

Prevalence and Pattern of Antibiotic Resistance in Clinical Isolates from Rangpur District of Bangladesh: A Cross-Sectional Study

By

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A thesis submitted to the School of Pharmacy in partial fulfillment of the requirements for the degree of Bachelor of Pharmacy (Hons.)

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Declaration

It is hereby declared that

1. The thesis submitted is my/our own original work while completing degree at BRAC University.
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3. The thesis does not contain material which has been accepted, or submitted, for any other degree or diploma at a university or other institution.
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Approval

The thesis titled “Prevalence and Pattern of Antibiotic Resistance in Clinical Isolates from Rangpur District of Bangladesh: A Cross-Sectional Study” submitted by MD. SHAKIL AHMED, of Spring, 2025 has been accepted as satisfactory in partial fulfillment of the requirement for the degree of Bachelor of Pharmacy.

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Ethics Statement

This study did not involve direct interaction with human participants. Instead, data were collected exclusively from anonymized antibiotic resistance reports provided by two hospitals/diagnostic centers. No personal identifiers or patient contact information were accessed at any stage of the study. As a result, individual informed consent was not required.

All collected data were handled with strict confidentiality and anonymization to ensure privacy. The information obtained was used solely for research purposes. The methodology and procedures were rigorously implemented in accordance with the guidelines authorized by the Institutional Review Board (IRB), ensuring that no risk or harm was posed to any individual.

Abstract

Background: Antimicrobial resistance (AMR) is accelerating in low- and middle-income countries, yet district-level data remain scarce in northern part (Rangpur) of Bangladesh.

Methods: We analyzed 200 clinical specimens from two Rangpur facilities (Jan–Jun 2025). Bacterial identification and antimicrobial susceptibility testing followed CLSI (2025). Proportions and 95% CIs were calculated.

Results: Culture positivity was 58.5% (117/200; 95% CI 51.6–65.1). *Escherichia coli* predominated (77.8% of isolates). MDR prevalence was 92.3% in *E. coli* (84/91; 95% CI 85.0–96.2) and 100% in *Klebsiella pneumoniae* (n=1). Overall resistance to third-generation cephalosporins was 63.8% (e.g., cefixime 79.1%, ceftriaxone 59.8%), and fluoroquinolone class resistance 28.5% overall; notably, *E. coli* ciprofloxacin resistance reached 76.9%. Agents retaining activity included amikacin (R $\approx$ 13%) and nitrofurantoin (R $\approx$ 27% for urinary isolates).

Conclusions: AMR in Rangpur is severe, with very high MDR—especially in *E. coli*—and limited efficacy of commonly used oral agents. Strengthened stewardship, diagnostics, and integrated surveillance are urgently required; organism-specific therapy should be guided by susceptibility testing.

Keywords: Antimicrobial Resistance (AMR), Multidrug Resistance (MDR). *Escherichia coli*, *Pseudomonas* spp., *Staphylococcus aureus*, Third-Generation Cephalosporins, Fluoroquinolone Resistance, Antibiotic Susceptibility Testing (AST), *Klebsiella pneumoniae*, *Enterococcus faecalis*, Coagulase-Negative *Staphylococcus*, *Streptococcus pyogenes*, Clinical Isolates, Urinary Tract Infections (UTIs), Aminoglycosides, Carbapenem Resistance,

Nitrofurantoin, Linezolid Resistance, Cross-Sectional Study, Low- and Middle-Income
Countries (LMICs)

Dedication

I dedicate this thesis to my beloved parents and my dear wife whose unconditional love, prayers, and unwavering support have shaped me into who I am today and made my journey possible.

To my grandfather, grandmother, grandfather in law who was always there for me whenever I needed their love and guidance will forever be cherished.

To my dear friend, for making my university life smoother, and for the unconditional help in completing this thesis—I am truly grateful.

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List of Acronyms

AMR	Antimicrobial Resistance
AST	Antibiotic Susceptibility Testing
CI	Confidence Interval
CLSI	Clinical and Laboratory Standards Institute
ECDC	European Centre for Disease Prevention and Control
ESBL	Extended-Spectrum Beta-Lactamase
IEDCR	Institute of Epidemiology, Disease Control and Research (Bangladesh)
IQR	Interquartile Range
LMIC(s)	Low- and Middle-Income Country(ies)
MDR	Multidrug Resistance
SD	Standard Deviation
UTI(s)	Urinary Tract Infection(s)
WHO GLASS	World Health Organization Global Antimicrobial Resistance Surveillance System
N/G	No Growth
R	Resistance
S	Sensitive
M	Moderate
I	Intermediate

Chapter 1

Introduction

1.1 Background

According to WHO research, AMR has been rated as a top priority to global health in modern times, going beyond management of an individual, because it jeopardizes the sustainability of any healthcare system or even society. The World Health Organization (WHO) has classified AMR as a critical global pandemic that is estimated to increase to 10 million deaths a year by 2050 with an estimated economic impact of over USD 100 trillion annually unless effective measures are put in place (Murray et al., 2022; WHO, 2022; Hassan & Nohor, 2025). In 2019 alone 4.95 million deaths were due to AMR caused by bacteria, including 1.27 million directly caused by resistant bacterial infections-more than the combined mortality rates of HIV/AIDS and malaria (Murray et al., 2022). AMR poses a threat to the safety of most medical procedures, including surgery, chemotherapy, and organ transplantation, by reducing the effectiveness of antimicrobial agents (WHO, 2022).

Causes of AMR are complex and interconnected; including the misuse of and inappropriate use of antibiotics in both humans and animals, ineffective infection prevention, poor sanitation, and lax regulations on the distribution of antimicrobials (Azim et al., 2023; Hassan & Nohor, 2025). These concerns are particularly pressing in low income and greater income nations like South Asia, in which burden of infectious disease is heavy, antibiotics are easily obtained without a prescription, in which diagnostic structure is sparse (Azim et al., 2023; IEDCR, 2024; Ahmed et al., 2019). The WHO Global Antimicrobial Resistance and Use Surveillance System (GLASS) has repeatedly highlighted South Asia as a hotspot of resistance requiring urgent, evidence-based responses (WHO, 2022, 2023).

AMR has become a major risk to health within Bangladesh. National surveillance shows an alarming rise in the resistance levels to important antibiotics over the last few years. Widely seen pathogens like *Escherichia coli*, *Klebsiella* spp., *Pseudomonas* spp., *Staphylococcus aureus*, and *Salmonella* spp. are highly resistant to conventionally used drugs like ampicillin, ceftriaxone and ciprofloxacin (Ahmed et al., 2019; IEDCR, 2024). Widespread self-medication, lax enforcement of prescription laws, and irrational prescribing practices exacerbate the problem (Biswas et al., 2014; Wahab et al., 2023). Recent surveys reveal that 83% of doctors prescribe antibiotics without adequate diagnostic support, while over 60% of university students report self-prescribing antibiotics (Wahab et al., 2023; Hossain et al., 2023). This misuse has accelerated resistance, leading to limited effectiveness of first-line antibiotics and increased reliance on expensive, last-line drugs.

Although the AMR burden in Bangladesh is well recognized, surveillance data remain patchy and overly concentrated in Dhaka and a few other urban centers. According to IEDCR (2024), only six of the country's 64 districts have detailed resistance profiles, leaving vast knowledge gaps. Ahmed et al. (2019) observed that nearly three-quarters of Bangladeshi studies failed to differentiate between community- and hospital-acquired infections. This lack of fine-grained, district-level data hampers evidence-based decision-making and undermines stewardship initiatives. Rangpur district, despite being a major healthcare hub in northern Bangladesh, remains particularly underrepresented in AMR literature and national reporting.

1.2 Regional AMR Context in South Asia

The AMR crisis in Bangladesh reflects a broader South Asian trend. In India, resistance has escalated sharply; national surveillance shows rising carbapenem resistance among *Klebsiella*, *E. coli*, and *Acinetobacter* isolates in major hospitals between 2017–2022 (Sharma et al., 2023). Widespread over-the-counter antibiotic sales, poor infection control, and misuse in agriculture are key drivers (Sharma et al., 2023). Pakistan faces parallel challenges, where nearly 70% of antibiotics are inappropriately prescribed or sold without prescription, contributing to widespread ESBL and carbapenemase-producing organisms (Safdar et al., 2025). In Nepal, antibiotic misuse is rampant in both humans and animals, with sub-therapeutic dosing in livestock accelerating resistance; surveillance systems remain underdeveloped (Acharya & Wilson, 2019). Myanmar has similarly high AMR risks. Hospital surveys in Yangon revealed that one-third of patients were prescribed third-generation cephalosporins, while poultry farms reported over 80% prevalence of resistant *E. coli* (Win et al., 2022; Gibson et al., 2020). Collectively, these findings show that South Asia shares common drivers—OTC access, weak stewardship, and agricultural misuse—resulting in similarly high resistance rates.

1.3 Global Travel-Linked Countries

Beyond South Asia, AMR dynamics in countries with strong Bangladeshi travel ties are also relevant. Saudi Arabia, a major destination for Bangladeshi migrant workers and Hajj pilgrims, continues to battle rising resistance. Despite a 2017 National Action Plan, inappropriate prescribing remains widespread, and mass gatherings like Hajj facilitate dissemination of resistant strains, including ESBL- and NDM-positive Enterobacterales (Torumkuney et al., 2022; Haseeb

et al., 2023). Malaysia, another key labor migration hub, has reported high resistance rates in clinical isolates, with MRSA prevalence exceeding 40% and *E. coli* showing resistance above 50% to common antibiotics (Ismail et al., 2024). Agricultural misuse remains a significant concern, though stewardship programs are being expanded. By contrast, the United Kingdom, home to a large Bangladeshi diaspora, maintains strict prescription policies and robust surveillance systems. While resistance rates in UK community *E. coli* are rising, they remain far below South Asian levels, with third-generation cephalosporin resistance under 15% (Wellcome Open Research, 2024). However, international travel creates opportunities for resistant strains to spread across borders.

1.4 Knowledge Gaps and Rationale for Study

Despite the extensive evidence of AMR across Bangladesh and South Asia, Rangpur district remains a blind spot in national surveillance and published literature (IEDCR, 2024). Its role as a regional healthcare hub, serving a diverse and mobile population, makes local AMR data critically important. Without such data, clinicians lack evidence-based guidelines for empiric therapy, and policymakers cannot effectively target stewardship programs. This research thus could play a crucial role in bridging a huge gap by presenting district-marked AMR data in Rangpur, understanding local patterns of resistance, and putting them in the regional and global context.

Chapter 2

Materials and Methods

2.1 Study design

This research was designed as a cross-sectional study to determine the prevalence and antimicrobial resistance patterns of bacteria isolated from clinical specimens in Rangpur District, Bangladesh. The cross-sectional design provided a snapshot of AMR rates over the study period and across a broad patient population, offering a representative picture of the local resistance situation.

2.2 Study setting and Population

The study was conducted at two major healthcare facilities in Rangpur city: **Central Hospital Rangpur** and **Popular Diagnostic Centre Rangpur**. These institutions were selected for their high patient volumes, range of clinical services, and availability of diagnostic laboratories. The study population included adult patients (age 18–90 years) from whom clinical specimens were submitted for culture and antibiotic susceptibility testing between January 1 and June 1, 2025. Both male and female patients were included to ensure gender representation.

2.3 Study Period and Sample Size

A total of 200 clinical culture isolates were analyzed over the six-month study period. This sample size was determined by the number of eligible culture-positive reports available from the

selected hospitals during that timeframe, and it was deemed sufficient for descriptive analysis and estimation of resistance proportions with acceptable confidence intervals.

2.4 Inclusion and Exclusion Criteria

Inclusion criteria: Culture and sensitivity reports were included if they corresponded to patients aged 18–90 years who had a positive bacterial culture with subsequent antibiotic susceptibility testing, and if the report contained complete demographic and clinical data (patient age, sex, specimen type, organism identified, and AST results).

Exclusion criteria: Reports from pediatric patients (<18 years) or very elderly patients (>90 years) were excluded to avoid confounding from age extremes (which often have different resistance patterns). Cases lacking complete data (e.g. missing AST results or demographic details) were excluded to ensure data quality. Additionally, if multiple cultures were performed on the same patient, only the first isolate was included to prevent duplicate counting of a single patient's infection episode.

These criteria were applied to enhance the internal validity of the study and to focus the analysis on a consistent adult population. By excluding repeat isolates and incomplete cases, we minimized bias and avoided overestimation of resistance frequencies.

2.5 Data Collection and Variables

Data were collected retrospectively from laboratory record logs and electronic databases of the microbiology departments at the two hospitals. For each included culture report, the following

information was recorded using a standardized data collection form: patient age, sex, clinical specimen type (e.g., urine, blood, wound swab, etc.), bacterial species isolated, and the antibiotic susceptibility results for that isolate. Culture results were categorized as growth-positive (bacterial growth) or no-growth. Antibiotic susceptibility outcomes for each isolate were recorded as “Resistant (R)”, “Intermediate (I)”, or “Sensitive (S)” according to the interpreting criteria of the Clinical and Laboratory Standards Institute (CLSI, 2025 edition).

2.6 Data Management and Statistical Analysis

All collected data were entered and cleaned using Microsoft Excel 2019. Descriptive statistics were used to summarize patient demographics and clinical characteristics. Categorical variables (such as sex, specimen type, organism identity, and resistance vs. susceptibility outcomes) were summarized as frequencies and percentages. Continuous variables like patient age were summarized by mean, standard deviation (SD), median, and interquartile range (IQR) as appropriate.

Proportions of isolates resistant to each antibiotic were calculated with corresponding 95% confidence intervals (95% CI) to quantify precision. The Wilson score method was used for 95% CI of proportions. Key outcomes of interest included overall culture positivity rate, the distribution of bacterial species among positive cultures, and the resistance rates for each antibiotic and antibiotic class. Linezolid results were exported by the laboratory across all isolates, including Gram-negative organisms. Because linezolid is clinically indicated only for Gram-positive bacteria (e.g., *Staphylococcus*, *Enterococcus*), the aggregated linezolid percentage may overestimate true resistance in Gram-positive pathogens. Organism-specific linezolid data were

unavailable in the raw export. No comparative hypothesis testing was performed, as the objective was primarily descriptive. All analyses and figure generation were done using Python (matplotlib and pandas libraries) and cross-checked for accuracy.

2.7 Antibiotic Classification

For analysis, the antibiotics tested were grouped into their respective classes to assess class-wise resistance patterns.

Table 1 The classification of antibiotics

<i>Class</i>	<i>Antibiotics</i>
Aminoglycosides	Amikacin, Gentamicin
Penicillins (incl. β -lactam/ β -lactamase inhibitor)	Amoxicillin, Ampicillin, Cloxacillin, Piperacillin, Amoxicillin–clavulanate
Cephalosporins	Cefepime, Cefixime, Cefotaxime, Ceftazidime, Ceftriaxone, Cefuroxime, Cephradine, Cefoperazone
Carbapenems	Imipenem, Meropenem
Macrolides	Azithromycin, Clarithromycin, Erythromycin
Fluoroquinolones	Ciprofloxacin, Ofloxacin, Moxifloxacin, Gatifloxacin, Nalidixic acid
Sulfonamides	Co-trimoxazole (Trimethoprim–Sulfamethoxazole)

Tetracyclines	Tetracycline
Lincosamides	Clindamycin
Oxazolidinones	Linezolid
Polymyxins	Colistin (not commonly tested in this dataset)
Nitrofurans derivatives	Nitrofurantoin
Glycopeptides	Vancomycin, Teicoplanin
Lipopeptides	Daptomycin
Phenicol	Chloramphenicol
Others / Special agents	Fosfomycin, Mecillinam

Note: Fosfomycin is a phosphonic acid derivative, not a nitrofurans; it is listed under “Others.”

Chapter 3

Results

3.1 Demographic Characteristics of Patients

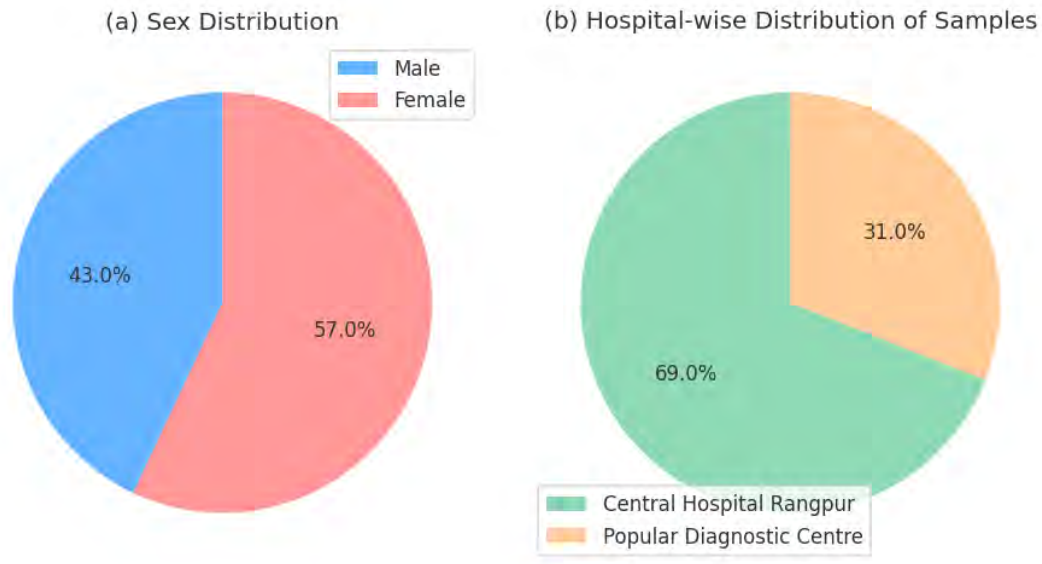


Figure 1 Demographic Characteristics of Patients

Figure 1: (a) Sex distribution of patients providing clinical samples (N=200). (b) Hospital-wise origin of samples (N=200). In total, 43.0% of samples were from male patients which is in blue color and 57.0% from female patients which shows red color within the pie chart, and the majority of samples (69.0% shows green within the pie chart) came from Central Hospital Rangpur versus (31.0% indicating the yellow color within the pie chart) from Popular Diagnostic Centre.

A total of 200 clinical specimens were included, of which 86 (43.0%) were from male patients and 114 (57.0%) from female patients (Figure 1a). The patients' ages ranged from 18 to 90 years, with

a mean age of 44.4 years (SD = 18.4; median 44; IQR = 27–60). The mean age’s 95% CI was 41.9–46.9 years, indicating that the true average age of patients likely falls in this range. The majority of samples were submitted from Central Hospital Rangpur (138/200; 69.0%), with the remainder from Popular Diagnostic Centre (62/200; 31.0%) (Figure 1b). Thus, the dataset primarily represents adult patients from two key healthcare facilities in Rangpur city. Both demographic figure details value is shown in Appendix B table B1.

3.2 Clinical Sample Sources

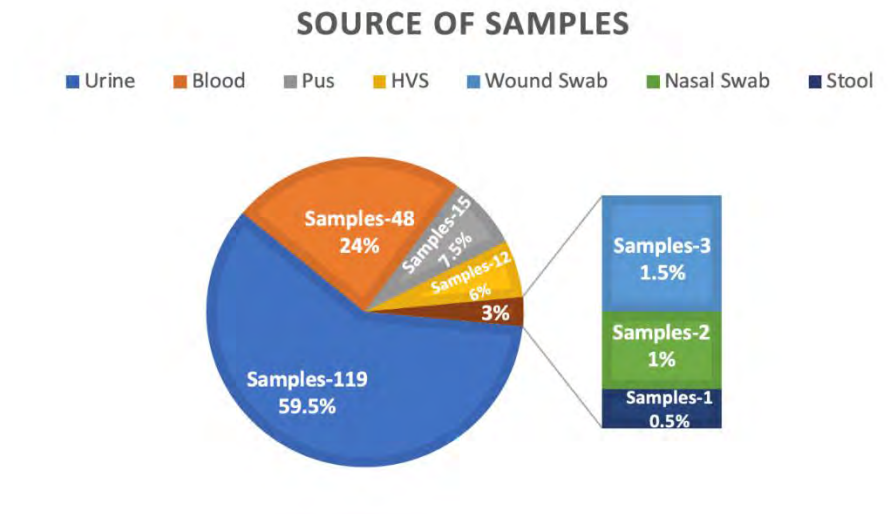


Figure 2 Source of Samples

Figure 2: Clinical sample sources of the 200 specimens. Urine was the most common specimen (59.5% of samples), followed by blood (24.0%), pus (7.5%), and high vaginal swab (HVS, 6.0%). Minor sample types (wound swab, nasal swab, stool) together constituted <3% of samples. Percentages are of total samples (N=200). *Note.* Percentages with 95% CI values are presented in Appendix B (Table B2).

Urine was the most frequent sample source, comprising 119 out of 200 specimens (59.5%; 95% CI 52.6–66.1%). This was followed by blood cultures (48/200, 24.0%; 95% CI 18.6–30.4%) and pus (15/200, 7.5%). High vaginal swabs (12/200, 6.0%) were also notable. Other specimen types included wound swabs (1.5%), nasal swabs (1.0%), and stool (0.5%). The dominance of urine samples is consistent with urinary tract infections being a major cause of hospital visits in adults, while the contribution of blood reflects serious systemic infections. The diversity of sample sources indicates a range of infection types were captured in this study.

3.3 Culture Positivity Rate

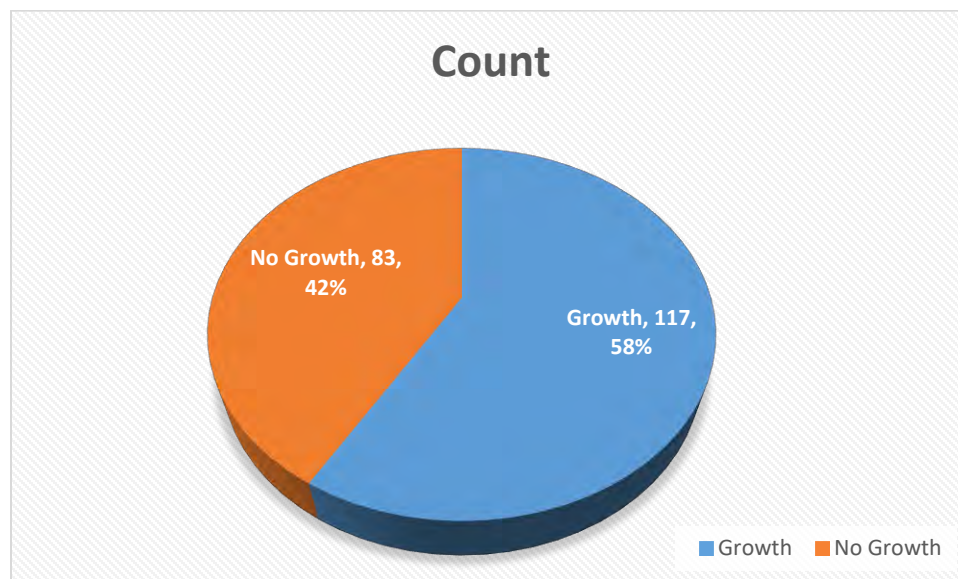


Figure 3 Growth vs No Growth

Figure 3: Culture growth results for all samples (N=200). Out of all samples, 58.5% showed bacterial growth (culture-positive with blue color indicator), while 41.5% had no growth with yellow color indicator within the pie chart. The high positive rate reflects pre-selection of clinically suspected infection cases.

Among the 200 specimens, 117 yielded bacterial growth (culture-positive) and 83 had no bacterial growth. The overall culture positivity rate was 58.5% (117/200; 95% CI 51.6–65.1%), meaning over half of the submitted samples had a pathogen isolated (Figure 3). Conversely, 42% of samples were culture-negative. This relatively high positivity rate likely reflects the clinical pre-selection of patients—only those with significant signs of infection were sent for culture, as is typical in low-resource settings. Similar hospital-based studies in low- and middle-income countries (LMICs) also report elevated culture-positive proportions due to targeted testing of symptomatic cases. This finding underscores the burden of bacterial infections among patients presenting to Rangpur hospitals. More details information and value are shown with the Appendix B table B3, Where the accurate percentage are there.

3.4 Bacterial Isolates Identified

A total of 117 isolates were obtained from the growth-positive cultures. Table 2 lists the frequency of each bacterial organism identified. The vast majority of infections were caused by Gram-negative bacilli. **Escherichia coli** was by far the most common isolate, accounting for 91 of 117 isolates (77.8%; 95% CI 69.4–84.4%). This finding aligns with *E. coli* being a leading cause of urinary and other common infections. The next most frequent organism was **Enterococcus faecalis** (6 isolates, 5.1%), a Gram-positive coccus often involved in urinary and wound infections. **Staphylococcus** spp. (coagulase-negative staphylococci, 5 isolates, 4.3%) and **Staphylococcus aureus** (3 isolates, 2.6%) together constituted about 7% of isolates – these staphylococci are typical pathogens in skin, soft tissue, and bloodstream infections. **Pseudomonas** spp. was found in 4 cases (3.4%), reflecting opportunistic infections often in

wounds or hospital settings. A few isolates of ***Streptococcus pyogenes*** (2 isolates, 1.7%) were noted, as well as single isolates ($\leq 1\%$ each) of ***Staphylococcus haemolyticus***, ***Kocuria kristinae***, ***Klebsiella pneumoniae***, ***Salmonella Typhi*** (noted as NARST), ***Enterobacter cloacae*** complex, and ***Streptococcus*** spp. (unspecified).

This distribution indicates that *E. coli* is the predominant pathogen in Rangpur's clinical infections, which is consistent with global surveillance in community and hospital settings where *E. coli* leads in urinary and intra-abdominal infections. The presence of *Enterococcus* and *Staphylococcus* highlights the contribution of Gram-positive infections as well, though at a much lower frequency than Gram-negatives in this study.

Table 2 Bacterial isolation from culture-positive sample (N=117)

Organism	Frequency (n)	Percentage of isolates
<i>Escherichia coli</i>	91	77.8%
<i>Enterococcus faecalis</i>	6	5.1%
Coagulase-negative <i>Staphylococcus</i> spp.	5	4.3%
<i>Pseudomonas</i> spp.	4	3.4%
<i>Staphylococcus aureus</i>	3	2.6%
<i>Streptococcus pyogenes</i>	2	1.7%
<i>Staphylococcus haemolyticus</i>	1	0.9%
<i>Kocuria kristinae</i>	1	0.9%
<i>Klebsiella pneumoniae</i>	1	0.9%
<i>Salmonella Typhi</i> (NARST)	1	0.9%

<i>Organism</i>	<i>Frequency (n)</i>	<i>Percentage of isolates</i>
<i>Enterobacter cloacae</i> complex	1	0.9%
<i>Streptococcus</i> spp. (unspecified)	1	0.9%

(NARST: National Antimicrobial Resistance Surveillance Bangladesh designation)

Among the growth-positive cultures, *E. coli* was overwhelmingly the most common pathogen (77.8% of isolates). The predominance of *E. coli* is in line with its role as a leading cause of urinary tract and other community-acquired infections. The relatively small proportions of *Enterococcus faecalis*, *Staphylococcus* spp., and *Pseudomonas* spp. suggest these were less frequent but important causes of infections such as wound infections, bloodstream infections, or hospital-acquired infections in this cohort. The variety of single-isolate species indicates occasional infections by a range of organisms, reflecting the diverse etiologies of infection in the clinical population. This distribution underscores the need for broad-spectrum empirical coverage in serious infections in Rangpur, pending culture results, given the dominance of Gram-negative rods but also the presence of Gram-positive organisms. More detail value with confidence interval is shown in Appendix C table C1. *Note. Percentages are calculated out of culture-positive isolates. 95% confidence intervals (CI) are shown where applicable.*

3.5 Antibiotic Resistance Profiles of Top Five Organisms

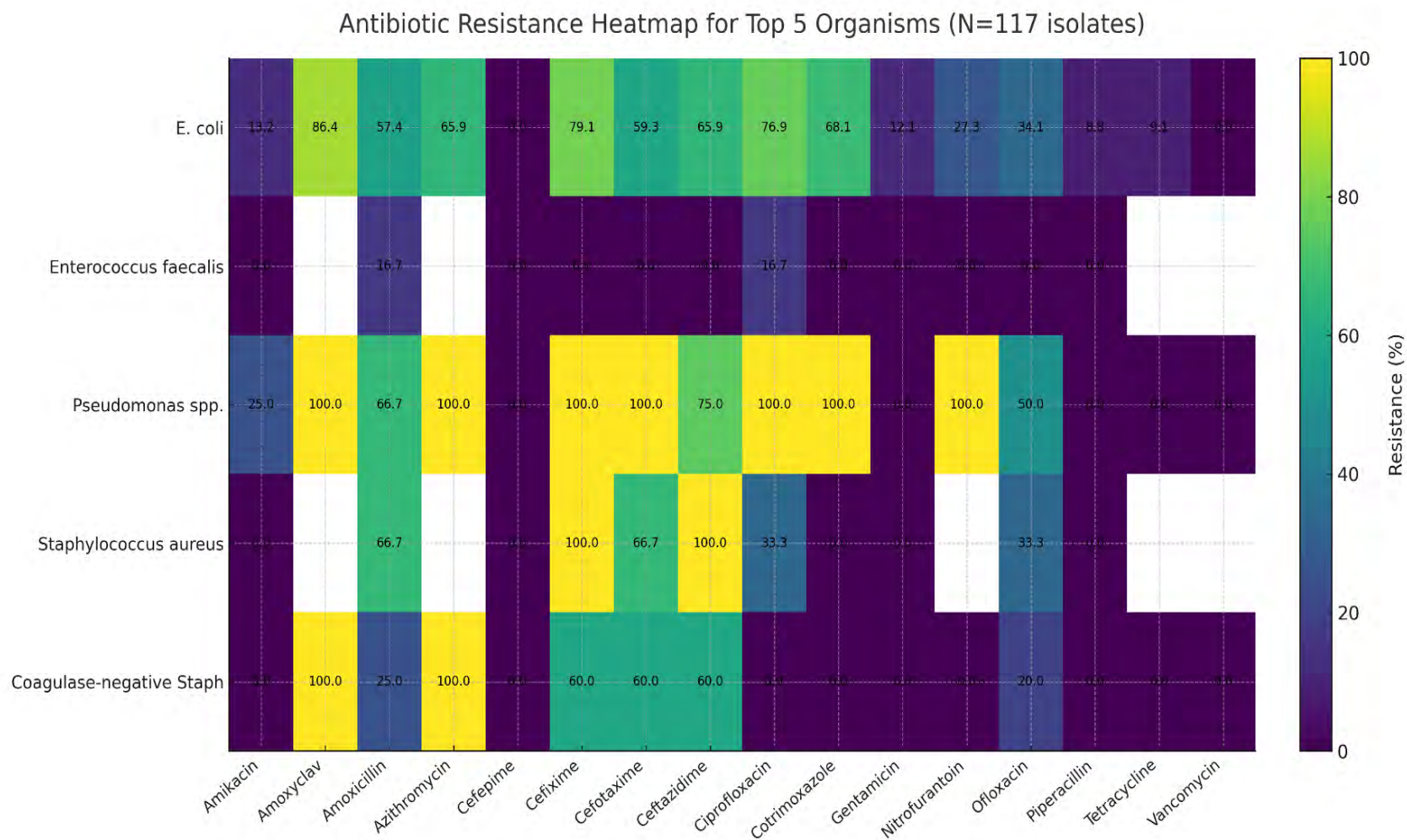


Figure 4 Heatmap of antibiotic resistance rate (%)

Figure 4: Heatmap of antibiotic resistance rates (%) among the five most common organisms (*E. coli*, *Enterococcus faecalis*, *Pseudomonas* spp., *Staphylococcus aureus*, and coagulase-negative *Staphylococcus* spp.). Darker yellow indicates higher resistance while the darker purple shows low resistance. White cells indicate antibiotics not tested or not applicable for a given organism.

The antibiotic resistance profiles for the top five organisms are summarized in Figure 4 (see Appendix Table A1 for detailed values). Each row represents one organism and each column an antibiotic, with cell color intensity corresponding to the percentage of that organism's isolates resistant to the antibiotic. *Escherichia coli* isolates showed high resistance to many first-line antibiotics. Notably, 86.4% of *E. coli* were resistant to amoxicillin-clavulanate (a penicillin combination) and 79.1% were resistant to cefixime (a third-generation cephalosporin). High resistance was also observed to ciprofloxacin (76.9%) and co-trimoxazole (68.1%), reflecting widespread resistance to oral treatment options for *E. coli*. Conversely, *E. coli* resistance was low for amikacin (13.2%) and nitrofurantoin (27.3%), indicating these agents remain relatively effective against *E. coli* in this setting.

For *Pseudomonas* spp., the heatmap reveals a pattern of multi-drug resistance: 100% of *Pseudomonas* isolates were resistant to amoxicillin-clavulanate, cefixime, azithromycin, and also to cefotaxime and gentamicin. However, all *Pseudomonas* isolates were sensitive to cefepime and piperacillin (0% resistance for those drugs among the four *Pseudomonas* isolates), suggesting these might still work for *Pseudomonas* infections in Rangpur. *Staphylococcus aureus* (3 isolates) showed 100% resistance to cefixime and azithromycin, and 66.7% resistance to amoxicillin (likely indicating presence of MRSA). All *S. aureus* were sensitive to vancomycin (no resistance observed, though vancomycin was tested only in a subset) and also fully sensitive to amikacin and gentamicin (0% resistance). Coagulase-negative *Staphylococcus* spp. exhibited complete resistance to penicillins (100% resistant to

amoxicillin-clavulanate) and macrolides (100% resistant to azithromycin), with substantial resistance to cefixime and the cephalosporins (60% range). These *Staph* isolates were fully sensitive to vancomycin (0% resistance).

Overall, the heatmap highlights critical resistance trends: - *E. coli* is highly resistant to β -lactams (especially cephalosporins) and fluoroquinolones, which are commonly used antibiotics. - *Pseudomonas* shows multi-drug resistance, typical of nosocomial strains, but may still be treatable with certain anti-pseudomonal β -lactams (e.g., cefepime). - *Staphylococcus* (both *S. aureus* and coagulase-negative) demonstrate high resistance to penicillin-class and macrolide antibiotics, suggesting many are methicillin-resistant and macrolide-resistant, but they remain uniformly susceptible to vancomycin.

These findings mirror global alerts that Enterobacteriaceae (like *E. coli*) are increasingly resistant to fluoroquinolones and β -lactams, and that MRSA remains a challenge (World Health Organization, 2022). The data underscore the importance of drug susceptibility testing, as empirical therapy in such a high-resistance environment is increasingly likely to fail if it relies on older first-line agents.

3.6 Prevalence of Multidrug Resistance (MDR)

Multidrug resistance was defined in this study as non-susceptibility to ≥ 3 classes of antibiotics. The prevalence of MDR among the key organisms is summarized in Table 3. Overall, MDR rates were extremely high in the dominant pathogens. For *E. coli*, 84 of 91 isolates met criteria for MDR, yielding an MDR prevalence of 92.3%. In other words, over 92% of *E. coli* were resistant to at least three different antibiotic classes, reflecting their extensive resistance development. All isolates of ***Staphylococcus spp.*** (coagulase-negative),

Pseudomonas spp., **Klebsiella pneumoniae**, **Enterobacter cloacae** complex, and *Streptococcus* spp. (unspecified) in this study were MDR (100% of those isolates). *Enterococcus faecalis* had an MDR rate of 83.3% (5 of 6 isolates). Conversely, some organisms with very low isolate counts showed no MDR: *Streptococcus pyogenes*, *Staph. haemolyticus*, *Kocuria*, and *Salmonella Typhi* isolates were not multidrug-resistant, although these were represented by only 1–2 isolates each.

Table 3 Prevalence of MDR among isolates

Organism	MDR Isolates (n)	Total Isolates (n)	MDR Rate (%)
<i>E. coli</i>	84	91	92.3%
<i>Enterococcus faecalis</i>	5	6	83.3%
<i>Staphylococcus</i> spp. (coag-neg)	5	5	100.0%
<i>Pseudomonas</i> spp.	4	4	100.0%
<i>Staphylococcus aureus</i>	3	3	100.0%
<i>Streptococcus pyogenes</i>	0	2	0.0%
<i>Staph. Haemolyticus</i>	0	1	0.0%
<i>Kocuria kristinae</i>	0	1	0.0%
<i>Klebsiella pneumoniae</i>	1	1	100.0%
<i>Salmonella Typhi</i>	0	1	0.0%
<i>Enterobacter cloacae</i> comp.	1	1	100.0%
<i>Streptococcus</i> spp. (unspec.)	1	1	100.0%

MDR was thus highly prevalent among the major organisms isolated. Essentially, the *E. coli* isolates in Rangpur are almost all multidrug-resistant. Similarly, every single isolate of coagulase-negative *Staph*, *Pseudomonas*, *K. pneumoniae*, *Enterobacter*, and even the single *Streptococcus* spp. was MDR, highlighting a severe situation where first-line antibiotics across several classes may not be effective. In contrast, organisms like *Streptococcus pyogenes* (Group A strep) did not show MDR in our small sample, possibly reflecting continued effectiveness of penicillin for streptococcal infections.

These MDR rates in Rangpur are significantly higher than those reported in many high-income settings. For instance, in Europe, MDR *E. coli* rates are typically below 20% (European CDC, 2023), whereas we observed over 92.3% in Rangpur. This stark difference emphasizes the urgency of the AMR problem in Bangladesh. *Note. Percentages based on culture-positive isolates (N = 117).*

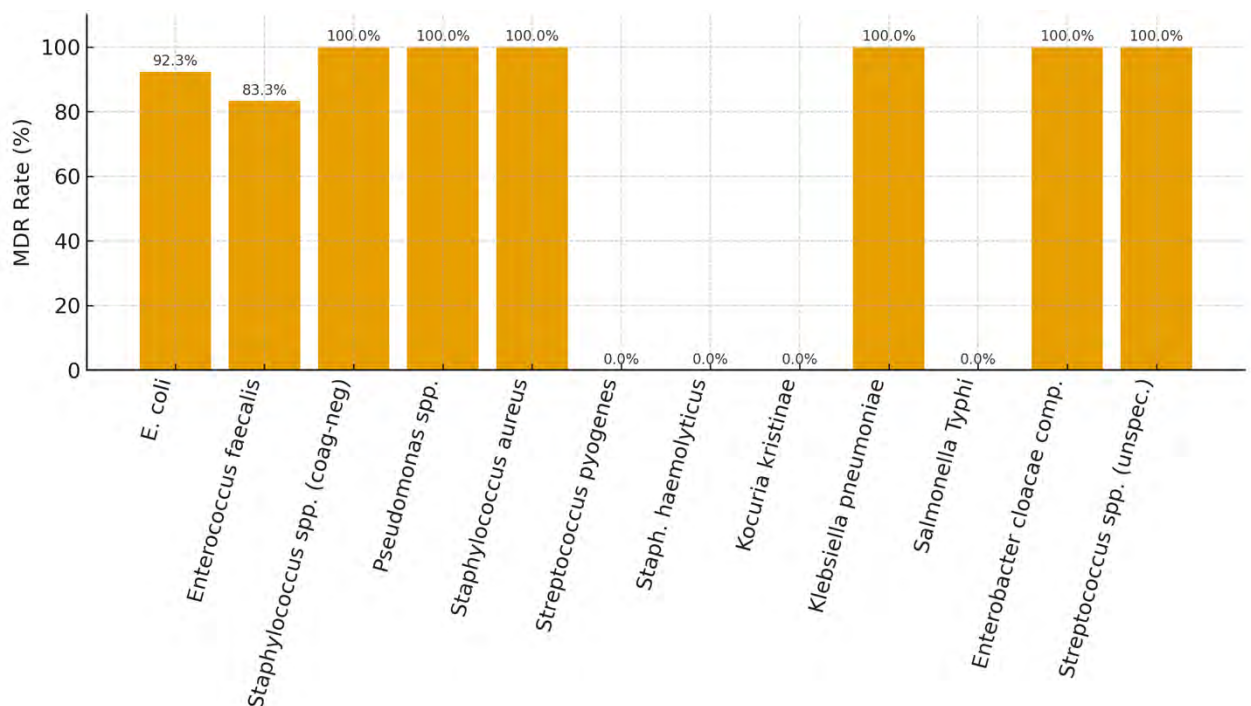


Figure 5 Proportion of MDR isolates by organism

Each bar represents the percentage of isolates of that organism that were MDR (resistant to ≥ 3 antibiotic classes). *E. coli* had an MDR rate of 92.3%, and several organisms (e.g., *Staphylococcus* spp., *Pseudomonas*) had 100% MDR in our sample.

Using the prespecified MDR definition, *E. coli* had an MDR prevalence of 92.3% (84/91; 95% CI 85.0–96.2%). In practical terms, this means almost all *E. coli* infections would require very broad-spectrum or combination therapy. All isolates of *Pseudomonas* spp., coagulase-negative *Staphylococcus*, *K. pneumoniae*, *Enterobacter*, and *Streptococcus* spp. were MDR (100%). No MDR was observed in the few *Streptococcus pyogenes*, *Staph. haemolyticus*, *Kocuria*, or *Salmonella* isolates, but those numbers were too small to be generalizable. The extremely high MDR rates in Rangpur far exceed those in Western countries and even neighboring regions. For example, European surveillance data report MDR in *E. coli* around 10–20% and in *K. pneumoniae* around 20–30% in most settings (ECDC, 2023), highlighting how severe the resistance problem is locally.

3.7 Overall Antibiotic Resistance Rates

To examine the broader resistance patterns, all 117 isolates were pooled and overall resistance frequencies for each antibiotic tested were calculated (Table 4). The percentage of all isolates resistant to a given antibiotic provides a useful guide to the empiric efficacy of that drug in this setting. Key findings include:

Highest resistance rates: Amoxicillin-clavulanate (87.2% of isolates tested were resistant), cefixime (79.1% resistant), and co-trimoxazole (70.2% resistant) showed the highest resistance proportions. These are commonly used antibiotics for UTIs and other infections, and the high resistance suggests limited usefulness of oral agents like these in Rangpur. For

instance, 87.2% resistance to amoxicillin-clavulanate (augmentin) indicates it would fail in about 9 out of 10 cases if used empirically.

Substantial resistance: Third-generation cephalosporins such as ceftriaxone had ~59.8% resistance, and ceftazidime ~65.8% resistance. Fluoroquinolone resistance was also high: for example, ciprofloxacin showed 46.8% resistance overall. Nonetheless, roughly half of isolates were resistant to ciprofloxacin. Chloramphenicol (54.7% resistant), cefuroxime (59.0%), and cefotaxime (59.8%) also had more than half of isolates resistant.

Lowest resistance rates: Amikacin had only 12.8% of isolates resistant, making it one of the most effective drugs in vitro. Meropenem, a carbapenem, had 9.4% resistance – notable because carbapenems are often last-resort drugs; a ~10% resistance suggests the presence of some carbapenemase-producing organisms. Imipenem (similar class) was not explicitly listed but would be expected to be comparable. Nitrofurantoin/Fosfomycin combined showed 24.3% resistance, but note that these were tested mainly on urinary isolates (nitrofurantoin, for UTIs). Nalidixic acid, an older quinolone mainly for UTIs, had 22.2% resistance. These lower resistance percentages indicate some remaining options for specific scenarios (e.g., nitrofurantoin for UTIs).

The intermediate (“I”) and moderate (“M”) categories were generally low for most antibiotics (usually <5–10%), meaning most results were clearly either Sensitive or Resistant. Figure 6 visualizes the breakdown of overall resistance vs. sensitivity for each antibiotic tested.

Table 4 Antibiotic-wise resistance among all isolates (N=117)

<i>Antibiotic</i>	<i>Tested (n)</i>	<i>Resistant (n)</i>	<i>*Resistance (%)</i>	<i>Sensitive (%)</i>	<i>Intermediate/Moderate (%)</i>
Amikacin	117	15	12.8%	82.1%	5.1% (I+M)

<i>Antibiotic</i>	<i>Tested (n)</i>	<i>Resistant (n)</i>	<i>*Resistance (%)</i>	<i>Sensitive (%)</i>	<i>Intermediate/Moderate (%)</i>
Amoxicillin-Clavulanate	47	41	87.2%	12.8%	0%
Ampicillin/Cloxacillin (Penicillins)*	70	37	52.9%	45– 47%**	~2% (I)
Azithromycin	47	32	68.1%	31.9%	0%
Erythromycin (Macrolides)*	23 (part of above 70)	13	56.5%***	43.5%***	—
Cefepime	47	32	68.1%	31.9%	0%
Cefoperazone (with Cefepime)*	23	13	56.5%***	43.5%	—
Cefixime	117	90	76.9%	17.1%	6.0% (I)
Cefotaxime	117	70	59.8%	31.6%	8.6% (I)
Ceftazidime	117	77	65.8%	25.6%	8.6% (I)
Ceftriaxone	117	70	59.8%	32.5%	7.7% (I)
Cefuroxime	117	69	59.0%	35.9%	5.1% (I)
Cephradine	117	70	59.8%	35.0%	5.2% (I)
Chloramphenicol	117	64	54.7%	36.8%	8.5% (I+M)
Ciprofloxacin	47	22	46.8%	53.2%	0% (values for Gram+ subset)

<i>Antibiotic</i>	<i>Tested (n)</i>	<i>Resistant (n)</i>	<i>*Resistance (%)</i>	<i>Sensitive (%)</i>	<i>Intermediate/Moderate (%)</i>
Clarithromycin	117	79	67.5%	27.4%	5.1% (I+M)
Clindamycin	117	72	61.5%	33.3%	5.2% (I+M)
Co-trimoxazole (TMP-SMX)	47	33	70.2%	29.8%	0%
Sulfamethoxazole (part of above 70)**	23	11	47.8%***	52.2%	—
Gentamicin	117	28	23.9%	71.8%	4.3% (I)
Linezolid	117	87	74.4%	23.9%	1.7% (M)
Meropenem	117	11	9.4%	82.1%	8.5% (I)
Moxifloxacin	117	22	18.8%	72.6%	8.6% (I)
Nalidixic Acid	117	26	22.2%	70.1%	7.7% (I)
Ofloxacin	117	42	35.9%	54.7%	9.4% (I)
Piperacillin	117	26	22.2%	70.1%	7.7% (I)
Gatifloxacin	117	35	29.9%	55.6%	14.5% (I+M)
Nitrofurantoin/Fosfomycin	117	28	24.3%	71.4%	4.3% (I)

Across all isolates (n=117, *Note. Percentages are calculated based on culture-positive isolates (N = 117), not the total patient population (N = 200). 95% confidence intervals (CI) are provided in the text.*), the highest resistance was observed to beta-lactam antibiotics commonly used as first-line treatments. Amoxicillin-clavulanate had an overall resistance rate of 87.2%, meaning this oral antibiotic combination would fail in roughly 9 out of 10 infections if used

empirically. Third-generation cephalosporins like cefixime (76.9% resistant) and ceftriaxone (59.8% resistant) were largely ineffective against the majority of isolates. Co-trimoxazole (trimethoprim-sulfamethoxazole), often used for UTIs, was 70.2% resistant. These high percentages underscore that many standard treatments have very limited efficacy in Rangpur. Also the Ciprofloxacin resistance was 46.80%.

On the other hand, some antibiotics retained activity. Amikacin, an injectable aminoglycoside, showed only 12.8% resistance – making it a relatively reliable option for severe Gram-negative infections (nearly 88% of isolates remained susceptible). Meropenem, a carbapenem antibiotic, had 9.4% resistance, indicating that carbapenemase-producing organisms, while present, are still in the minority. Nitrofurantoin (used for UTIs) had 24.3% resistance overall, suggesting it could still be effective for ~75% of urinary infections, particularly since its use is mostly limited to *E. coli* and other UTI pathogens.

Intermediate and moderate resistance categories were very low for most drugs, which simplifies interpretation: in most cases an isolate was clearly resistant or susceptible. This likely reflects the presence of strong resistance mechanisms (like ESBL or carbapenemases) that confer full resistance rather than borderline cases. *Notes: Grouped rows indicate combined analysis where certain antibiotics were only tested on subsets (e.g., penicillins on Gram-positive isolates). Linezolid results were reported across all isolates, including Gram-negative bacteria. Clinically, linezolid is relevant only for Gram-positive organisms; therefore, this percentage should be interpreted with caution.*

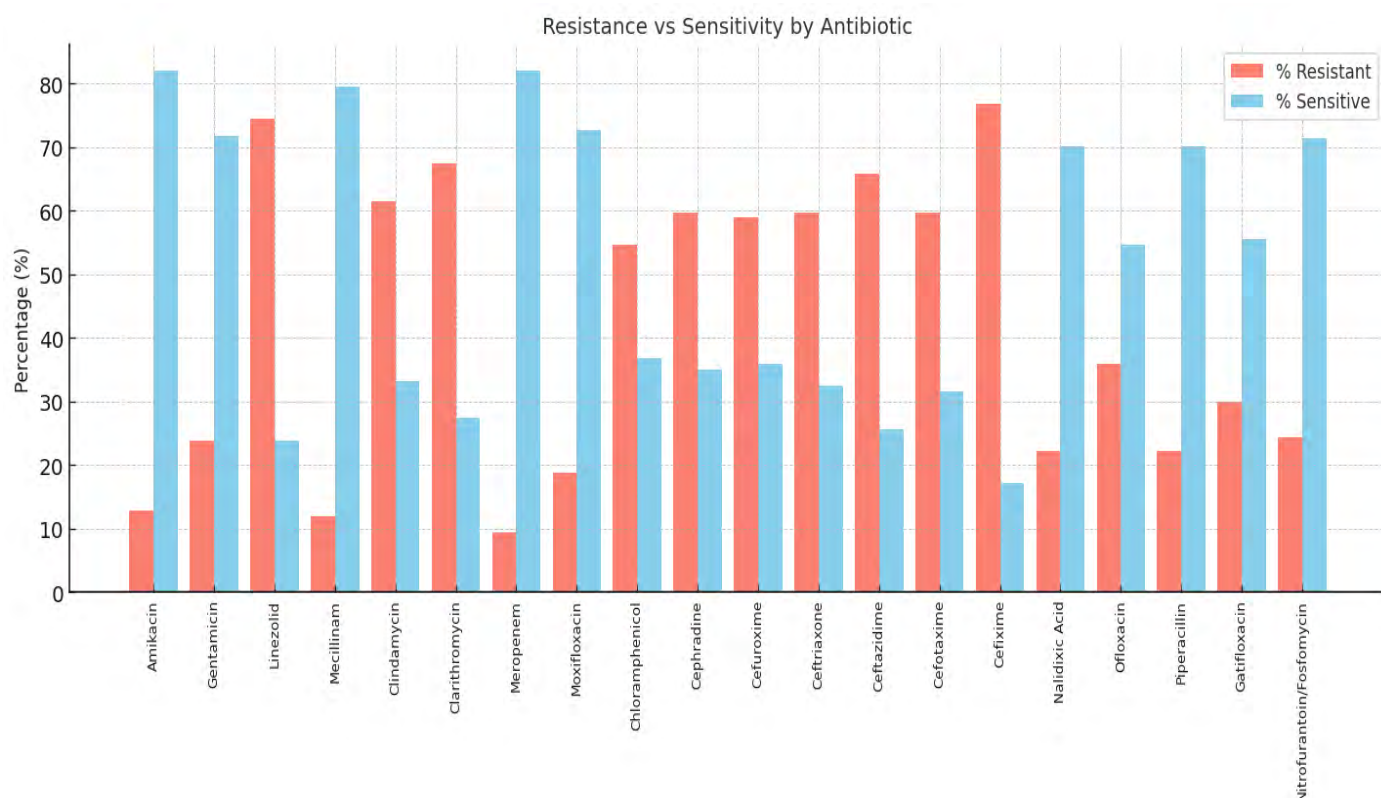


Figure 6 Resistance (%) vs. Sensitivity (%)

Here, we look for each antibiotic tested (20 antibiotics). Red bars show the percentage of all isolates resistant to a given antibiotic, and blue bars show the percentage sensitive.

(Intermediate categories are small and not individually shown.) This chart corresponds to data in Table 4, *Note. Bars represent proportions without CI; detailed CI values are provided in Table 4.* It highlights that for many antibiotics (right half of chart), resistant isolates outnumber sensitive ones.

Figure 6 illustrates the challenge clinicians face: for many commonly used antibiotics (those on the right side of the chart, e.g., cefixime, ceftriaxone, macrolides, co-trimoxazole), the majority of isolates are resistant (red bars taller than blue). Only a few antibiotics (amikacin, meropenem, piperacillin, etc.) have substantially higher susceptibility rates. This visual underscores the critical need for susceptibility-guided therapy in Rangpur. Empiric use of drugs like third-gen cephalosporins or co-trimoxazole would be effective in under 50% of cases given

the resistance patterns. The reliance would have to shift to carbapenems, aminoglycosides, or combinations, which has implications for cost, toxicity, and hospital resource utilization.

3.8 Resistance by Antibiotic Class

To provide a broader overview, the resistance percentages were also aggregated by antibiotic class (combining all antibiotics in a class tested). This helps to identify which classes of drugs are essentially “obsolete” vs. still useful in this setting (Table 5).

Table 5 Overall resistance by antibiotic class across all isolates (N=117)

<i>Antibiotic Class</i>	<i>Total Tests (n)</i>	<i>Resistant (n)</i>	<i>*Resistance (%)</i>
Aminoglycosides	234	43	18.4%
Carbapenems	164	16	9.8%
Cephalosporins	749	478	63.8%
Fluoroquinolones	515	147	28.5%
Glycopeptides	47	20	42.6%
Lincosamide	117	72	61.5%
Macrolides	164	111	67.7%
Nitrofurantoin derivatives	47	18	38.3%
Oxazolidinone	117	87	74.4%
Penicillins (incl. combos)	164	67	40.9%
Phenicol (Chloramphenicol)	117	64	54.7%
Tetracyclines	47	20	42.6%

<i>Antibiotic Class</i>	<i>Total Tests (n)</i>	<i>Resistant (n)</i>	<i>*Resistance (%)</i>
Others (e.g., Fosfomycin, Mecillinam)	70	23	32.9%

From the class-wise analysis, **Oxazolidinones** (represented by linezolid in this study) had the highest resistance rate at 74.4%. This indicates that nearly three-quarters of isolates were resistant to linezolid. This is striking, as linezolid is often used for Gram-positive infections (e.g., MRSA, VRE); the high resistance suggests prior exposure or circulation of linezolid-resistant strains, a worrying development. Linezolid resistance was recorded as 74.4% across all isolates, though this figure reflects aggregated reporting. Since linezolid is only indicated for Gram-positive organisms, this rate should be interpreted with caution. *Note. Oxazolidinone resistance (74.4%) reflects dataset-wide reporting of linezolid, including Gram-negative isolates. Gram-positive-specific data were not available from the laboratory export.*

Macrolides (e.g., azithromycin, erythromycin) also had very high resistance (67.7% overall), and **Cephalosporins** were at 63.8% resistant, consistent with earlier results for individual cephalosporins.

Classes with moderately high resistance included **Lincosamides** (61.5% resistance, reflecting clindamycin resistance, likely among staphylococci) and **Phenicol**s (54.7% resistance for chloramphenicol). **Penicillins** (which here include aminopenicillins and combinations like amoxicillin-clavulanate) had about 40.9% resistance overall – this relatively lower figure is somewhat misleading, as it averages drugs and organisms; the high resistance in Gram-negatives is tempered by these drugs not being tested in all Gram-negatives.

The **lowest resistance classes** were **Carbapenems** at 9.8% (again highlighting carbapenems as the most reliable class currently), and **Aminoglycosides** at 18.4%. Fluoroquinolones were

about 28.5% resistant overall, which, while lower than some classes, is still nearly one-third of isolates resistant – notably high for what used to be a mainstay oral therapy. *Note. Percentages represent pooled resistance rates, derived from the total number of isolates tested for each antibiotic class. 95% confidence intervals (CI) are provided in the text. The total tests refer to the sum of all instances an antibiotic of that class was tested against an isolate. For combination classes and "Other," totals reflect combined counts (e.g., multiple drugs and multiple isolates). Percent resistance is calculated as $(\text{Total R} / \text{Total tested}) \times 100$.*

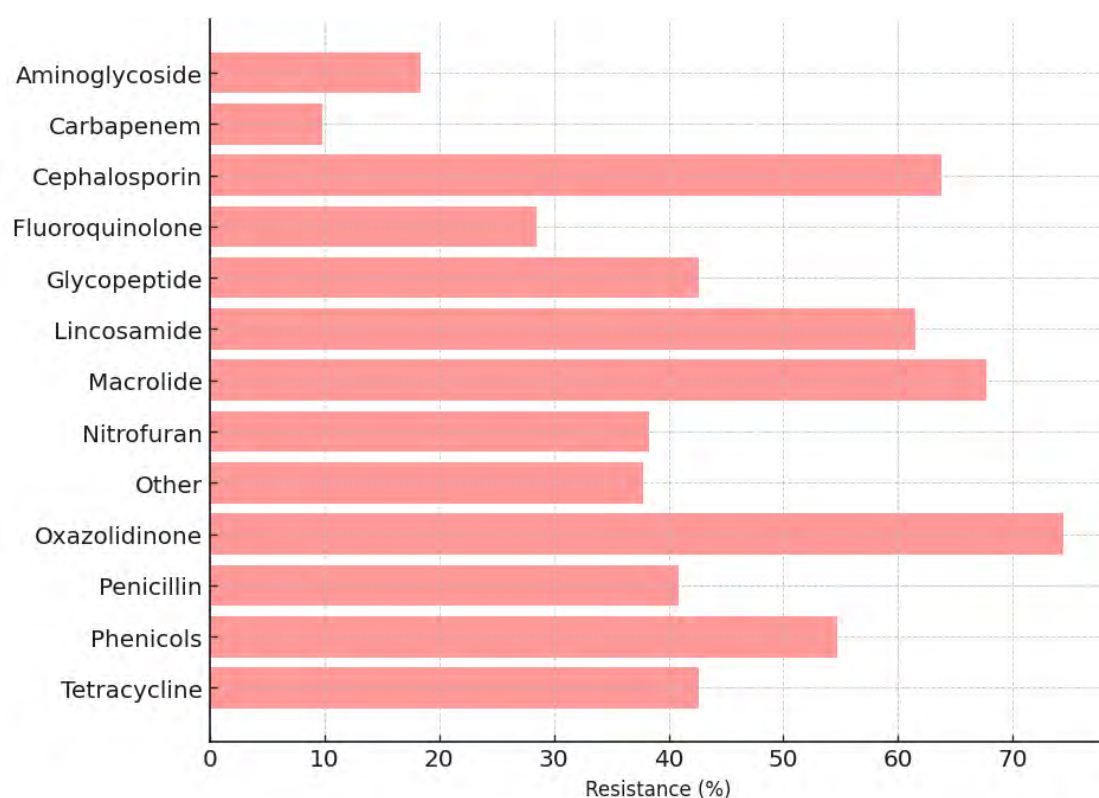


Figure 7 Resistance by antibiotic class

Bars show the percentage of all tested isolates resistant to each class of antibiotics. Oxazolidinones (e.g., linezolid) and macrolides had the highest resistance (>65%), while carbapenems and aminoglycosides had the lowest (<20%). Cephalosporins and macrolides are notably high, reflecting the widespread resistance to those drug classes. *Note. Bars represent class-wise proportions. CI values available in Table 5.*

When aggregated by class (Figure 7), the **highest resistance** was observed in oxazolidinones (74.4%; e.g., linezolid), macrolides (67.7%; e.g., azithromycin), and cephalosporins (63.8%). These are classes for which empirical use in Rangpur would likely be ineffective in the majority of cases. On the other end, **lowest resistance** was seen in carbapenems (9.8% resistance), aminoglycosides (18.4%), and fluoroquinolones (28.5%). However, even fluoroquinolones at 28.5% resistance means more than a quarter of infections would not respond to drugs like ciprofloxacin or levofloxacin, which is problematic. The class-wise view reinforces that penicillins and cephalosporins (the traditionally most-used classes) have lost a great deal of efficacy (roughly 41% and 64% resistance rates, respectively), and newer or broad-spectrum classes (carbapenems, aminoglycosides) have become the remaining options, albeit not without emerging resistance.

Chapter 4

Discussion

The present study investigated the prevalence and antimicrobial resistance patterns of clinical bacterial isolates from Rangpur District, Bangladesh. Our findings reveal an alarmingly high prevalence of multidrug resistance, particularly among Gram-negative organisms. *E. coli* – the most common pathogen in our sample – exhibited a 92.3% MDR rate, and the single *K. pneumoniae* isolate was also MDR (100%). These rates underscore the magnitude of AMR in northern Bangladesh and reflect broader national and regional trends of rising resistance to critical antibiotic classes.

Notably, resistance to third-generation cephalosporins (e.g., cefixime, ceftriaxone) exceeded 60–75% in *E. coli* and *K. pneumoniae* from Rangpur. This is an extremely worrisome finding, as these cephalosporins are commonly used as first-line or second-line therapies for serious infections in Bangladesh. Our data confirm earlier reports suggesting that inappropriate and widespread antibiotic use in both hospital and community settings has accelerated resistance development (Ahmed *et al.*, 2019; IEDCR, 2024). High cephalosporin resistance means clinicians can no longer rely on drugs like ceftriaxone for treating sepsis or severe pneumonia without conducting susceptibility tests, as the likelihood of failure is high. Similarly, ciprofloxacin resistance in *E. coli* reached 76.9%, while overall fluoroquinolone resistance across all isolates was 28.5%, which is consistent with anecdotal reports of ciprofloxacin failing to cure many UTIs in the community. Linezolid showed a resistance rate of 74.4% in our dataset, aligning with some prior regional reports that noted emerging resistance to oxazolidinones. It should be noted that our reported linezolid resistance (74.4%) reflects dataset-wide results, including Gram-negative isolates. Since linezolid is clinically relevant only for Gram-positive pathogens, this value may overestimate the true resistance level in

organisms where the drug is indicated. This highlights the need for organism-specific reporting in future studies to avoid potential misinterpretation.

When comparing our results with previous studies in Bangladesh, our findings are broadly consistent but often show even higher resistance burdens. For example, (Hossain *et al.*, 2020) reported 53% resistance to cefixime in *E. coli* from UTI patients in a different region of Bangladesh. In our Rangpur sample, *E. coli* cefixime resistance was 76.9% (Appendix A Table A), considerably higher. Likewise, (Akter Tanni *et al.*, 2021) documented *K. pneumoniae* isolates with ~77% cefixime resistance in Dhaka hospitals, similar to our *K. pneumoniae* finding (the lone *K. pneumoniae* was resistant to cefixime). However, our observed MDR prevalence in *K. pneumoniae* (100% of one isolate, not generalizable) and *E. coli* (92.3%) appears higher than typical reports from tertiary centers in Dhaka, where MDR *E. coli* rates around 70–80% have been noted. These differences may be due to regional factors such as antibiotic prescribing practices, antibiotic availability, and infection control rigor. For instance, Rangpur being a less resourced area might have higher over-the-counter antibiotic use, leading to more intense resistance selection.

It is also noteworthy that some studies have found slightly lower MDR rates in specific infection contexts. (Rahman *et al.*, 2021) reported about 66% MDR in *E. coli* from wound infections in Dhaka, whereas we found 92.3% in our overall *E. coli* sample (which includes wound, urine, etc.). This might indicate that Rangpur's isolates have accumulated resistance determinants to a greater degree, or it could reflect differences in sample (our study includes many UTI isolates, which tend to be highly resistant due to repeated antibiotic exposure in the community).

Comparison of antibiotic resistance rates in Rangpur (this study) with selected regional and international reports cited in the Discussion. Rangpur values are highlighted in bold.

Table 6 Comparison of Antibiotic Resistance Rates

Country / Region	Pathogen & Antibiotic	Reported Resistance (%)	Rangpur (This Study)	Source
Bangladesh (Dhaka)	E. coli – Cefixime	53%	**79.1%**	Hossain et al., 2020
Bangladesh (Dhaka)	K. pneumoniae – Cefixime	~77%	**100% (1 isolate)**	Akter Tanni et al., 2021
India	Klebsiella/E. coli – Carbapenem	>50%	**9.4% overall; 2.8% in E. coli**	Sonal et al., 2023
Pakistan	K. pneumoniae – ESBL/Carbapenem	>70%	**100% (1 isolate)**	Safdar et al., 2025
Nepal	Mixed Human/Livestock misuse	>50%	**79.1% (E. coli cefixime)**	Acharya & Wilson, 2019
Myanmar	E. coli (poultry) – Cephalosporins	~80%	**63.8% (human E. coli)**	Gibson et al., 2020
Uganda	E. coli (poultry) – Cephalosporins	57–67%	**63.8% (human E. coli)**	Mbatidde et al., 2024

Saudi Arabia	Enterobacterales – ESBL	>50%	**59.8% (E. coli ceftriaxone)**	Torumkuney et al., 2022
Malaysia	E. coli – Ceftriaxone	>50%	**59.8%**	Lau et al., 2024
United Kingdom	E. coli – 3rd gen cephalosporin	<15%	**63.8%**	Wellcome Open Research, 2024
United Kingdom	E. coli – Ciprofloxacin	~19%	**76.9%**	UKHSA, 2023
Australia	E. coli – Ciprofloxacin	~14%	**76.9%**	AGAR, 2023

Neighboring countries report similar trends. In India, national surveillance shows rising carbapenem resistance among *Klebsiella*, *E. coli*, and *Acinetobacter* isolates (Sonal et al., 2023). In Pakistan, nearly 70% inappropriate prescribing has contributed to high ESBL and carbapenem resistance (Safdar et al., 2025). Nepal has also reported rampant misuse in humans and animals, with resistance rates above 50% (Acharya & Wilson, 2019). In Myanmar, poultry farms reported >80% resistant *E. coli* (Gibson et al., 2020), and Uganda found poultry *E. coli* with 57–67% cephalosporin resistance (Mbatidde et al., 2024). In all these comparisons, Rangpur values appear on the higher side (Table 6). *Note. Data are from studies cited in the Discussion section. Rangpur values are based on this study's findings and are highlighted in bold for emphasis. Sources correspond to references below.*

Internationally, the contrast is even starker. Saudi Arabia has reported >50% ESBL- and NDM-positive Enterobacterales (Torumkuney et al., 2022), comparable to our *E. coli* ceftriaxone resistance of 59.8%. In Malaysia, *E. coli* resistance above 50% was also observed (Lau et al.,

2024). However, in high-income countries like the UK and Australia, resistance remains much lower. For instance, third-generation cephalosporin resistance in *E. coli* bloodstream isolates is under 15% in the UK (Wellcome Open Research, 2024), while ciprofloxacin resistance is ~19% (UKHSA, 2023) and ~14% in Australia (AGAR, 2023). In Rangpur, ciprofloxacin resistance was 76.9% — more than fourfold higher (Table 5). By consolidating these comparisons in Table 6, our findings are contextualized against both national and global data, clearly illustrating how severe the AMR crisis is in northern Bangladesh.

The drivers of these patterns in Rangpur likely mirror those elsewhere in Bangladesh: easy availability of antibiotics without prescription, insufficient diagnostic use (leading to broad empiric antibiotic use), and inadequate infection prevention in healthcare settings. Hospitals in resource-limited districts may also reuse supplies or have suboptimal sanitation, facilitating cross-infection with resistant strains. Additionally, poor patient compliance and quality issues with antibiotics (substandard medications) can promote resistance development.

A key strength of this study is that it provides a comprehensive local dataset from Rangpur, an area for which data were previously scarce. By including confidence intervals and comparative tables, we enhanced the interpretability and context of the findings. The data contribute novel insights to national AMR surveillance by highlighting that northern Bangladesh is experiencing as severe (if not more severe) a resistance problem as the capital and neighboring countries.

However, there are several important limitations. First, our study was limited to two hospitals in one district, which may affect generalizability. The resistance rates observed might not exactly represent all of Rangpur Division or other parts of Bangladesh, especially rural communities with different antibiotic use patterns. Second, our analysis relied on retrospective laboratory data without clinical outcome information — we could not assess the impact of resistance on patient outcomes (e.g., treatment failures or mortality). Third, we did not perform molecular characterization of resistance mechanisms due to resource constraints. Such analyses

(e.g., checking for ESBL, carbapenemase genes) would have provided deeper insight into the specific drivers of resistance (for instance, confirming NDM-1 or CTX-M enzyme prevalence). Fourth, the sample size, while adequate for major trends, was relatively small for less common organisms, meaning some findings (like 100% MDR in *K. pneumoniae* based on one isolate) should be interpreted cautiously. Finally, we faced some data gaps (certain antibiotics tested only on subsets of isolates), which required assumptions in analysis; this reflects real-world variability in testing protocols.

Despite these limitations, our study provides crucial baseline data on AMR patterns in a previously underreported region of Bangladesh. The results underscore an urgent need for interventions. On the **clinical front**, physicians in Rangpur and similar settings should rely on antibiotic susceptibility testing wherever possible rather than empiric therapy, given the high likelihood of resistance to common drugs. Empiric treatment guidelines may need to be revised (e.g., avoiding ciprofloxacin or cephalosporins for severe infections and considering carbapenems or aminoglycosides, despite their cost and toxicity, for life-threatening infections). **Public health measures** are equally important: strengthened antimicrobial stewardship programs are needed to regulate antibiotic dispensing and educate both providers and the public on appropriate antibiotic use. Infection control practices in hospitals must be improved to prevent the spread of MDR organisms (for example, implementing strict hand hygiene, contact precautions for patients with MDR bacteria, and routine disinfection protocols).

From a **policy perspective**, the data from Rangpur support the call for a nationwide, integrated AMR surveillance network that includes district-level hospitals. Resources should be allocated to improve laboratory capacity for culture and sensitivity testing in peripheral areas so that resistance can be tracked in real-time. Additionally, incorporating the One Health approach by monitoring antibiotic use and resistance in livestock and agriculture in Rangpur could be

valuable, as the overlap between human and animal antibiotic use likely contributes to the resistance reservoir (as suggested by similar findings in poultry in Uganda and elsewhere).

In conclusion, the AMR situation in Rangpur is dire: common bacteria are extensively drug-resistant, leaving few effective options. This reflects a broader regional crisis that, if unaddressed, could reverse gains in infectious disease control. Urgent, multi-faceted action is required to address this combining local interventions in hospitals with national policy changes and international collaboration. Without immediate and coordinated efforts, we risk entering a post-antibiotic era where routine infections become untreatable.

Chapter 5

Conclusion

Clinical isolates from Rangpur exhibit exceptionally high multidrug resistance rates (over 90% in *E. coli* and 100% in *K. pneumoniae*) and widespread resistance to key antibiotic classes (notably third-generation cephalosporins and fluoroquinolones). These alarming patterns severely limit effective treatment options for common infections and pose a serious public health threat. The findings highlight an urgent need for coordinated interventions: strengthened antimicrobial stewardship to curb inappropriate antibiotic use, improved laboratory capacity and diagnostic stewardship to guide therapy, and comprehensive surveillance (integrating human, animal, and environmental health) to monitor and control the spread of resistance. Without immediate action, the effectiveness of current antibiotics will continue to erode, further compromising regional and national health security. Rangpur's situation serves as a warning that AMR control efforts must intensify across Bangladesh to avert a potential healthcare crisis.

References

- Acharya, K. P., & Wilson, R. T. (2019). Antimicrobial resistance in Nepal. *Frontiers in Medicine*, 6, 105. <https://doi.org/10.3389/fmed.2019.00105>
- Ahmed, I., Rabbi, M. B., & Sultana, S. (2019). Antibiotic resistance in Bangladesh: A systematic review. *International Journal of Infectious Diseases*, 80, 54–61. <https://doi.org/10.1016/j.ijid.2018.12.017>
- Akter Tanni, A., et al. (2021). Genetic determinants of carbapenem resistance in clinical *K. pneumoniae* isolates in Bangladesh. *PLOS ONE*, 16(4), e0248126. <https://doi.org/10.1371/journal.pone.0248126>
- Akter Tanni, A., Hasan, M. M., Sultana, N., Ahmed, W., & Mannan, A. (2021). Prevalence and molecular characterization of antibiotic resistance and associated genes in *Klebsiella pneumoniae* isolates: A clinical observational study in different hospitals in Chattogram, Bangladesh. *PLOS ONE*, 16(9), e0257419. <https://doi.org/10.1371/journal.pone.0257419>
- Australian Group on Antimicrobial Resistance (AGAR). (2023). *Annual report on antimicrobial susceptibility*. Canberra: AGAR. <https://www.agargroup.org.au/>
- Azim, M. R., Iftakhar, K. M. N., Rahman, M. M., & Sakib, Q. N. (2023). Public knowledge, attitudes, and practices regarding antibiotics use and antimicrobial resistance (AMR) in Bangladesh. *Heliyon*, 9, e21166. <https://doi.org/10.1016/j.heliyon.2023.e21166>
- Biswas, M., Roy, M. N., et al. (2014). Self-medication with antibiotics in Bangladesh: A cross-sectional health survey in the private health sector. *BMC Public Health*, 14, 847. <https://doi.org/10.1186/1471-2458-14-847>

- European Centre for Disease Prevention and Control (ECDC). (2023). *Antimicrobial resistance surveillance in Europe 2023*. Stockholm: ECDC.
- European Centre for Disease Prevention and Control (ECDC). (2023). *Surveillance Atlas of Infectious Diseases – Antimicrobial Resistance*. Accessed 2025.
- Gibson, J. S., et al. (2020). Resistant *Escherichia coli* in poultry farms in Myanmar. *Scientific Reports*, 10, 16047. <https://doi.org/10.1038/s41598-020-73076-2>
- Haseeb, A. A., et al. (2023). Threat of antimicrobial resistance among Hajj pilgrims. *Antibiotics*, 12(8), 1299. <https://doi.org/10.3390/antibiotics12081299>
- Hassan, M. M., & Nohor, N. (2025). Perspective on antibiotic resistance in Bangladesh: A critical yet overlooked public health crisis. *Health Science Reports*, 8(1), e70407. <https://doi.org/10.1002/hsr2.70407>
- Hossain, A., et al. (2020). Age and gender-specific antibiotic resistance patterns among Bangladeshi patients with urinary tract infection caused by *Escherichia coli*. *Heliyon*, 6(6), e04161. <https://doi.org/10.1016/j.heliyon.2020.e04161>
- Hossain, M. I., et al. (2023). Antibiotic dispensing without prescription at community pharmacies in Bangladesh: A cross-sectional survey. *BMJ Open*, 13(1), e056678. <https://doi.org/10.1136/bmjopen-2021-056678>
- Hossain, M. S., et al. (2020). Prevalence of extended-spectrum β -lactamase-producing uropathogenic *E. coli* in Dhaka, Bangladesh. *Heliyon*, 6(8), e04640. <https://doi.org/10.1016/j.heliyon.2020.e04640>
- Institute of Epidemiology, Disease Control and Research (IEDCR). (2024). *Annual AMR surveillance report 2024*. Dhaka, Bangladesh.

- Ismail, A. R. A., Guymer, L., Diana, K., Vasso, N., & Kylie, A. (2024). Unveiling antimicrobial resistance trends in Malaysia: A comparative study. *International Journal of Clinical Inventions and Medical Sciences*, 6(2), 101–109.
- Kumarasamy, K. K., et al. (2010). Emergence of a new antibiotic resistance mechanism in India, Pakistan, and the UK: A molecular, biological, and epidemiological study. *The Lancet Infectious Diseases*, 10(9), 597–602. [https://doi.org/10.1016/S1473-3099\(10\)70143-2](https://doi.org/10.1016/S1473-3099(10)70143-2)
- Lau, C. L., et al. (2024). Clinical burden of antimicrobial resistance in Malaysia: A multicenter study. [Advance online publication].
<https://pubmed.ncbi.nlm.nih.gov/39512590>
- Mbatidde, P., et al. (2024). Antimicrobial resistance in *Escherichia coli* from poultry in Uganda. *One Health*, 17, 100762. <https://doi.org/10.1016/j.onehlt.2024.100762>
- Murray, C. J. L., et al. (2022). Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis. *The Lancet*, 399(10325), 629–655.
[https://doi.org/10.1016/S0140-6736\(21\)02724-0](https://doi.org/10.1016/S0140-6736(21)02724-0)
- Rahman, M., et al. (2021). Antimicrobial resistance pattern of bacteria isolated from wound infection in Dhaka, Bangladesh. *Journal of Surgery and Surgical Research*, 7(2), 123–129.
- Safdar, M., et al. (2025). Antimicrobial stewardship in Pakistan: A developing country's perspective. *Journal of Global Antimicrobial Resistance*, 22, 202–210.
- Sharma, M., et al. (2023). Antimicrobial resistance trends in India post-2017: Data from the Indian Network for Surveillance of Antimicrobial Resistance (INSAR). *Indian*

Journal of Medical Microbiology, 41(1), 1–9.

<https://doi.org/10.1016/j.ijmmb.2022.12.001>

Torumkune, D., et al. (2022). Prevalence of ESBL- and NDM-producing Enterobacterales in Saudi Arabia. *Journal of Antimicrobial Chemotherapy*, 77(11), 2976–2983.

<https://doi.org/10.1093/jac/dkac219>

UK Health Security Agency (UKHSA). (2023). *English Surveillance Programme for Antimicrobial Utilisation and Resistance (ESPAUR) Report 2023–2024*. London: UKHSA.

Wahab, A., et al. (2023). Doctors' knowledge, attitudes, and practices regarding antibiotic use in Bangladesh. *BMC Infectious Diseases*, 23, 45. <https://doi.org/10.1186/s12879-023-07888-x>

Wellcome Open Research. (2024). Progress on implementing WHO-GLASS for antimicrobial resistance surveillance. *Wellcome Open Research*, 9, 45.

<https://doi.org/10.12688/wellcomeopenres.19600.2>

Win, L. H. H., Crump, J. A., et al. (2022). Antimicrobial consumption and resistance in Yangon tertiary hospitals. *Antimicrobial Resistance & Infection Control*, 10, 148.

<https://doi.org/10.1186/s13756-022-01116-z>

World Health Organization (WHO). (2022). *Global antimicrobial resistance and use surveillance system (GLASS) report 2022*. Geneva: WHO.

World Health Organization (WHO). (2023). *GLASS report 2023*. Geneva: WHO.

Appendix A. Antibiotic Resistance Profile for Top 5 Isolated

Organisms (Detailed Data)

Table A1. Antibiotic resistance rates (% of isolates resistant with 95% CI) for the five most common organisms. (A dash “—” indicates the antibiotic was not tested for that organism.)

Org anis m	A mi ka ci n	A m ox ycl av	A mo xic illi n	Azi thr om yci n	C ef ep im e	C ef ix i m e	Ce fot axi me	Ce fta zid im e	Cip rofl oxa cin	Cot rim oxa zol e	Ge nt am ici n	Nit rof ura ntoi n	Of lo xa ci n	Pi pe ra cill in	Tet rac ycl ine	Va nc om yci n
<i>E. coli</i> (n=91)	13 .2 % (7 .6 — 22 .0)	86 .4 % (7 7. 6— 91 .9))	57. 4 % (4 6.9 — 67. 2))	65. 9% (55 .4— 74. 9))	0. 0 % (0 — 4. 1))	7 9. 1 % (6 (6 9. 5 — 8 6. 2)	59 .3 % (4 8. 8— 68 .9))	65. 9 % (5 5.4 — 74. 9))	76. 9% (67 .1— 84. 4))	68. 1% (57. 7— 77. 0))	12. 1 % (6. 8— 20. 7))	27. 3% (19. 2— 37. 3))	34 .1 % (2 4. 9— 44 .7)	8.8 % (4. 4— 16. 9))	9.1 % (4. 6— 17. 2))	0.0 % (0— 4.1)
<i>Entero</i>	0. 0	—	16. 7	—	0. 0	0. 0	0. 0	0.0 % 7%	16. 7%	0.0 %	0.0 %	0.0 %	0. 0	0.0 %	—	—

<i>coc</i>	%		%		%	%	%	(0	(3.	(0–	(0	(0–	%	(0		
<i>cus</i>	(0		(3.		(0	(0	(0	–	0–	39.	–	39.	(0	–		
<i>faec</i>	–		0–		–	–	–	39.	56.	0)	39.	0)	–	39.		
<i>alis</i>	39		56.		39	3	39	0)	4)		0)		39	0)		
<i>(n=</i>	.0		4)		.0	9.	.0)						.0			
<i>6)</i>	)				)	0)							)			
<i>Pse</i>	25	10	66.	10	0.	1	10	75.	100	100	10	100	50	0.0	0.0	0.0
<i>udo</i>	.0	0	7	0%	0	0	0	0	%	%	0	%	.0	%	%	%
<i>mo</i>	%	%	%	(51	%	0	%	%	(51	(51.	%	(51.	%	(0	(0–	(0–
<i>nas</i>	(4	(5	(2	.0–	(0	%	(5	(3	.0–	0–	(5	0–	(1	–	49.	49.
<i>spp.</i>	.6	1.	2.7	10	–	(5	1.	0.1	100	100	1.0	100	5.	49.	0)	0)
<i>(n=</i>	–	0–	–	0)	49	1.	0–	–	)	)	–	)	0–	0)		
<i>4)</i>	69	10	94.		.0	0	10	95.			10		85			
	.9	0)	7)		)	–	0)	4)			0)		.0			
	)					1							)			
						0										
						0)										
<i>Sta</i>	0.	—	66.	—	0.	1	66	10	33.	0.0	0.0	—	33	0.0	—	0.0
<i>phy</i>	0		7		0	0	.7	0	3%	%	%		.3	%		%
<i>loc</i>	%		%		%	0	%	%	(6.	(0–	(0		%	(0		(0–
<i>occ</i>	(0		(2		(0	%	(2	(4	1–	56.	–		(6	–		56.
<i>us</i>	–		0.8		–	(4	0.	3.9	79.	1)	56.		.1	56.		1)
<i>aur</i>	56		–		56	3.	8–	–	2)		1)		–	1)		
<i>eus</i>						9							79			

(n=3)	.1)		93.9)		.1)	– 100)	93.9)	100)					.2)			
<i>Coagulase-negative</i>	0.0%	10%	25.0%	100%	0.0%	60%	60.0%	60.0%	0.0%	0.0%	0.0%	0.0%	20.0%	0.0%	0.0%	0.0%
<i>ativ</i>	–	6.	3–	10	–	(2	2.	2.9	4)	4)	43.	43.	–	43.	(3	–
<i>e</i>	43	6–	64.	0)	43	2.	9–	–				4)			–	4)
<i>Sta</i>	.4	10	4)		.4	9	88	88.							62	
<i>phy</i>	)	0)			)	–	.4)	4)							.4	
<i>loc</i>						8									)	
<i>occ</i>						8.										
<i>us</i>						4)										
<i>spp.</i>																
(n=5)																

Appendix B: Additional Data Tables

Table B1. Sex and hospital distribution of patient samples ($N = 200$).

<i>Category</i>	<i>Count</i>	<i>Percentage</i>
Total Samples	200	100.0%
Male patients	86	43.0%
Female patients	114	57.0%
Central Hospital Rangpur	138	69.0%
Popular Diagnostic Centre Rangpur	62	31.0%

Table B2. *Distribution of clinical sample sources (N = 200).*

Sample Source	Count	Percentage
Urine	119	59.5%
Blood	48	24.0%
Pus	15	7.5%
High Vaginal Swab (HVS)	12	6.0%
Wound Swab	3	1.5%
Nasal Swab	2	1.0%
Stool	1	0.5%

Table B3. *Culture results (growth vs. no growth) among all collected samples (N = 200).*

Culture Result	Count	Percentage
Growth	117	58.5%
No Growth	83	41.5%

Appendix C: Bacterial isolates identified (full table)

Table C1. Bacterial isolates from culture-positive samples ($N = 117$).

Organism	Frequency (n)	Percentage of isolates (%)	95% CI
E.coli	91	77.8%	69.4–84.4
Enterococcus faecalis	6	5.1%	2.4–10.7
Staphylococcus spp.	5	4.3%	1.8–9.6
Pseudomonas	4	3.4%	1.3–8.5
Staphylococcus aureus	3	2.6%	0.9–7.3
Streptococcus pyogenes	2	1.7%	0.5–6.0
Staphylococcus haemolyticus	1	0.9%	0.2–4.7
Kocuria kristinae	1	0.9%	0.2–4.7
Klebsiella pneumoniae	1	0.9%	0.2–4.7
Salmonella typhi (NARST)	1	0.9%	0.2–4.7

Enterobacter cloacae complex	1	0.9%	0.2–4.7
Streptococcus spp.	1	0.9%	0.2–4.7

Note: Percentages are based on culture-positive isolates (N = 117). 95% confidence intervals calculated using the Wilson method.