Northwestern Ethiopia Region. *Biomed Res. Int.* **2022**, *2022*, 5727638. [[CrossRef](#)]
40. Hendriksen, R.S.; Munk, P.; Njage, P.; van Bunnik, B.; McNally, L.; Lukjancenko, O.; Röder, T.; Nieuwenhuijse, D.; Pedersen, S.K.; Kjeldgaard, J.; et al. Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage. *Nat. Commun.* **2019**, *10*, 1124. [[CrossRef](#)]
41. Allocati, N.; Masulli, M.; Alexeyev, M.F.; Di Ilio, C. *Escherichia coli* in Europe: An overview. *Int. J. Environ. Res. Public Health* **2013**, *10*, 6235–6254. [[CrossRef](#)]
42. Irek, E.O.; Amupitan, A.A.; Obadare, T.O.; Aboderin, A.O. A systematic review of healthcare-associated infections in Africa: An antimicrobial resistance perspective. *Afr. J. Lab. Med.* **2018**, *7*, a796. [[CrossRef](#)] [[PubMed](#)]
43. Teklu, D.S.; Negeri, A.A.; Legese, M.H.; Bedada, T.L.; Woldemariam, H.K.; Tullu, K.D. Extended-spectrum beta-lactamase production and multi-drug resistance among Enterobacteriaceae isolated in Addis Ababa, Ethiopia. *Antimicrob. Resist. Infect. Control* **2019**, *8*, 39. [[CrossRef](#)]
44. Park, S.; So, H.J.; Kim, M.N.; Lee, J. Initial empirical antibiotics of non-carbapenems for ESBL-producing *E. coli* and *K. pneumoniae* bacteremia in children: A retrospective medical record review. *BMC Infect. Dis.* **2022**, *22*, 866. [[CrossRef](#)] [[PubMed](#)]
45. Robert, E.; Grippa, M.; Nikiema, D.E.; Kergoat, L.; Koudougou, H.; Auda, Y.; Rochelle-Newall, E. Environmental determinants of *E. coli*, link with the diarrheal diseases, and indication of vulnerability criteria in tropical west africa (kapore, burkina faso). *PLoS Neglected Trop. Dis.* **2021**, *15*, e0009634. [[CrossRef](#)] [[PubMed](#)]
46. Mfoutou Mapanguy, C.C.; Adedaja, A.; Kecka, L.G.V.; Vouvougui, J.C.; Nguimbi, E.; Velavan, T.P.; Ntoumi, F. High prevalence of antibiotic-resistant *Escherichia coli* in Congolese students. *Int. J. Infect. Dis.* **2021**, *103*, 119–123. [[CrossRef](#)] [[PubMed](#)]
47. Silva, A.; Silva, V.; Pereira, J.E.; Maltez, L.; Igrejas, G.; Valentão, P.; Falco, V.; Poeta, P. Antimicrobial Resistance and Clonal Lineages of *Escherichia coli* from Food-Producing Animals. *Antibiotics* **2023**, *12*, 1061. [[CrossRef](#)]
48. Ramos, S.; Silva, V.; de Lurdes Enes Dapkevicius, M.; Caniça, M.; Tejedor-Junco, M.T.; Igrejas, G.; Poeta, P. *Escherichia coli* as commensal and pathogenic bacteria among food-producing animals: Health implications of extended-spectrum β -lactamase (ESBL) production. *Animals* **2020**, *10*, 2239. [[CrossRef](#)]
49. Ribeiro, J.; Silva, V.; Monteiro, A.; Vieira-Pinto, M.; Igrejas, G.; Reis, F.S.; Barros, L.; Poeta, P. Antibiotic Resistance among Gastrointestinal Bacteria in Broilers: A Review Focused on *Enterococcus* spp. and *Escherichia coli*. *Animals* **2023**, *13*, 1362. [[CrossRef](#)]
50. Bumbangi, F.N.; Llarena, A.-K.; Skjerve, E.; Hang'ombe, B.M.; Mpundu, P.; Mudenda, S.; Mutombo, P.B.; Muma, J.B. Evidence of Community-Wide Spread of Multi-Drug Resistant *Escherichia coli* in Young Children in Lusaka and Ndola Districts, Zambia. *Microorganisms* **2022**, *10*, 1684. [[CrossRef](#)]

51. Choudhuri, A.H.; Ahuja, B.; Biswas, P.S.; Uppal, R. Epidemiology of multidrug-resistant infections after inter ICU transfer in India. *Indian J. Crit. Care Med.* **2019**, *23*, 1–6. [[CrossRef](#)]
52. Ema, F.A.; Shanta, R.N.; Rahman, M.Z.; Islam, M.A.; Khatun, M.M. Isolation, identification, and antibiogram studies of *Escherichia coli* from ready-to-eat foods in Mymensingh, Bangladesh. *Vet. World* **2022**, *15*, 1497–1505. [[CrossRef](#)] [[PubMed](#)]
53. Mahmud, Z.H.; Kabir, M.H.; Ali, S.; Moniruzzaman, M.; Imran, K.M.; Nafiz, T.N.; Islam, M.S.; Hussain, A.; Hakim, S.A.I.; Worth, M.; et al. Extended-Spectrum Beta-Lactamase-Producing *Escherichia coli* in Drinking Water Samples From a Forcibly Displaced, Densely Populated Community Setting in Bangladesh. *Front. Public Health* **2020**, *8*, 228. [[CrossRef](#)] [[PubMed](#)]
54. Peirano, G.; Chen, L.; Nobrega, D.; Finn, T.J.; Kreiswirth, B.N.; DeVinney, R.; Pitout, J.D.D. Genomic Epidemiology of Global Carbapenemase-Producing *Escherichia coli*, 2015–2017. *Emerg. Infect. Dis.* **2022**, *28*, 924–931. [[CrossRef](#)] [[PubMed](#)]
55. Martischang, R.; François, P.; Cherkaoui, A.; Gaïa, N.; Renzi, G.; Agostinho, A.; Perez, M.; Graf, C.E.; Harbarth, S. Epidemiology of ESBL-producing *Escherichia coli* from repeated prevalence studies over 11 years in a long-term-care facility. *Antimicrob. Resist. Infect. Control* **2021**, *10*, 148. [[CrossRef](#)] [[PubMed](#)]
56. Castanheira, M.; Simner, P.J.; Bradford, P.A. Extended-spectrum β -lactamases: An update on their characteristics, epidemiology and detection. *JAC-Antimicrob. Resist.* **2021**, *3*, dlab092. [[CrossRef](#)]
57. Mora-Ochomogo, M.; Lohans, C.T. β -Lactam antibiotic targets and resistance mechanisms: From covalent inhibitors to substrates. *RSC Med. Chem.* **2021**, *12*, 1623–1639. [[CrossRef](#)]
58. Kayastha, K.; Dhungel, B.; Karki, S.; Adhikari, B.; Banjara, M.R.; Rijal, K.R.; Ghimire, P. Extended-Spectrum β -Lactamase-Producing *Escherichia coli* and *Klebsiella* Species in Pediatric Patients Visiting International Friendship Children’s Hospital, Kathmandu, Nepal. *Infect. Dis. Res. Treat.* **2020**, *13*, 117863372090979. [[CrossRef](#)]
59. Franciczek, R.; Sobieszczkańska, B.; Turniak, M.; Kasprzykowska, U.; Krzyzanowska, B.; Jermakow, K.; Mokracka-Latajka, G. ESBL-producing *Escherichia coli* isolated from children with acute diarrhea—Antimicrobial susceptibility, adherence patterns and phylogenetic background. *Adv. Clin. Exp. Med.* **2012**, *21*, 187–192.
60. Kumar, N.; Chatterjee, K.; Deka, S.; Shankar, R.; Kalita, D. Increased Isolation of Extended-Spectrum Beta-Lactamase-Producing *Escherichia coli* From Community-Onset Urinary Tract Infection Cases in Uttarakhand, India. *Cureus* **2021**, *13*, e13837. [[CrossRef](#)]
61. Mboya, E.A.; Sanga, L.A.; Ngocho, J.S. Irrational use of antibiotics in the moshi municipality Northern Tanzania: A cross-sectional study. *Pan Afr. Med. J.* **2018**, *31*, 165. [[CrossRef](#)]
62. Urban-Chmiel, R.; Marek, A.; Stępień-Pyśniak, D.; Wieczorek, K.; Dec, M.; Nowaczek, A.; Osek, J. Antibiotic Resistance in Bacteria—A Review. *Antibiotics* **2022**, *11*, 1079. [[CrossRef](#)]
63. Mudenda, S.; Nsofu, E.; Chisha, P.; Daka, V.; Chabalenge, B.; Mufwambi, W.; Kainga, H.; Kanaan, M.H.G.; Mfuno, R.L.; Mwaba, F.; et al. Prescribing Patterns of Antibiotics According to the WHO AWaRe Classification during the COVID-19 Pandemic at a Teaching Hospital in Lusaka, Zambia: Implications for Strengthening of Antimicrobial Stewardship Programmes. *Pharmacoepidemiology* **2023**, *2*, 42–53. [[CrossRef](#)]
64. Mudenda, S.; Chomba, M.; Chabalenge, B.; Hikaambo, C.N.; Banda, M.; Daka, V.; Zulu, A.; Mukesela, A.; Kasonde, M.; Lukonde, P.; et al. Antibiotic Prescribing Patterns in Adult Patients According to the WHO AWaRe Classification: A Multi-Facility Cross-Sectional Study in Primary Healthcare Hospitals in Lusaka, Zambia. *Pharmacol. Pharm.* **2022**, *13*, 379–392. [[CrossRef](#)]
65. Bush, K.; Bradford, P.A. β -lactams and β -lactamase inhibitors: An overview. *Cold Spring Harb. Perspect. Med.* **2016**, *6*, a025247. [[CrossRef](#)] [[PubMed](#)]
66. Kasanga, M.; Mudenda, S.; Siyanga, M.; Chileshe, M.; Mwiikisa, M.J.; Kasanga, M.; Solochi, B.B.; Gondwe, T.; Kantenga, T.; L Shimbema, A.; et al. Antimicrobial susceptibility patterns of bacteria that commonly cause bacteremia at a tertiary hospital in Zambia. *Future Microbiol.* **2020**, *15*, 1735–1745. [[CrossRef](#)] [[PubMed](#)]
67. Kasanga, M.; Mukosha, R.; Kasanga, M.; Siyanga, M.; Mudenda, S.; Solochi, B.B.; Chileshe, M.; Mwiikisa, M.J.; Gondwe, T.; Kantenga, T.; et al. Antimicrobial resistance patterns of bacterial pathogens their distribution in university teaching hospitals in Zambia. *Future Microbiol.* **2020**, *16*, 811–824. [[CrossRef](#)]
68. Badulla, W.F.S.; Alshakka, M.; Mohamed Ibrahim, M.I. Antimicrobial Resistance Profiles for Different Isolates in Aden, Yemen: A Cross-Sectional Study in a Resource-Poor Setting. *Biomed Res. Int.* **2020**, *2020*, 1810290. [[CrossRef](#)]
69. Kasanga, M.; Chileshe, M.; Mudenda, S.; Mukosha, R.; Kasanga, M.; Daka, V.; Mudenda, T.; Chisembele, M.; Musuku, J.; Solochi, B.B.; et al. Antibiotic Prescribing Patterns and Prevalence of Surgical Site Infections in Caesarean Section Deliveries at Two Tertiary Hospitals in Lusaka, Zambia. *Pharmacol. Pharm.* **2022**, *13*, 313–330. [[CrossRef](#)]
70. Seman, A.; Mihret, A.; Sebre, S.; Awoke, T.; Yitayew, B.; Aseffa, A.; Asrat, D.; Abebe, T.; Yeshitela, B. Prevalence and Molecular Characterization of Extended Spectrum β -Lactamase and Carbapenemase-Producing Enterobacteriaceae Isolates from Bloodstream Infection Suspected Patients in Addis Ababa, Ethiopia. *Infect. Drug Resist.* **2022**, *15*, 1367–1382. [[CrossRef](#)]
71. Hassell, J.M.; Ward, M.J.; Muloi, D.; Bettridge, J.M.; Robinson, T.P.; Kariuki, S.; Ogendo, A.; Kiiru, J.; Imboma, T.; Kang’ethe, E.K.; et al. Clinically relevant antimicrobial resistance at the wildlife–livestock–human interface in Nairobi: An epidemiological study. *Lancet Planet. Health* **2019**, *3*, e259–e269. [[CrossRef](#)]
72. Enany, M.E.; Algammal, A.M.; Nasef, S.A.; Abo-Eillil, S.A.M.; Bin-Jumah, M.; Taha, A.E.; Allam, A.A. The occurrence of the multidrug resistance (MDR) and the prevalence of virulence genes and QACs resistance genes in *E. coli* isolated from environmental and avian sources. *AMB Express* **2019**, *9*, 192. [[CrossRef](#)] [[PubMed](#)]
73. Guardabassi, L.; Butaye, P.; Dockrell, D.H.; Fitzgerald, J.R.; Kuijper, E.J. One Health: A multifaceted concept combining diverse approaches to prevent and control antimicrobial resistance. *Clin. Microbiol. Infect.* **2020**, *26*, 1604–1605. [[CrossRef](#)] [[PubMed](#)]

74. World Health Organization. *Global Action Plan on Antimicrobial Resistance*; World Health Organization: Geneva, Switzerland, 2015; pp. 1–28.
75. Rhouma, M.; Soufi, L.; Cenatus, S.; Archambault, M.; Butaye, P. Current Insights Regarding the Role of Farm Animals in the Spread of Antimicrobial Resistance from a One Health Perspective. *Vet. Sci.* **2022**, *9*, 480. [CrossRef]
76. Meier, H.; Spinner, K.; Crump, L.; Kuenzli, E.; Schuepbach, G.; Zinsstag, J. State of Knowledge on the Acquisition, Diversity, Interspecies Attribution and Spread of Antimicrobial Resistance between Humans, Animals and the Environment: A Systematic Review. *Antibiotics* **2023**, *12*, 73. [CrossRef] [PubMed]
77. Saleem, Z.; Godman, B.; Cook, A.; Khan, M.A.; Campbell, S.M.; Seaton, R.A.; Siachalinga, L.; Haseeb, A.; Amir, A.; Kurdi, A.; et al. Ongoing Efforts to Improve Antimicrobial Utilization in Hospitals among African Countries and Implications for the Future. *Antibiotics* **2022**, *11*, 1824. [CrossRef]
78. Siachalinga, L.; Mufwambi, W.; Lee, I.H. Impact of antimicrobial stewardship interventions to improve antibiotic prescribing for hospital inpatients in Africa: A systematic review and meta-analysis. *J. Hosp. Infect.* **2022**, *129*, 124–143. [CrossRef]
79. Dyar, O.J.; Huttner, B.; Schouten, J.; Pulcini, C. What is antimicrobial stewardship? *Clin. Microbiol. Infect.* **2017**, *23*, 793–798. [CrossRef]
80. Lammie, S.L.; Hughes, J.M. Antimicrobial Resistance, Food Safety, and One Health: The Need for Convergence. *Annu. Rev. Food Sci. Technol.* **2016**, *7*, 287–312. [CrossRef]
81. Godman, B.; Ekwuenu, A.; Haque, M.; Malande, O.O.; Schellack, N.; Kumar, S.; Saleem, Z.; Sneddon, J.; Hoxha, I.; Islam, S.; et al. Strategies to improve antimicrobial utilization with a special focus on developing countries. *Life* **2021**, *11*, 528. [CrossRef]
82. Republic of Zambia NAP on AMR Multi-Sectoral National Action Plan on Antimicrobial Resistance. Available online: <https://www.afro.who.int/publications/multi-sectoral-national-action-plan-antimicrobial-resistance-2017-2027> (accessed on 24 July 2022).
83. Kapona, O. Zambia successfully launches the first multi-sectoral national action plan on antimicrobial resistance (AMR). *Health Press Zamb. Bull* **2017**, *1*, 5–7.
84. Mwikuma, G.; Kainga, H.; Kallu, S.A.; Nakajima, C.; Suzuki, Y.; Hang’ombe, B.M. Determination of the Prevalence and Antimicrobial Resistance of *Enterococcus Faecalis* and *Enterococcus Faecium* Associated with Poultry in Four Districts in Zambia. *Antibiotics* **2023**, *12*, 657. [CrossRef] [PubMed]
85. Mudenda, S.; Malama, S.; Munyeme, M.; Matafwali, S.K.; Kapila, P.; Katemangwe, P.; Mainda, G.; Mukubesa, A.N.; Hadunka, M.A.; Muma, J.B. Antimicrobial Resistance Profiles of *Escherichia Coli* Isolated from Laying Hens in Zambia: Implications and Significance on One Health. *JAC-Antimicrob. Resist.* **2023**, *5*, dlad060. [CrossRef]
86. Mudenda, S.; Hankombo, M.; Saleem, Z.; Sadiq, M.J.; Banda, M.; Munkombwe, D.; Mwila, C.; Kasanga, M.; Zulu, A.C.; Hangoma, J.M.; et al. Knowledge, Attitude, and Practices of Community Pharmacists on Antibiotic Resistance and Antimicrobial Stewardship in Lusaka, Zambia. *J. Biomed. Res. Environ. Sci.* **2021**, *2*, 1005–1014. [CrossRef]
87. Tembo, N.; Mudenda, S.; Banda, M.; Chileshe, M.; Matafwali, S. Knowledge, Attitudes and Practices on Antimicrobial Resistance among Pharmacy Personnel and Nurses at a Tertiary Hospital in Ndola, Zambia: Implications for Antimicrobial Stewardship Programmes. *JAC-Antimicrob. Resist.* **2022**, *4*, dlac107. [CrossRef]
88. Mudenda, S.; Malama, S.; Munyeme, M.; Hang’ombe, B.M.; Mainda, G.; Kapona, O.; Mukosha, M.; Yamba, K.; Bumbangi, F.N.; Mfuno, R.L.; et al. Awareness of Antimicrobial Resistance and Associated Factors among Layer Poultry Farmers in Zambia: Implications for Surveillance and Antimicrobial Stewardship Programs. *Antibiotics* **2022**, *11*, 383. [CrossRef]
89. Mudenda, S.; Matafwali, S.K.; Malama, S.; Munyeme, M.; Yamba, K.; Katemangwe, P.; Siluchali, G.; Mainda, G.; Mukuma, M.; Bumbangi, F.N.; et al. Prevalence and Antimicrobial Resistance Patterns of *Enterococcus* Species Isolated from Laying Hens in Lusaka and Copperbelt Provinces of Zambia: A Call for AMR Surveillance in the Poultry Sector. *JAC-Antimicrob. Resist.* **2022**, *4*, dlac126. [CrossRef]
90. Mudenda, S.; Mukosha, M.; Godman, B.; Fadare, J.; Malama, S.; Munyeme, M.; Hikaambo, C.N.; Kalungia, A.C.; Hamachila, A.; Kainga, H.; et al. Knowledge, Attitudes and Practices of Community Pharmacy Professionals on Poultry Antimicrobial Dispensing, Use and Resistance in Zambia: Implications on Antibiotic Stewardship and WHO AWaRe Classification of Antibiotics. *Antibiotics* **2022**, *11*, 1210. [CrossRef]
91. Yamba, K.; Lukwesa-Musyani, C.; Samutela, M.T.; Kapesa, C.; Hang’ombe, M.B.; Mpabalwani, E.; Hachaambwa, L.; Fwoloshi, S.; Chanda, R.; Mpundu, M.; et al. Phenotypic and Genotypic Antibiotic Susceptibility Profiles of Gram-Negative Bacteria Isolated from Bloodstream Infections at a Referral Hospital, Lusaka, Zambia. *PLOS Glob. Public Health* **2023**, *3*, e0001414. [CrossRef]
92. ZamStats Total Number of Households by Province, Zambia 2022. Available online: <https://www.zamstats.gov.zm/total-number-of-household-by-province-zambia-2022/> (accessed on 24 January 2023).
93. ZamStats Population Size by Province, Zambia 2010 and 2022. Available online: <https://www.zamstats.gov.zm/population-size-by-province-zambia-2010-and-2022/#> (accessed on 24 January 2023).
94. Clinical and Laboratory Standards Institute Performance Standards for Antimicrobial Susceptibility Testing, Thirtieth Edition: M100. Available online: <https://unitedvrg.com/2021/05/20/m100-performance-standards-for-antimicrobial-susceptibility-testing-30th-edition-2020-pdf/> (accessed on 26 August 2021).
95. Magiorakos, A.P.; Srinivasan, A.; Carey, R.B.; Carmeli, Y.; Falagas, M.E.; Giske, C.G.; Harbarth, S.; Hindler, J.F.; Kahlmeter, G.; Olsson-Liljequist, B.; et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clin. Microbiol. Infect.* **2012**, *18*, 268–281. [CrossRef]

96. O'Neill, J. Tackling Drug-Resistant Infections Globally: Final Report and Recommendations. The Review on Antimicrobial Resistance. 2016, pp. 1–84. Available online: https://amr-review.org/sites/default/files/160518_Final%20paper_with%20cover.pdf (accessed on 27 May 2023).
97. Bush, K.; Bradford, P.A. Epidemiology of β -lactamase-producing pathogens. *Clin. Microbiol. Rev.* **2020**, *33*, e00047-19. [[CrossRef](#)] [[PubMed](#)]
98. Ullah, W.; Ali, S. Antimicrobial Resistance in *Escherichia coli*. In *Escherichia coli—Old and New Insights*; IntechOpen: London, UK, 2023; ISBN 978-1-83969-870-5.
99. Osińska, A.; Korzeniewska, E.; Korzeniowska-Kowal, A.; Wzorek, A.; Harnisz, M.; Jachimowicz, P.; Buta-Hubeny, M.; Zieliński, W. The challenges in the identification of *Escherichia coli* from environmental samples and their genetic characterization. *Environ. Sci. Pollut. Res.* **2023**, *30*, 11572–11583. [[CrossRef](#)] [[PubMed](#)]
100. Akbar, A.; Naeem, W.; Liaqat, F.; Sadiq, M.B.; Shafee, M.; Gul, Z.; Khan, S.A.; Mengal, H.; Chein, S.H.; Qasim, S.; et al. Hospital Acquired Pathogenic *Escherichia coli* from Clinical and Hospital Water Samples of Quetta Balochistan. *J. Trop. Med.* **2022**, *2022*, 6495044. [[CrossRef](#)]
101. Velazquez-Meza, M.E.; Galarde-López, M.; Carrillo-Quiróz, B.; Alpuche-Aranda, C.M. Antimicrobial resistance: One Health approach. *Vet. World* **2022**, *15*, 743–749. [[CrossRef](#)]
102. Roberts, L.W.; Hoi, L.T.; Khokhar, F.A.; Hoa, N.T.; Van Giang, T.; Bui, C.; Ninh, T.H.; Co, D.X.; Binh, N.G.; Long, H.B.; et al. Genomic characterisation of multidrug-resistant *Escherichia coli*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii* in two intensive care units in Hanoi, Viet Nam: A prospective observational cohort study. *Lancet Microbe* **2022**, *3*, e857–e866. [[CrossRef](#)] [[PubMed](#)]
103. Reza Mortazavi-Tabatabaei, S.; Ghaderkhani, J.; Nazari, A.; Sayehmiri, K.; Sayehmiri, F.; Pakzad, I. Pattern of antibacterial resistance in urinary tract infections: A systematic review and meta-analysis. *Int. J. Prev. Med.* **2019**, *10*, 169. [[CrossRef](#)]
104. Dela Peña, L.B.R.O.; Nacario, M.A.G.; Bolo, N.R.; Rivera, W.L. Multiple Antibiotic Resistance in *Escherichia coli* Isolates from Fecal and Water Sources in Laguna Lake, Philippines. *Water* **2022**, *14*, 1517. [[CrossRef](#)]
105. Salvador-Membreve, D.M.; Rivera, W.L. Predominance of *bla*TEM and *tetA* genes in antibiotic-resistant *Escherichia coli* isolates from laguna lake, Philippines. *J. Water Sanit. Hyg. Dev.* **2021**, *11*, 814–823. [[CrossRef](#)]
106. Naqid, I.A.; Balatay, A.A.; Hussein, N.R.; Saeed, K.A.; Ahmed, H.A.; Yousif, S.H. Antibiotic Susceptibility Pattern of *Escherichia coli* Isolated from Various Clinical Samples in Duhok City, Kurdistan Region of Iraq. *Int. J. Infect.* **2020**, *7*, e103740. [[CrossRef](#)]
107. Ramatla, T.; Ramaili, T.; Lekota, K.E.; Ndou, R.; Mphuti, N.; Bezuidenhout, C.; Thekisoe, O. A systematic review and meta-analysis on prevalence and antimicrobial resistance profile of *Escherichia coli* isolated from water in africa (2000–2021). *Heliyon* **2023**, *9*, e16123. [[CrossRef](#)]
108. Pormohammad, A.; Nasiri, M.J.; Azimi, T. Prevalence of antibiotic resistance in *Escherichia coli* strains simultaneously isolated from humans, animals, food, and the environment: A systematic review and meta-analysis. *Infect. Drug Resist.* **2019**, *12*, 1181–1197. [[CrossRef](#)]
109. Agbagwa, O.E.; Okorafor, O.N.; Horsfall, S.J. Multidrug Resistant Pattern and Plasmid Detection of *Escherichia coli* from Various Sources within the University of Port Harcourt. *Open J. Med. Microbiol.* **2022**, *12*, 11–23. [[CrossRef](#)]
110. Chiyangi, H.; Muma, B.; Malama, S.; Manyahi, J.; Abade, A.; Kwenda, G.; Matee, M. Identification and antimicrobial resistance patterns of bacterial enteropathogens from children aged 0–59 months at the University Teaching Hospital, Lusaka, Zambia: A prospective cross-sectional study. *BMC Infect. Dis.* **2017**, *17*, 117. [[CrossRef](#)] [[PubMed](#)]
111. Li, H.; Liu, Y.; Yang, L.; Wu, X.; Shao, B. Prevalence of *Escherichia coli* and Antibiotic Resistance in Animal-Derived Food Samples—Six Districts, Beijing, China, 2020. *China CDC Wkly.* **2021**, *3*, 999–1004. [[CrossRef](#)] [[PubMed](#)]
112. Park, J.H.; Kim, Y.J.; Binn-Kim; Seo, K.H. Spread of multidrug-resistant *Escherichia coli* harboring integron via swine farm waste water treatment plant. *Ecotoxicol. Environ. Saf.* **2018**, *149*, 36–42. [[CrossRef](#)] [[PubMed](#)]
113. Sula, I.; Alreshidi, M.A.; Alnasr, N.; Hassaneen, A.M.; Saquib, N. Urinary Tract Infections in the Kingdom of Saudi Arabia, a Review. *Microorganisms* **2023**, *11*, 952. [[CrossRef](#)]
114. Aworh, M.K.; Kwaga, J.K.P.; Hendriksen, R.S.; Okolocha, E.C.; Harrell, E.; Thakur, S. Quinolone-resistant *Escherichia coli* at the interface between humans, poultry and their shared environment- a potential public health risk. *One Heal. Outlook* **2023**, *5*, 2. [[CrossRef](#)]
115. Almagor, J.; Temkin, E.; Benenson, I.; Fallach, N.; Carmeli, Y. The impact of antibiotic use on transmission of resistant bacteria in hospitals: Insights from an agent-based model. *PLoS ONE* **2018**, *13*, e0197111. [[CrossRef](#)]
116. Mwansa, M.; Mukuma, M.; Mulilo, E.; Kwenda, G.; Mainda, G.; Yamba, K.; Bumbangi, F.N.; Muligisa-Muonga, E.; Phiri, N.; Silwamba, I.; et al. Determination of antimicrobial resistance patterns of *Escherichia coli* isolates from farm workers in broiler poultry production and assessment of antibiotic resistance awareness levels among poultry farmers in Lusaka, Zambia. *Front. Public Health* **2023**, *10*, 998860. [[CrossRef](#)]
117. Öztürk, R.; Tazegul, G. Bacteria Causing Community-Acquired Urinary Tract Infections and Their Antibiotic Susceptibility Patterns in Outpatients Attending at a State Hospital in Turkey. *Cureus* **2021**, *13*, e17753. [[CrossRef](#)]
118. Abraham, R.; Allison, H.S.; Lee, T.; Pavic, A.; Chia, R.; Hewson, K.; Lee, Z.Z.; Hampson, D.J.; Jordan, D.; Abraham, S. A national study confirms that *Escherichia coli* from Australian commercial layer hens remain susceptible to critically important antimicrobials. *PLoS ONE* **2023**, *18*, e0281848. [[CrossRef](#)]

119. Schuts, E.C.; Boyd, A.; Muller, A.E.; Mouton, J.W.; Prins, J.M. The effect of antibiotic restriction programs on prevalence of antimicrobial resistance: A systematic review and meta-analysis. *Open Forum Infect. Dis.* **2021**, *8*, ofab070. [[CrossRef](#)] [[PubMed](#)]
120. Tang, K.L.; Caffrey, N.P.; Nóbrega, D.B.; Cork, S.C.; Ronksley, P.E.; Barkema, H.W.; Polachek, A.J.; Ganshorn, H.; Sharma, N.; Kellner, J.D.; et al. Restricting the use of antibiotics in food-producing animals and its associations with antibiotic resistance in food-producing animals and human beings: A systematic review and meta-analysis. *Lancet Planet. Health* **2017**, *1*, e316–e327. [[CrossRef](#)]
121. Bhatnagar, K.; Wong, A. The mutational landscape of quinolone resistance in *Escherichia coli*. *PLoS ONE* **2019**, *14*, e0224650. [[CrossRef](#)]
122. Röderova, M.; Halova, D.; Papousek, I.; Dolejska, M.; Masarikova, M.; Hanulik, V.; Pudova, V.; Broz, P.; Htoutou-Sedlakova, M.; Sauer, P.; et al. Characteristics of quinolone resistance in *Escherichia coli* isolates from humans, animals, and the environment in the Czech Republic. *Front. Microbiol.* **2017**, *7*, 2147. [[CrossRef](#)] [[PubMed](#)]
123. Slettemeås, J.S.; Sunde, M.; Ulstad, C.R.; Norström, M.; Wester, A.L.; Urdahl, A.M. Occurrence and characterization of quinolone resistant *Escherichia coli* from Norwegian Turkey meat and complete sequence of an IncX1 plasmid encoding qnrS1. *PLoS ONE* **2019**, *14*, e0212936. [[CrossRef](#)] [[PubMed](#)]
124. Dirar, M.H.; Bilal, N.E.; Ibrahim, M.E.; Hamid, M.E. Prevalence of extended-spectrum β -lactamase (Esb1) and molecular detection of bla TEM, bla SHV and bla CTX-M genotypes among enterobacteriaceae isolates from patients in khartoum, sudan. *Pan Afr. Med. J.* **2020**, *37*, 213. [[CrossRef](#)]
125. Odongo, L.; Ssemambo, R.; Kungu, J.M. Prevalence of *Escherichia Coli* and Its Antimicrobial Susceptibility Profiles among Patients with UTI at Mulago Hospital, Kampala, Uganda. *Interdiscip. Perspect. Infect. Dis.* **2020**, *2020*, 8042540. [[CrossRef](#)]
126. Bhowmik, A.; Shah, S.T.; Goswami, S.; Sirajee, A.S.; Ahsan, S. Predominance of Multidrug-Resistant *Escherichia coli* of Environmental Phylotype in Different Environments of Dhaka, Bangladesh. *Trop. Med. Infect. Dis.* **2023**, *8*, 226. [[CrossRef](#)]
127. Gottesman, B.S.; Carmeli, Y.; Shitrit, P.; Chowers, M. Impact of quinolone restriction on resistance patterns of *Escherichia coli* isolated from urine by culture in a community setting. *Clin. Infect. Dis.* **2009**, *49*, 869–875. [[CrossRef](#)]
128. Malema, M.S.; Abia, A.L.K.; Tandlich, R.; Zuma, B.; Kahinda, J.M.M.; Ubomba-Jaswa, E. Antibiotic-resistant pathogenic *Escherichia coli* isolated from rooftop rainwater-harvesting tanks in the Eastern Cape, South Africa. *Int. J. Environ. Res. Public Health* **2018**, *15*, 892. [[CrossRef](#)] [[PubMed](#)]
129. Jalil, M.B.; Al Atbee, M.Y.N. The prevalence of multiple drug resistance *Escherichia coli* and *Klebsiella pneumoniae* isolated from patients with urinary tract infections. *J. Clin. Lab. Anal.* **2022**, *36*, e24619. [[CrossRef](#)] [[PubMed](#)]
130. Gelaw, L.Y.; Bitew, A.A.; Gashey, E.M.; Ademe, M.N. Ceftriaxone resistance among patients at GAMBY teaching general hospital. *Sci. Rep.* **2022**, *12*, 12000. [[CrossRef](#)]
131. Chilawa, S.; Mudenda, S.; Daka, V.; Chileshe, M.; Matafwali, S.; Chabalenge, B.; Mpundu, P.; Mufwambi, W.; Mohamed, S.; Mfuno, R.L.; et al. Knowledge, Attitudes, and Practices of Poultry Farmers on Antimicrobial Use and Resistance in Kitwe, Zambia: Implications on Antimicrobial Stewardship. *Open J. Anim. Sci.* **2023**, *13*, 60–81. [[CrossRef](#)]
132. Joya, M.; Aalemi, A.K.; Baryali, A.T. Prevalence and Antibiotic Susceptibility of the Common Bacterial Uropathogen Among UTI Patients in French Medical Institute for Children. *Infect. Drug Resist.* **2022**, *15*, 4291–4297. [[CrossRef](#)] [[PubMed](#)]
133. Ibrahim, D.R.; Dodd, C.E.R.; Stekel, D.J.; Meshioye, R.T.; Diggle, M.; Lister, M.; Hobman, J.L. Multidrug-Resistant ESBL-Producing *E. coli* in Clinical Samples from the UK. *Antibiotics* **2023**, *12*, 169. [[CrossRef](#)]
134. Kumar, D.; Singh, A.K.; Ali, M.R.; Chander, Y. Antimicrobial Susceptibility Profile of Extended Spectrum β -Lactamase (ESBL) Producing *Escherichia coli* from Various Clinical Samples. *Infect. Dis. Res. Treat.* **2014**, *7*, IDRT-S13820. [[CrossRef](#)]
135. Odonkor, S.T.; Addo, K.K. Prevalence of Multidrug-Resistant *Escherichia coli* Isolated from Drinking Water Sources. *Int. J. Microbiol.* **2018**, *2018*, 7204013. [[CrossRef](#)]
136. Ramírez-Castillo, F.Y.; Moreno-Flores, A.C.; Avelar-González, F.J.; Márquez-Díaz, F.; Harel, J.; Guerrero-Barrera, A.L. An evaluation of multidrug-resistant *Escherichia coli* isolates in urinary tract infections from Aguascalientes, Mexico: Cross-sectional study. *Ann. Clin. Microbiol. Antimicrob.* **2018**, *17*, 34. [[CrossRef](#)] [[PubMed](#)]
137. Gonçalves, V.D.; Meirelles-Pereira, F.; Cataldo, M.; Fonseca, B.D.O.; Nogueira, B.A.; Olivella, J.G.B.; Esteves, F.D.A.; Mattos-Guaraldi, A.L.; de Andrade, A.F.B.; Bello, A.R.; et al. Detection of multidrug-resistant Enterobacteria isolated from river waters flowing to Guanabara Bay (Rio de Janeiro, Brazil) and from clinical samples of hospital origin. *Biomedica* **2019**, *39*, 135–149. [[CrossRef](#)]
138. Paniagua-Contreras, G.L.; Monroy-Pérez, E.; Rodríguez-Moctezuma, J.R.; Domínguez-Trejo, P.; Vaca-Paniagua, F.; Vaca, S. Virulence factors, antibiotic resistance phenotypes and O-serogroups of *Escherichia coli* strains isolated from community-acquired urinary tract infection patients in Mexico. *J. Microbiol. Immunol. Infect.* **2017**, *50*, 478–485. [[CrossRef](#)] [[PubMed](#)]
139. Jain, P.; Bepari, A.K.; Sen, P.K.; Rafe, T.; Imtiaz, R.; Hossain, M.; Reza, H.M. High prevalence of multiple antibiotic resistance in clinical *E. coli* isolates from Bangladesh and prediction of molecular resistance determinants using WGS of an XDR isolate. *Sci. Rep.* **2021**, *11*, 22859. [[CrossRef](#)] [[PubMed](#)]
140. Ali, I.; Rfaque, Z.; Ahmed, S.; Malik, S.; Dasti, J.I. Prevalence of multi-drug resistant uropathogenic *Escherichia coli* in Potohar region of Pakistan. *Asian Pac. J. Trop. Biomed.* **2016**, *6*, 60–66. [[CrossRef](#)]
141. Fani, R.; Dioli, C.; Pappa, O.; Siatravani, E.; Bratakou, S.; Tatsiopoulos, A.; Giakkoupi, P.; Miriagou, V.; Beloukas, A. Molecular Characterization and Prevalence of Antimicrobial-Resistant *Escherichia coli* Isolates Derived from Clinical Specimens and Environmental Habitats. *Microorganisms* **2023**, *11*, 1399. [[CrossRef](#)]

142. Shaikh, S.; Fatima, J.; Shakil, S.; Rizvi, S.M.D.; Kamal, M.A. Antibiotic resistance and extended spectrum beta-lactamases: Types, epidemiology and treatment. *Saudi J. Biol. Sci.* **2015**, *22*, 90–101. [[CrossRef](#)]
143. Brolund, A. Overview of ESBL-producing Enterobacteriaceae from a Nordic perspective. *Infect. Ecol. Epidemiol.* **2014**, *4*, 24555. [[CrossRef](#)]
144. Erb, S.; D’Mello-Guyett, L.; Malebo, H.M.; Njee, R.M.; Matwewe, F.; Ensink, J.; Hinic, V.; Widmer, A.; Frei, R. High prevalence of ESBL-Producing *E. coli* in private and shared latrines in an informal urban settlement in Dar es Salaam, Tanzania. *Antimicrob. Resist. Infect. Control* **2018**, *7*, 3. [[CrossRef](#)]
145. Peirano, G.; Pitout, J.D.D. Molecular epidemiology of Escherichia coli producing CTX-M β -lactamases: The worldwide emergence of clone ST131 O25:H4. *Int. J. Antimicrob. Agents* **2010**, *35*, 316–321. [[CrossRef](#)]
146. Quan, J.; Dai, H.; Liao, W.; Zhao, D.; Shi, Q.; Zhang, L.; Shi, K.; Akova, M.; Yu, Y. Etiology and prevalence of ESBLs in adult community-onset urinary tract infections in East China: A prospective multicenter study. *J. Infect.* **2021**, *83*, 175–181. [[CrossRef](#)]
147. Yadav, K.K.; Adhikari, N.; Khadka, R.; Pant, A.D.; Shah, B. Multidrug-resistant Enterobacteriaceae and extended spectrum β -lactamase producing Escherichia coli: A cross-sectional study in National Kidney Center, Nepal. *Antimicrob. Resist. Infect. Control* **2015**, *4*, 42. [[CrossRef](#)]
148. Mukherjee, M.; Basu, S.; Mukherjee, S.K.M.; Majumder, M. Multidrug-resistance and extended spectrum beta-lactamase production in uropathogenic *E. coli* which were isolated from hospitalized patients in Kolkata, India. *J. Clin. Diagn. Res.* **2013**, *7*, 449–453. [[CrossRef](#)]
149. Tian, G.B.; Wang, H.N.; Zhang, A.Y.; Zhang, Y.; Fan, W.Q.; Xu, C.W.; Zeng, B.; Guan, Z.B.; Zou, L.K. Detection of clinically important β -lactamases in commensal Escherichia coli of human and swine origin in western China. *J. Med. Microbiol.* **2012**, *61*, 233–238. [[CrossRef](#)] [[PubMed](#)]
150. Serwecińska, L. Antimicrobials and antibiotic-resistant bacteria: A risk to the environment and to public health. *Water* **2020**, *12*, 3313. [[CrossRef](#)]
151. Tigabie, M.; Biset, S.; Belachew, T.; Amare, A.; Moges, F. Multidrug-resistant and extended-spectrum beta-lactamase-producing Enterobacteriaceae isolated from chicken droppings in poultry farms at Gondar City, Northwest Ethiopia. *PLoS ONE* **2023**, *18*, e0287043. [[CrossRef](#)]
152. Ludden, C.; Coll, F.; Gouliouris, T.; Restif, O.; Blane, B.; Blackwell, G.A.; Kumar, N.; Naydenova, P.; Crawley, C.; Brown, N.M.; et al. Defining nosocomial transmission of Escherichia coli and antimicrobial resistance genes: A genomic surveillance study. *Lancet Microbe* **2021**, *2*, e472–e480. [[CrossRef](#)] [[PubMed](#)]
153. Jia, P.; Zhu, Y.; Li, X.; Kudinha, T.; Yang, Y.; Zhang, G.; Zhang, J.; Xu, Y.; Yang, Q. High Prevalence of Extended-Spectrum Beta-Lactamases in Escherichia coli Strains Collected From Strictly Defined Community-Acquired Urinary Tract Infections in Adults in China: A Multicenter Prospective Clinical Microbiological and Molecular Study. *Front. Microbiol.* **2021**, *12*, 663033. [[CrossRef](#)]
154. Siriphap, A.; Kittit, T.; Khuekankaew, A.; Boonlao, C.; Thephinlap, C.; Thepmalee, C.; Suwannasom, N.; Khoothiam, K. High prevalence of extended-spectrum beta-lactamase-producing Escherichia coli and Klebsiella pneumoniae isolates: A 5-year retrospective study at a Tertiary Hospital in Northern Thailand. *Front. Cell. Infect. Microbiol.* **2022**, *12*, 955774. [[CrossRef](#)]
155. Al-Jamei, S.A.; Albsoul, A.Y.; Bakri, F.G.; Al-Bakri, A.G. Extended-spectrum β -lactamase producing *E. coli* in urinary tract infections: A two-center, cross-sectional study of prevalence, genotypes and risk factors in Amman, Jordan. *J. Infect. Public Health* **2019**, *12*, 21–25. [[CrossRef](#)]
156. Hays, J.P.; Safain, K.S.; Almogbel, M.S.; Habib, I.; Khan, M.A. Extended Spectrum- and Carbapenemase-Based β -Lactam Resistance in the Arabian Peninsula—A Descriptive Review of Recent Years. *Antibiotics* **2022**, *11*, 1354. [[CrossRef](#)]
157. Ranjan Dash, N.; Albatineh, M.T.; Alhourani, N.; Khoudeir, A.M.; Ghanim, M.; Wasim, M.; Mahmoud, I. Community-acquired urinary tract infections due to extended-spectrum β -lactamase-producing organisms in United Arab Emirates. *Travel Med. Infect. Dis.* **2018**, *22*, 46–50. [[CrossRef](#)] [[PubMed](#)]
158. Ikram, R.; Psutka, R.; Carter, A.; Priest, P. An outbreak of multi-drug resistant Escherichia coli urinary tract infection in an elderly population: A case-control study of risk factors. *BMC Infect. Dis.* **2015**, *15*, 224. [[CrossRef](#)]
159. Aabed, K.; Moubayed, N.; Alzahrani, S. Antimicrobial resistance patterns among different Escherichia coli isolates in the Kingdom of Saudi Arabia. *Saudi J. Biol. Sci.* **2021**, *28*, 3776–3782. [[CrossRef](#)]
160. Shrestha, A.; Shrestha, R.; Koju, P.; Tamrakar, S.; Rai, A.; Shrestha, P.; Madhup, S.K.; Katuwal, N.; Shrestha, A.; Shrestha, A.; et al. The Resistance Patterns in *E. coli* Isolates among Apparently Healthy Adults and Local Drivers of Antimicrobial Resistance: A Mixed-Methods Study in a Suburban Area of Nepal. *Trop. Med. Infect. Dis.* **2022**, *7*, 133. [[CrossRef](#)]
161. Sahuquillo-Arce, J.M.; Selva, M.; Perpiñán, H.; Gobernado, M.; Armero, C.; López-Quílez, A.; González, F.; Vanaclocha, H. Antimicrobial resistance in more than 100,000 Escherichia coli isolates according to culture site and patient age, gender, and location. *Antimicrob. Agents Chemother.* **2011**, *55*, 1222–1228. [[CrossRef](#)]
162. Pariyar, M.; Adhikari, S.; Regmi, R.S.; Dhungel, B.; Banjara, M.R.; Rijal, B.P.; Rijal, K.R.; Ghimire, P. Beta-Lactamase-Producing Gram-Negative Bacterial Isolates Among the Patients Attending a Tertiary Care Hospital, Kathmandu, Nepal. *Microbiol. Insights* **2023**, *16*, 117863612211507. [[CrossRef](#)]
163. Bora, A.; Sanjana, R.; Jha, B.K.; Narayan Mahaseth, S.; Pokharel, K. Incidence of metallo-beta-lactamase producing clinical isolates of Escherichia coli and Klebsiella pneumoniae in central Nepal. *BMC Res. Notes* **2014**, *7*, 557. [[CrossRef](#)]

164. Bao, D.; Xu, X.; Wang, Y.; Zhu, F. Emergence of a Multidrug-Resistant Escherichia coli Co-Carrying a New mcr-1.33 Variant and blaNDM-5 Genes Recovered from a Urinary Tract Infection. *Infect. Drug Resist.* **2022**, *15*, 1499–1503. [[CrossRef](#)]
165. Niranjan, V.; Malini, A. Antimicrobial resistance pattern in Escherichia coli causing urinary tract infection among inpatients. *Indian J. Med. Res.* **2014**, *139*, 945–948.
166. Kourtis, A.P.; Sheriff, E.A.; Weiner-Lastinger, L.M.; Elmore, K.; Preston, L.E.; Dudeck, M.; McDonald, L.C. Antibiotic Multidrug Resistance of Escherichia coli Causing Device- and Procedure-related Infections in the United States Reported to the National Healthcare Safety Network, 2013–2017. *Clin. Infect. Dis.* **2021**, *73*, E4552–E4559. [[CrossRef](#)]
167. Muters, N.T.; Mampel, A.; Kropidowski, R.; Biehler, K.; Günther, F.; Bălu, I.; Malek, V.; Frank, U. Treating urinary tract infections due to MDR *E. coli* with Isothiocyanates—A phytotherapeutic alternative to antibiotics? *Fitoterapia* **2018**, *129*, 237–240. [[CrossRef](#)]
168. Kaye, K.S.; Gupta, V.; Mulgirigama, A.; Joshi, A.V.; Scangarella-Oman, N.E.; Yu, K.; Ye, G.; Mitrani-Gold, F.S. Antimicrobial Resistance Trends in Urine Escherichia coli Isolates From Adult and Adolescent Females in the United States From 2011 to 2019: Rising ESBL Strains and Impact on Patient Management. *Clin. Infect. Dis.* **2021**, *73*, 1992–1999. [[CrossRef](#)]
169. Reaver, K.M.; Levy, J.; Nyambe, I.; Hay, M.C.; Mutiti, S.; Chandipo, R.; Meiman, J. Drinking Water Quality and Provision in Six Low-Income, Peri-Urban Communities of Lusaka, Zambia. *GeoHealth* **2021**, *5*, e2020GH000283. [[CrossRef](#)] [[PubMed](#)]
170. Seguni, N.Z.; Kimera, Z.I.; Msafiri, F.; Mgaya, F.X.; Joachim, A.; Mwingwa, A.; Matee, M.I. Multidrug-resistant Escherichia coli and Klebsiella pneumoniae isolated from hospital sewage flowing through community sewage system and discharging into the Indian Ocean. *Bull. Natl. Res. Cent.* **2023**, *47*, 66. [[CrossRef](#)]
171. Farrell, M.L.; Chueiri, A.; O'Connor, L.; Duane, S.; Maguire, M.; Miliotis, G.; Cormican, M.; Hooban, B.; Leonard, A.; Gaze, W.H.; et al. Assessing the impact of recreational water use on carriage of antimicrobial resistant organisms. *Sci. Total Environ.* **2023**, *888*, 164201. [[CrossRef](#)]
172. Leonard, A.F.C.; Zhang, L.; Balfour, A.J.; Garside, R.; Hawkey, P.M.; Murray, A.K.; Ukoumunne, O.C.; Gaze, W.H. Exposure to and colonisation by antibiotic-resistant *E. coli* in UK coastal water users: Environmental surveillance, exposure assessment, and epidemiological study (Beach Bum Survey). *Environ. Int.* **2018**, *114*, 326–333. [[CrossRef](#)]
173. Lyimo, B.; Buza, J.; Subbiah, M.; Smith, W.; Call, D.R. Comparison of antibiotic-resistant Escherichia coli obtained from drinking water sources in northern Tanzania: A cross-sectional study. *BMC Microbiol.* **2016**, *16*, 254. [[CrossRef](#)]
174. Chen, Z.; Yu, D.; He, S.; Ye, H.; Zhang, L.; Wen, Y.; Zhang, W.; Shu, L.; Chen, S. Prevalence of antibiotic-resistant Escherichia coli in drinking water sources in Hangzhou City. *Front. Microbiol.* **2017**, *8*, 267763. [[CrossRef](#)]
175. Kalakonda, S.P.; Parameswarreddy, G.; Skariah, E.N.; George, B.; Suchithra, T.V.; Sindhu, T.K. Treatment of Escherichia coli contaminated water with different pulse-powered NTP configurations and analysis for post treatment efficacy. *Sci. Rep.* **2022**, *12*, 20380. [[CrossRef](#)]

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