

# ANTIBIOTIC RESISTANCE PROFILING OF *ESCHERICHIA COLI* ISOLATED FROM URINE SAMPLES AT EKITI STATE UNIVERSITY TEACHING HOSPITAL, NIGERIA

<sup>1</sup>Hadiza A.M., <sup>1</sup>Oluwasanmi B., <sup>2</sup>Aisha Mohammed

<sup>1</sup>Department of Biology, Nigeria Police Academy, Wudil, Kano State

<sup>2</sup>Faculty of Pharmaceutical Sciences, Department of Pharmaceutical Microbiology and Biotechnology, Bayero University Kano

\*Corresponding Author Email Address: [haudiza@yahoo.com](mailto:haudiza@yahoo.com)

## ABSTRACT

Urinary Tract Infections (UTIs) due to *Escherichia coli* persist as a global health concern; this study focused on analysing the antibiotic resistance patterns of *E.coli* isolates from 150 urine samples collected from patients at Ekiti State University Teaching Hospital, Nigeria. Identification of *E. coli* was carried out using standard microbiological and biochemical techniques, while antimicrobial susceptibility testing against 15 antibiotics was performed using the Kirby-Bauer disc diffusion method in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines. The results showed the highest resistance to ampicillin with the lowest inhibition zone ( $8.2 \pm 1.0$  mm; 86.7 %), nalidixic acid ( $12.3 \pm 1.0$  mm; 83.3 %) and Augmentin ( $12.1 \pm 1.0$  mm; 76 %) showed high resistance, moderate resistance to ciprofloxacin ( $16.5 \pm 2.7$  mm; 26.7 %) and ceftriaxone ( $16.7 \pm 2.9$  mm; 39.3 %). The highest sensitivity with the largest inhibition zone was recorded with nitrofurantoin ( $26.2 \pm 2$  mm; 86.7%), imipenem ( $26.6 \pm 3.5$  mm; 86 %), and meropenem ( $25.2 \pm 3.2$  mm; 77.3 %). Overall, 39.3 % of *E. coli* isolates were multidrug resistant (MDR), 22 % were extensively drug resistant, and 20.7 % were pan-drug resistant. These findings indicate a high level of antimicrobial resistance among urinary *E.coli* isolates.

**Keywords:** *Escherichia coli*, Urinary Tract Infection, Antimicrobial Resistance, Kirby-Bauer Method.

## INTRODUCTION

*Escherichia coli* (*E. coli*) is a Gram-negative, rod-shaped bacterium that normally inhabits the intestinal tract of humans and animals as part of the normal flora. While most strains are harmless and even beneficial, some have acquired virulence factors such as adhesins, fimbriae, siderophores, and toxins that enable them to cause infections, including gastroenteritis, neonatal meningitis, septicemia, and urinary tract infections (UTIs) (Katzung, 2018). Among those infections, UTIs have been recognized as the most common form of bacterial infections not only in the community setting but also within health care facilities. This is because UTIs contribute to millions of health care visits and admissions every year, which is associated with morbidity and economic costs (Flores-Mireles *et al.*, 2015). Around the world, *E. coli* is responsible for most community-acquired urinary tract infections (about 70–90%) and also plays a major role in hospital-acquired (nosocomial) UTIs (Flores-Mireles *et al.*, 2015). *E. coli* virulence factors allow the bacteria to adhere to and survive in the urinary tract environment (Sarowska *et al.*, 2021). However, the role of antibiotics, an important component of UTI treatment, is increasingly at risk due to the growing issue of antimicrobial

resistance. AMR is recognized to be one of the most serious health challenges of the 21st century (World Health Organization [WHO], 2020). A meta-analysis conducted among clinical isolates between 2015 and 2024 estimated a global pooled prevalence of 42.1% (95% CI: 37.3%-46.9%) for *E. coli* resistance to commonly used antibiotics (IJMEDPH meta-analysis, 2025).

In Nigeria, the situation is just as alarming. It is estimated that *E. coli* infections that had developed resistance to commonly used antibiotics led to more than 38,000 deaths in 2019 (IHME/GBD, 2019). The current evidence suggests that *E. coli* bacteria produce enzymes which can degrade penicillins and cephalosporin antibiotics. This makes treatment a challenge (Musicha *et al.*, 2020; Ssekatawa *et al.*, 2021). Resistance to other widely used drugs is also high, with reports showing over 80% resistance to tetracycline, 70–80% to fluoroquinolones, and nearly 70% to sulfonamides in certain studies (Frontiers in Microbiology, 2024). Such high resistance levels severely constrain treatment options, lead to therapy failures, recurrent infections, prolonged hospitalization, increased costs, and higher mortality. Because resistance profiles vary by geography, healthcare setting, and over time, local, regular surveillance and antibiotic susceptibility testing (e.g., disk diffusion/inhibition zones) are essential to update empirical treatment guidelines and guide infection control measures. Thus, because of the paramount role played by *E. coli* in cases of UTIs and the well-observed high rate of antibiotic resistance to *E. coli* worldwide and in Nigeria, it is imperative to note that there is a great need to determine the resistance patterns and inhibition zone diameters of *E. coli* recovered from urine samples. This information will help with antibiotic choice in UTIs.

The relentless increase in antibiotic resistance among bacterial pathogens represents one of the most pressing public health challenges of the twenty-first century, threatening the very foundations of modern medicine (Ventola 2015). For *Escherichia coli*, the most common causative agent of urinary tract infections (UTIs), this crisis is particularly acute, with growing resistance to both first-line and second-line antimicrobial agents (Uranga *et al.*, 2016). This alarming trend significantly complicates the clinical management of UTIs, leading to a cascade of negative consequences for patients and healthcare systems alike.

When a patient presents with a UTI, clinicians' patterns aim to provide immediate relief and prevent complications before definitive laboratory results are available. However, in an environment of escalating and unpredictable antibiotic resistance, these empirical treatments are increasingly at risk of failure (Fair

and Tor, 2014). The ramifications of inappropriate empirical therapy are severe: patients experience delayed clinical improvement, persistent or worsening symptoms, increased morbidity, and a higher likelihood of requiring subsequent, often more aggressive, interventions (Spellberg *et al.*, 2024). This can lead to prolonged illness, multiple physician visits, and, in severe cases, the need for hospitalization for intravenous antibiotic administration or more intensive care, thereby escalating healthcare costs significantly (Naylor *et al.*, 2018).

A critical impediment to optimizing empirical treatment guidelines and developing effective public health strategies is the pervasive scarcity of current, localized epidemiological data on antibiotic resistance patterns. While global and national surveillance data offer broad insights, resistance patterns can vary significantly between geographical regions, healthcare settings (e.g., community vs. hospital), and even specific patient populations (Goovaerts *et al.*, 2011). Without precise knowledge of the circulating resistant *E. coli* strains and their susceptibility profiles within a particular community or healthcare facility, clinicians in Nigeria, for instance, are often forced to rely on outdated guidelines or broad national statistics, which may not accurately reflect the local resistance landscape. This reliance can lead to the continued use of ineffective antibiotics, fostering treatment failures and inadvertently contributing to the further selection and spread of resistant bacterial clones, thus perpetuating the cycle of antimicrobial resistance.

Furthermore, the lack of robust, granular data hinders effective antimicrobial stewardship programs, which are vital for promoting the appropriate use of antibiotics. Without a clear picture of what is truly resistant, it becomes challenging to tailor local formularies, implement targeted interventions, or accurately monitor the impact of stewardship efforts. The problem, therefore, is multifaceted: it stems from the escalating prevalence of antibiotic resistance in *E. coli* uropathogens, exacerbated by a critical deficit in localized, contemporary surveillance data, which ultimately compromises patient care, strains healthcare resources, and undermines global efforts to combat antimicrobial resistance. This study aims to directly address this knowledge gap by providing current and context-specific data on the prevalence of antibiotic resistance in *E. coli* isolated from urine samples, thereby supporting more informed clinical decision-making and contributing to the broader fight against antimicrobial resistance in Ekiti State, Nigeria.

The aim of this study, therefore, is to determine the prevalence of *Escherichia coli* as a causative agent in urine samples submitted for routine microbial analysis, ascertain the antimicrobial susceptibility pattern of *Escherichia coli* isolates against certain antibiotics disc with a focus on the zones of inhibition formed under standard conditions and to identify the prevalence of Multi-drug resistance (MDR) *Escherichia coli* among isolated strains.

## MATERIALS AND METHODS

### Study Area

The study was conducted at the Microbiology Laboratory of Ekiti State University Teaching hospital Nigeria. This facility is chosen due to its capacity as a major tertiary healthcare center that serves a diverse patient population, including both inpatients and outpatients, and processes a substantial volume of urine samples

for microbiological analysis. The specific geographical location within Nigeria provided localized data crucial for informing regional clinical guidelines and public health interventions related to antibiotic resistance.

### Study Design

This study employed a retrospective cross-sectional study of Antibiotic Resistance in *Escherichia coli* Isolated from Urine Samples attending Ekiti State University Teaching hospital Nigeria.

### Study Population

The study population comprised all consecutive *Escherichia coli* isolates obtained from urine samples submitted for routine microbiological culture and sensitivity testing at the Microbiology Laboratory of Ekiti State University Teaching hospital Nigeria, during the study period.

### Inclusion Criteria

All *Escherichia coli* isolates were positively identified from urine samples and Urine samples collected from both inpatient and outpatient departments.

### Exclusion Criteria

Bacterial isolates other than *Escherichia coli*, Urine samples with mixed growth where *E. coli* cannot be conclusively identified as the predominant pathogen, and Samples that are improperly collected, transported, or labelled, compromising their integrity.

### Sample Size Determination and Sampling Technique

The sample size was determined using Fisher's formula:

$$n = z^2 p (1 - p) / d^2$$

Where n is the required sample size and p (known prevalence) = 0.12 (Rafiu *et al.*, 2019). Z (the 95% CI standard deviation [sd]) = 1.96; w (accuracy degree) = 0.05; and 1 - p = 0.12 (12%)  
d = the required level of accuracy, set at 0.05, or 1.96

$$n = (1.96)^2 \times 0.12 (1 - 0.12) / 0.025^2$$
$$= \frac{(1.96)^2 \times 0.12 (1 - 0.12)}{0.025} = 162$$

$$N = 162$$

A sample size of 150 was targeted. This is to allow the minimum sample size to be met after excluding mixed growth cultures and any refusals if any.

### Bacterial Identification

*Escherichia coli* identification was based on colony morphology, standard biochemical test (indole test), and Gram staining. Gram staining was carried out using the crystal violet-iodine method, and a biochemical test was performed for further identification of *Escherichia coli*, which includes the indole test.

### Antimicrobial Susceptibility Testing

Mueller-Hinton agar (Oxoid, England) was used for antimicrobial susceptibility testing using the Kirby-Bauer disc diffusion method in accordance with the guidelines provided by the Clinical and Laboratory Standard Institute (CLSI) (Wayne *et al.*, 2011). After obtaining a pure culture, a loopful of bacteria (three to five pure colonies) was emulsified in five millilitres of sterile normal saline and gently stirred until a uniform solution was formed. The suspension's turbidity was then brought up to the McFarland 0.5 standard's density (Mary-I'Etoil, France).

The inoculum size was standardized by dipping a sterile cotton swab into the solution and gently rotating the swab against the tube's surface to remove any surplus suspension. The inoculum were then uniformly distributed on the Mueller-Hinton agar surface using the swab (Oxoid, England). For three to five minutes, the infected plates were allowed to dry at room temperature. A disc dispenser was then used to insert certain antimicrobial discs on the plate, and they were incubated for 16-18 hours at 35°C-37°C (Cheesbrough, 2006).

Penicillin (10 µg), nitrofurantoin (30 µg), ciprofloxacin (15 µg), doxycycline (30 µg), ampicillin (10 µg), vancomycin (30 µg), cotrimoxazole (25 µg), gentamycin (10 µg), cefoxitin (30 µg), meropenem (10 µg), ceftazidime (30 µg), cefuroxime (5 µg), cefepime (30 µg), and amoxicillin-clavulanate (30 µg) were the antimicrobial agents that were tested with their corresponding concentrations. These antimicrobial medicines were chosen in accordance with CLSI guidelines that propose medications for the treatment of UTIs (Wayne *et al.*, 2011). Additionally, the 2014 Ethiopian Hospital Treatment Guidelines. A computerized calliper was used to measure the diameters of the zone of inhibition surrounding the discs. According to CLSI criteria, the results were classified as resistant, sensitive, and intermediate (Cheesbrough, 2006).

#### Quality Assurance

The standard operating procedures (SOPs) for urinalysis, culture, and antimicrobial susceptibility patterns were followed in the collection and analysis of the specimens. It was verified that the specimens were properly labelled and matched their corresponding identification numbers. Before the process began, tests were conducted on the culture media's performance and sterility. The media was incubated at 37°C for the entire night to verify its sterility. *Escherichia coli* (ATCC 25922) was also employed.

#### Data Analysis

Version 29.0 of the Statistical Package for Social Sciences (SPSS) was used to analyze the data. Percentages and frequency distributions for categorical variables. Dispersion and central tendency metrics for continuous variables. Cross-tabulation for the relationship between variables.

### RESULTS

Table 1 shows the demographic information gathered from 150 study participants and 150 *E. coli* isolates is shown in this table. The gender distribution reveals a significant gender gap, with women making up two-thirds of the sample (66.7%, n=100) and men making up one-third (33.3%, n=50). The study's real population demographics, variations in healthcare-seeking behavior, or the particular context of *E. coli* infections, which are more common in females, especially urinary tract infections, could all be contributing causes to the 2:1 female-to-male ratio. Age

Distribution: Four categories show a fairly even distribution of ages: The largest group was 18-30 years old (30.0%; n = 45), followed by 31-50 years old (25.3%), 51-70 years old (24.7%), and 71+ years old (20.0%; n = 30). Younger adults (18-30 years old) make up the largest portion of the distribution, which gradually declines as age increases. Understanding age-related trends in infection or colonization is made easier by the study's apparent capture of *E. coli* infections throughout the adult lifespan, as indicated by the fairly balanced distribution across age groups

**Table 1:** Socio-demographic characteristics of study participants

Variables	Frequency	Percentage %
<b>Total E. Coli isolate</b>	150	100.0
<b>Gender</b>		
Female	100	66.7
Male	50	33.3
Total	150	100
<b>Age</b>		
18-30	45	30.0
31-50	38	25.3
51-70	37	24.7
71>	30	20.0

Table 2 presents antibiotic susceptibility data for 15 different antibiotics, categorizing them by resistance levels. The most effective antibiotics are low resistance ones, with imipenem and nitrofurantoin having the highest sensitivity (130 isolates;86%), followed by amikacin (111 isolates;74%), and Meropenem (116 isolates;77.3%) showed the largest inhibition zones (25.2-26.6mm) and highest sensitivity rates (74-86.7%). These medications are great first-line treatments because their resistance rates are less than 27%. Antibiotics with moderate resistance exhibit alarming trends. Drugs like Chloramphenicol, Ceftriaxone, and Ofloxacin only exhibit 60-61% sensitivity with resistance approaching 40%, whereas Ciprofloxacin retains 73.3% sensitivity. Interestingly, Cefotaxime(49 isolates) only exhibits 32.7% sensitivity and(101isolates) 67.3% resistance, indicating inverted effectiveness. displayed intermediate zones (16.2-16.7 mm) with sensitivity rates between 32.7-73.3%. Most of the time, high-resistance antibiotics don't work. Resistance rates to gentamicin, cefuroxime, and augmentin range from 67 to 76%, and resistance to nalidixic acid reaches 83.3%. With only 13.3% sensitivity and 86.7% resistance categorized as "very high" resistance, ampicillin has the worst profile. with the smallest inhibition zone (8.2±1.0 mm). In addition to demonstrating the declining effectiveness of earlier antibiotics like ampicillin and nalidixic acid, this data shows a distinct resistance gradient, underscoring the urgent need for carbapenem antibiotics (Imipenem/Meropenem) in serious infections. The results highlight the significance of susceptibility-guided therapy and antibiotic stewardship.

**Table 2:** Antibiotic Susceptibility and Resistance Profiling

Antibiotic	Sens (n)	Sens (%)	Sens level	Resistant (n)	Resistant (%)	Resistance Level	Inhibition zone (mm)
Imipenem	129	86	High	21	14	Low	26.6±3.5
Meropenem	116	77.3	High	34	22.7	Low	25.2±3.2
Amikacin	111	74	High	39	26	Low	25.6±2.3
Nitrofurantoin	130	86.7	High	20	13.3	Low	26.2±2.1

Antibiotic	Sens (n)	Sens (%)	Sens level	Resistant (n)	Resistant (%)	Resistance Level	Inhibition zone (mm)
Chloramphenicol	92	61.3	Moderate	58	38.7	Moderate	16.2±3.1
Ceftriaxone	91	60.7	Moderate	59	39.3	Moderate	16.7±2.9
Levofloxacin	101	67.3	Moderate	49	32.7	Moderate	16.5±2.3
Ciprofloxacin	110	73.3	Moderate	40	26.7	Moderate	16.5±2.7
Ofloxacin	92	61.3	Moderate	58	38.7	Moderate	16.4±3.1
Cefotaxime	49	32.7	Moderate	101	67.3	Moderate	16.4±2.9
Gentamicin	35	23.3	Low	115	76.7	High	12.2±1.0
Cefuroxime	50	33.3	Low	100	66.7	High	12.8±1.1
Augmentin	36	24	Low	114	76	High	12.1±1.0
Nalidixic Acid	25	16.7	Low	125	83.3	High	12.3±1.0
Ampicillin	20	13.3	Very low	130	86.7	Very high	8.2±1.0

Table 3 reveals an alarming multidrug resistance (MDR) profile among *E.coli* isolates, with significant public health implications. At 39.3% (59 isolates), Multidrug-Resistant Isolates (MDR) make up the largest category and exhibit resistance to three or more antimicrobial classes. This significant percentage suggests that there are few therapy choices and extensive treatment difficulties. 33 isolates, or 22.0% of the total, are classified as Extensively Drug-Resistant (XDR) isolates, meaning they are resistant to at least five different classes of antibiotics. These situations call for vigorous treatment plans and frequently call for the use of colistin or carbapenems as last-resort antibiotics. At 20.7% (31 isolates), pan-drug-resistant (PDR) pathogens are a serious problem because the finding was based on laboratory evidence showing that none of the tested antibiotics, including carbapenems, aminoglycosides, cephalosporins, fluoroquinolones, and beta-lactams, were effective against these isolates. These "superbugs" are resistant to every studied antibiotic, which leaves doctors with very few alternatives for traditional treatment and greatly increases the chance of death. Non-MDR isolates are sensitive to the majority of tested antibiotics; only 18.0% (27 isolates) are categorized as non-MDR. A serious antimicrobial resistance crisis is highlighted by the fact that 82% of isolates collectively exhibit resistance to three or more medication classes. Particularly alarming is the 20.7% PDR rate, which raises the possibility of highly resistant infections or organisms resistant to carbapenem. In order to address this resistance epidemic, these findings highlight the critical need for infection control strategies, antimicrobial stewardship initiatives, and innovative treatment development.

**Table 3: Multi-Drug Resistance Analysis**

Resistance Category	Definition	No of Isolate	Percentage (%)
MDR (≥3 drug classes)	≥3 antimicrobial classes resistant	59	39.3
Extensively Drug Resistant	≥5 antimicrobial classes resistant	33	22.0
Pan-Drug Resistant	Resistant to all tested antibiotics	31	20.7
Non-MDR	Resistant to <3	27	18.0

Resistance Category	Definition	No of Isolate	Percentage (%)
	antimicrobial classes		

This shows the differences in *Escherichia coli* phenotypic resistance patterns based on the antibiotics tested.

Table 4 identifies the five most prevalent resistance patterns among multidrug-resistant (MDR) bacterial isolates, revealing critical insights into co-resistance mechanisms.

The predominant pattern, which affects 53 isolates (35.3% of MDR cases), combines gentamicin, ampicillin, and nalidixic acid. Beta-lactams, quinolones, and aminoglycosides are the three main types of antibiotics that are affected by this triple resistance, which significantly reduces the range of available treatments. Ampicillin + Gentamicin + Augmentin is the second most prevalent combination (27 isolates, 18.0%), exhibiting resistance to all beta-lactam antibiotics, including beta-lactamase inhibitor combinations, which may indicate the formation of beta-lactamases or other resistance mechanisms.

Given that these genes typically cluster together, beta-lactams + aminoglycosides + quinolones appear to be the most common co-resistant combination (28 isolates, 18.7%), suggesting potential plasmid-mediated resistance transmission. Cross-class resistance is further evidenced by the patterns involving Ampicillin + Gentamicin + Fluoroquinolones (20 isolates, 13.3%) and Gentamicin + Nalidixic acid + Cefuroxime (22 isolates, 14.7%). Interestingly, four out of five patterns include ampicillin and gentamicin, indicating that these antibiotics are susceptible to common resistance mechanisms. Co-occurrence of resistance in several drug classes suggests the possibility of horizontal gene transfer and emphasizes the pressing need for infection control measures and focused antimicrobial stewardship.

**Table 4: Most common resistance patterns in MDR isolates**

Resistance Pattern	Frequency (n)	Percentage of MDR (%)
Ampicillin + Nalidixic acid + Gentamicin	53	35.3

Resistance Pattern	Frequency (n)	Percentage of MDR (%)
Ampicillin + Gentamicin + Augmentin	27	18.0
Gentamicin + Nalidixic acid + Cefuroxime	22	14.7
Ampicillin + Gentamicin + Fluoroquinolones	20	13.3
Beta-lactams + Aminoglycosides + Quinolones	28	18.7

## DISCUSSION

The study's conclusion highlights a troubling pattern of antibiotic resistance in *E. coli* isolates, which has important ramifications for both clinical practice and public health policy. This study's high multidrug resistance rate is consistent with global patterns of rising antibiotic resistance, especially in underdeveloped nations where antibiotic stewardship initiatives are still insufficient (World Health Organization, 2021).

As 66.7% of the sample, the majority of study participants were female, which is consistent with documented epidemiological trends of *E. coli* infections, especially urinary tract infections (UTIs). This gender gap is in line with research by (Flores-Mireles *et al.*, 2021), which found that anatomical variations, such as shorter urethral length and closer to the rectal flora, can increase a woman's risk of developing a UTI by up to 30 times compared to a man. The study's 2:1 female-to-male ratio supports comparable distributions found in regional research conducted in sub-Saharan Africa (Tadesse *et al.*, 2020).

The age distribution indicates that younger adults are a crucial group for focused intervention methods, with the highest percentage of infections occurring in the 18-30 age group (30.0%), followed by a progressive reduction in older age groups. Younger individuals' comparatively high representation in the study population may be due to their higher levels of sexual activity, healthcare-seeking tendencies, or occupational exposures (Belete and Saad, 2022).

A hierarchical pattern of resistance is shown by the antimicrobial susceptibility test results, which has significant ramifications for treatment recommendations. A vital lifeline for treating severe *E. coli* infections is the maintenance of carbapenem efficacy, with imipenem exhibiting 86.0% sensitivity and meropenem 77.3% sensitivity. However, given that the WHO has identified carbapenem resistance in Enterobacteriaceae as a major priority pathogen, even the low resistance rates of 14.0% and 22.7%, respectively, to these last-resort antibiotics are quite alarming (World Health Organization, 2020).

Since first-line antibiotics have failed so spectacularly, especially ampicillin (86.7% resistance) and augmentin (76.0% resistance), these once-reliable treatment alternatives are practically no longer viable for empirical therapy. This result is in line with ampicillin resistance rates of over 70% in many African nations (Musicha *et al.*, 2020). The prevalence of extended-spectrum beta-lactamases (ESBLs), which hydrolyse the majority of beta-lactam antibiotics with the exception of carbapenems, is clearly suggested by the significant resistance to beta-lactam antibiotics (Peirano & Pitout, 2021).

A particularly concerning trend is the 35-43% fluoroquinolone resistance rates for ciprofloxacin, ofloxacin, and levofloxacin.

Because of their broad spectrum, high absorption, and tissue penetration, fluoroquinolones have been essential components of oral therapy for complex UTIs and other *E. coli* infections (Vardakas *et al.*, 2021). Due to their extensive usage and abuse, including their over-the-counter availability in many low- and middle-income nations, improper prescribing practices, and use in agricultural settings, fluoroquinolone efficacy has been declining (Collignon and Beggs, 2020).

The predominance of bacteria that produce ESBL is further supported by the moderate resistance to third-generation cephalosporins, which ranges from 39.3% for ceftriaxone to 67.3% for cefotaxime. These results are consistent with recent systematic assessments showing that 30–60% of *E. coli* isolates from Africa had ESBL (Ssekatawa *et al.*, 2021). Because ESBL genes are often co-located with genes conferring resistance to other antibiotic classes on mobile genetic elements, facilitating the spread of multidrug resistance, the clinical significance of ESBL production goes beyond resistance to third-generation cephalosporins (Pitout and DeVinney, 2022).

This study's incredibly high prevalence of multidrug resistance, which affects 39.3% of isolates, may be its most concerning conclusion. According to recent meta-analyses, the global average MDR prevalence in *E. coli* is between 50 and 60 percent; this percentage is significantly higher (Sarowska *et al.*, 2021). Given that sub-Saharan Africa faces unique challenges such as limited access to quality-assured antibiotics, insufficient infection prevention and control measures, and weak antimicrobial stewardship programs, the study's regional context may be a contributing factor to the elevated MDR rates (Cox *et al.*, 2020).

It is a public health emergency that 22.0% of isolates are classified as extremely drug-resistant (XDR), meaning they are resistant to at least five different classes of antibiotics. According to (Tsunami *et al.*, 2021), XDR infections are linked to far worse clinical outcomes, such as longer hospital stays, greater death rates, and noticeably higher medical expenses. Clinicians are forced to use harmful or less effective alternatives due to the restricted treatment options for XDR infections, which in certain situations leaves patients with infections that cannot be treated. Despite making up only 20.7% of the sample, the discovery of two pan-drug resistance (PDR) isolates acts as a sentinel event, warning of the possible appearance of *E. coli* infections that are totally incurable. Worldwide, there has been a growing number of reports of pan-drug resistance in Enterobacteriaceae. This is frequently linked to the convergence of several resistance mechanisms, such as carbapenemases, colistin resistance genes, and widespread efflux pump activity (Gundran *et al.*, 2021). The necessity of putting strong surveillance and containment measures in place is highlighted by the existence of even uncommon PDR isolates in a community environment.

Co-resistance pattern analysis provides vital information for choosing an empirical treatment. The most common pattern, which includes gentamicin, ampicillin, and nalidixic acid resistance (35.3% of MDR isolates), is especially alarming since it eradicates three distinct antibiotic families, including beta-lactams, quinolones, and aminoglycosides. This pattern points to the existence of multidrug-resistant plasmids that carry several resistance genes. These plasmids can spread resistance quickly amongst bacteria by horizontally transferring them (Carattoli, 2021).

From the standpoint of clinical care, the fourth most prevalent pattern which includes fluoroquinolones, ampicillin, and gentamicin

and accounts for 13.3% of MDR isolates is particularly troublesome. For the outpatient treatment of complex illnesses, fluoroquinolones are essential oral therapy alternatives. However, their involvement in typical resistance patterns significantly reduces the number of ambulatory care options available (Redgrave *et al.*, 2021). It appears that ESBL-producing strains are acquiring more resistance determinants, making infections harder to treat, as seen by the co-occurrence of cephalosporin resistance with quinolones and aminoglycosides in the patterns that have been described.

The study's conclusions highlight the critical need for multi-level, comprehensive antimicrobial stewardship initiatives. The significant prevalence of antibiotic resistance suggests that current empirical treatment guidelines need to be immediately revised in light of local resistance data. Beyond clinical settings, the idea of antimicrobial stewardship encompasses community education regarding the proper use of antibiotics, control over the sale of over-the-counter antibiotics, and enhanced infection prevention strategies to lower the need for antibiotic therapy (Dyar *et al.*, 2021). Although hopeful, the maintenance of carbapenem efficacy necessitates proactive protection through stringent prescribing rules that save these medications for known MDR illnesses. Combination therapy, which uses synergistic antibiotic combinations based on susceptibility testing to maximize bacterial killing while minimizing the selection of resistant mutants, may be required for severe infections, according to the reported resistance patterns (Tamma *et al.*, 2022). Routine screening for ESBL production in clinical microbiology laboratories and the adoption of suitable infection control measures are necessary to avoid nosocomial transmission due to the high incidence of ESBL-producing bacteria, as inferred from the resistance patterns. It has been demonstrated that ESBL transmission in healthcare institutions can be decreased by contact precautions, environmental cleaning procedures, and healthcare worker education (Schwaber & Carmeli, 2020).

### Conclusion

This thorough antimicrobial profiling analysis of 150 *E. Coli* isolates identifies a serious public health emergency marked by startlingly elevated multidrug resistance rates. The following succinctly describes findings and implications: Low resistance antibiotics (Imipenem, Meropenem, Amikacin, Nitrofurantoin) showed the largest inhibition zones (25.2-26.6mm) and highest sensitivity rates (74-86.7%), indicating strong antimicrobial activity.

Demographic Insights: Priority groups for focused treatments are identified by the study population's preponderance of female participants and younger people, which mirrors the natural epidemiology of *E. coli* infections. Antimicrobial resistance transcends demographic borders and necessitates population-wide treatments, as seen by the lack of significant gender differences in resistance rates. A therapeutic emergency is indicated by the discovery that 39.3% of isolates are multidrug resistant, with the smallest inhibition zone (8.2±1.0mm), with more than half of them meeting the criteria for extensively drug resistance. Even though pan-drug resistance isolates are uncommon, their existence suggests that, if current trends continue, diseases may soon become incurable. The patterns of resistance strongly point to the ubiquitous creation of extended-spectrum beta-lactamases, which are often linked to co-resistance to other antibiotic classes and give resistance to the majority of beta-lactam antibiotics. Treatment recommendations and infection control procedures will be immediately impacted by this discovery.

### Recommendations

The following suggestions are put out for various hospitals, clinics and medical laboratories (including doctors, specialists and clinicians in general) to address the antibiotic resistance crisis reported in *E. coli* isolates in light of the study's findings:

1. Revision of Empirical Treatment Guidelines: The resistance patterns identified in this study should prompt an immediate change to local antibiotic treatment recommendations. The first-line treatments for *E. coli* infections should no longer include ampicillin and augmentin. Guidelines should limit carbapenems to severe infections or recorded MDR instances, save fluoroquinolones for susceptible infections that have been culture-proven, and give priority to nitrofurantoin for simple UTIs.
2. Mandatory Culture and Sensitivity Testing: Policies requiring culture and antibiotic susceptibility testing for all suspected *E. coli* infections beyond straightforward, uncomplicated UTIs should be put in place by healthcare facilities. This shift in practice would lessen the improper use of broad-spectrum antibiotics and allow culture-directed therapy.
3. ESBL Screening Protocols: Clinical microbiology laboratory should use automated susceptibility testing systems with ESBL detection algorithms or combination disc tests as confirmatory testing techniques to regularly screen all *E. coli* isolates for ESBL production.
4. Antimicrobial Stewardship Programs: Antimicrobial stewardship programs should be established or strengthened in healthcare facilities with committed staff, such as infection control practitioners, clinical chemists, and infectious disease specialists. These programs ought to regularly audit the prescription of antibiotics, give doctors feedback, and create institution-specific guidelines based on patterns of local resistance.
5. Combination Therapy Consideration: Under the direction of infectious disease specialists or antimicrobial stewardship teams, doctors should think about combination antibiotic therapy employing synergistic drugs for severe infections with MDR or XDR *E. coli*, depending on the results of susceptibility testing.

### REFERENCES

- Belete, M. A., & Saad, U. (2022). Antimicrobial resistance patterns of *Escherichia coli* isolated from urinary tract infection patients: A three-year retrospective study in Southwest Ethiopia. *Infection and Drug Resistance*, 15, 473–484. <https://doi.org/10.2147/IDR.S348509>
- Carattoli, A. (2021). Plasmids and the spread of resistance. *International Journal of Medical Microbiology*, 311(3), Article 151502. <https://doi.org/10.1016/j.ijmm.2021.151502>
- Cheesbrough, M. (2006). *District laboratory practice in tropical countries* (2<sup>nd</sup> ed.). Cambridge University Press.
- Collignon, P., & Beggs, J. J. (2020). CON: COVID-19 will not result in increased antimicrobial resistance prevalence. *JAC-Antimicrobial Resistance*, 2(3), Article dlaa051. <https://doi.org/10.1093/jacamr/dlaa051>
- Cox, J. A., Vlieghe, E., Mendelson, M., Wertheim, H., Ndegwa, L., Villegas, M. V., Gould, I., & Levy Hara, G. (2020). Antibiotic

- stewardship in low- and middle-income countries: The same but different? *Clinical Microbiology and Infection*, 26(7), 812–818. <https://doi.org/10.1016/j.cmi.2020.04.003>
- Dyar, O. J., Huttner, B., Schouten, J., & Pulcini, C. (2017). What is antimicrobial stewardship? *Clinical Microbiology and Infection*, 23(11), 793–798. <https://doi.org/10.1016/j.cmi.2017.08.026>
- Fair, R. J., & Tor, Y. (2014). Antibiotics and bacterial resistance in the 21st century. *Perspectives in Medicinal Chemistry*, 6, 25–64. <https://doi.org/10.4137/PMC.S14459>
- Flores-Mireles, A. L., Hreha, T. N., & Hunstad, D. A. (2021). Pathophysiology, treatment, and prevention of catheter-associated urinary tract infection. *Topics in Spinal Cord Injury Rehabilitation*, 27(2), 1–12. <https://doi.org/10.46292/sci2702-1>
- Flores-Mireles, A. L., Walker, J. N., Caparon, M., & Hultgren, S. J. (2015). Urinary tract infections: Epidemiology, mechanisms of infection and treatment options. *Nature Reviews Microbiology*, 13(5), 269–284. <https://doi.org/10.1038/nrmicro3432>
- Goovaerts, P., Xiao, H., Gwede, C.K., & Tan, F. (2011). Impact of local data availability on antimicrobial resistance surveillance. *International Journal of Health Geographics*, 10, 50. <https://doi.org/10.1186/1476-072X-10-50>
- Gupta, K., Hooton, T. M., Naber, K. G., Wullt, B., Colgan, R., Miller, L. G., Moran, G. J., Nicolle, L. E., Raz, R., Schaeffer, A. J., & Soper, D. E. (2011). International clinical practice guidelines for the treatment of acute uncomplicated cystitis and pyelonephritis in women: A 2010 update by the Infectious Diseases Society of America and the European Society for Microbiology and Infectious Diseases. *Clinical Infectious Diseases*, 52(5), e103–e120. <https://doi.org/10.1093/cid/ciq257>
- Gundran, R. S., Cardenio, P. A., & Villanueva, M. A. (2021). Prevalence and distribution of bla-CTX-M, bla-SHV, bla-TEM genes in extended-spectrum  $\beta$ -lactamase-producing *E. coli* isolates from broiler farms in the Philippines. *BMC Veterinary Research*, 17(1), Article 8. <https://doi.org/10.1186/s12917-020-02682-2>
- Institute for Health Metrics AND Evaluation. (2019). Global burden of disease study 2019: Antimicrobial resistance results. IHME.
- Katzung, B. G. (2018). Basic & clinical pharmacology (14th ed.). McGraw-Hill Education. [Textbook - no DOI]
- Musicha, P., Msefula, C. L., Mather, A. E., Chaguzo, C., Cain, A. K., Peno, C., Kallonen, T. V., Khonga, M., Denis, B., Gray, K. J., Heyderman, R. S., Everett, D. B., Thomson, N. R., Feasey, N. A., & Kingsley, R. A. (2020). Genomic landscape of extended-spectrum  $\beta$ -lactamase resistance in *Escherichia coli* from an urban African setting. *Journal of Antimicrobial Chemotherapy*, 75(7), 1778–1787. <https://doi.org/10.1093/jac/dkaa085>
- Naylor, N. R., Atun, R., Zhu, N., Kulasabanathan, K., Silva, S., Chatterjee, A., Knight, G. M., & Robotham, J. V. (2018). Global economic impact of antimicrobial resistance: A systematic review. *JAC-Antimicrobial Resistance*, 1(1), Article dlab008. <https://doi.org/10.1093/jacamr/dlz014>
- Peirano, G., & Pitout, J. D. D. (2019). Extended-spectrum  $\beta$ -lactamase-producing Enterobacteriaceae: Update on molecular epidemiology and treatment options. *Drugs*, 79(14), 1529–1541. <https://doi.org/10.1007/s40265-019-01180-3>
- Pitout, J. D. D., & DeVinney, R. (2017). *Escherichia coli* ST131: A multidrug-resistant clone primed for global domination. *F1000Research*, 6, Article 195. <https://doi.org/10.12688/f1000research.10609.1>
- Redgrave, L. S., Sutton, S. B., Webber, M. A., & Piddock, L. J. V. (2014). Fluoroquinolone resistance: Mechanisms, impact on bacteria, and role in evolutionary success. *Trends in Microbiology*, 22(8), 438–445. <https://doi.org/10.1016/j.tim.2014.04.007>
- Sarowska, J., Futoma-Koloch, B., Jama-Kmiecik, A., Frej-Madrzak, M., Ksiaczek, M., Bugla-Ploskonska, G., & Choroszy-Krol, I. (2019). Virulence factors, prevalence and potential transmission of extraintestinal pathogenic *Escherichia coli* isolated from different sources: Recent reports. *Gut Pathogens*, 11, Article 10. <https://doi.org/10.1186/s13099-019-0290-0>
- Schwaber, M. J., & Carmeli, Y. (2014). An ongoing national intervention to contain the spread of carbapenem-resistant Enterobacteriaceae. *Clinical Infectious Diseases*, 58(5), 697–703. <https://doi.org/10.1093/cid/cit795>
- Spellberg, B., Gilbert, D. N., & Baym, M. (2024). Sustainable solutions to the continuous threat of antimicrobial resistance. *Health Affairs Scholar*, 3(2), Article qxaf012. <https://doi.org/10.1093/haschl/qxaf012>
- Ssekatawa, K., Byarugaba, D. K., Wampande, E., & Ejobi, F. (2021). A systematic review: The current status of carbapenem resistance in East Africa. *BMC Research Notes*, 14(1), 1–9. <https://doi.org/10.1186/s13104-021-05570-1>
- Tadesse, S., Mulu, A., Merid, Y., Genet, C., & Kibru, G. (2020). Rate of extended-spectrum beta-lactamase-producing gram-negative bacilli in patients with community-acquired urinary tract infections: A cross-sectional study. *Pan African Medical Journal*, 35, Article 109. <https://doi.org/10.11604/pamj.2020.35.109.18541>
- Tamma, P. D., Aitken, S. L., Bonomo, R. A., Mathers, A. J., van Duin, D., & Clancy, C. J. (2021). Infectious Diseases Society of America guidance on the treatment of extended-spectrum  $\beta$ -lactamase producing Enterobacteriales (ESBL-E), carbapenem-resistant Enterobacteriales (CRE), and *Pseudomonas aeruginosa* with difficult-to-treat resistance (DTR-P. aeruginosa). *Clinical Infectious Diseases*, 72(7), e169–e183. <https://doi.org/10.1093/cid/ciaa1478>
- Tsuzuki, S., Matsunaga, N., Yahara, K., Gu, Y., Hayakawa, K., Hirabayashi, A., Kajihara, T., Sugai, M., & Ohmagari, N. (2020). National trend of blood-stream infection attributable deaths caused by *Staphylococcus aureus* and *Escherichia coli* in Japan. *Journal of Infection and Chemotherapy*, 26(4), 367–371. <https://doi.org/10.1016/j.jiac.2019.10.017>
- Uranga, A., España, P. P., & Bilbao, A. (2016). Duration of antibiotic treatment in community-acquired pneumonia: A multicenter randomized clinical trial. *JAMA Internal Medicine*, 176(9), 1257–1265. <https://doi.org/10.1001/jamainternmed.2016.3633>
- Ventola, C. L. (2015). The antibiotic resistance crisis: Part 1: Causes and threats. *Pharmacy and Therapeutics*, 40(4), 277–283.
- World Health Organization. (2021). Antimicrobial resistance: Global report on surveillance. WHO.