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Burden and Trends of Antimicrobial Resistance Among Major Clinical Bacterial Pathogens in Bangladesh (2019–2024): A Systematic Review and Meta-Analysis

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Abstract

Antimicrobial resistance (AMR) poses a severe global public health threat, particularly in low- and middle-income countries like Bangladesh, where factors such as unregulated antibiotic use, weak surveillance, and inadequate healthcare infrastructure exacerbate the problem. A unified, up-to-date assessment of recent resistance trends is crucial to guide effective public health interventions and optimize clinical decision-making. This systematic review and meta-analysis aimed to evaluate the prevalence and antimicrobial resistance patterns of major clinical bacterial pathogens in Bangladesh between 2019 and 2024. The analysis followed PRISMA guidelines, with data sourced from PubMed, Google Scholar, ResearchGate, and DOAJ. A random-effects model was employed to synthesize data from 30 eligible studies encompassing over 270,000 clinical specimens, providing estimates for the pooled prevalence and resistance patterns of eight major bacterial pathogens. Median resistance (MR) and interquartile ranges (IQR) were also calculated to determine resistance levels for each pathogen–antibiotic pair. The findings revealed that Gram-negative bacteria were most prevalent, with *Escherichia coli* (12%), *Klebsiella* spp. (8%), and *Pseudomonas* spp. (7%) as the most common pathogens. Alarmingly high antibiotic resistance rates were observed across all species, particularly in *Enterococcus* spp. (70%), *Pseudomonas* spp. (56%), *Acinetobacter* spp. (53%), *E. coli* (46%), *Proteus* spp. (44%), *Staphylococcus aureus* (43%), *Klebsiella* spp. (41%), and *Enterobacter* spp. (40%). Resistance was notably high for conventional antibiotics such as β-lactams, cephalosporins, and fluoroquinolones, while concerning levels of resistance were also detected against last-resort antibiotics including carbapenems, colistin, and certain aminoglycosides. These findings highlight the urgent need for national antimicrobial stewardship programs, enhanced surveillance, and coordinated public health strategies to mitigate the escalating threat of AMR.

Introduction

Antibiotics are life-saving medications that revolutionized the treatment of infectious diseases, and their discovery is regarded as one of the most significant scientific breakthroughs of the 20th century [1].Over the past decades, antibiotics have been essential in reducing morbidity and mortality, preventing the spread of infections, and minimizing postoperative and treatment-related complications [2].However, the widespread use of these drugs has led to antimicrobial resistance (AMR), an evolutionary process in which bacteria develop the ability to withstand previously effective treatments [3]. Misuse and overuse of antibiotics have further accelerated this problem, leading to treatment failures, increased morbidity and mortality, rising healthcare costs, and posing a severe threat to global public health[4]. The World Health Organization (WHO) has identified AMR as one of the top ten global public health threats [5]. Projections suggest that by 2050, antibiotic-resistant infections could cause up to 10 million deaths annually and impose an estimated economic burden of USD 100 trillion worldwide [6].

The global issue of antimicrobial resistance (AMR) poses a severe and immediate threat to public health, accounting for an estimated 1.27 million deaths and contributing to nearly 5 million fatalities in 2019 [7]. Each year approximately 2.8 million antibiotic-resistant infections affect people in the United States while more than 35,000 deaths result from these infections [8]. World Health Organization (WHO) declared ESKAPE pathogens (*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and Enterobacter* spp.) to be the highest priority because multiple antibiotics do not work against them [9]. According to the 2022 GLASS report, antimicrobial resistance remains a major concern, with third-generation cephalosporin-resistant *Escherichia coli* reported at 42% and methicillin-resistant *S. aureus* (MRSA) at 35% across 76 countries [10].

Antimicrobial resistance (AMR) poses a disproportionate burden on low- and middle-income countries , where weak healthcare systems, inadequate laboratory infrastructure, limited surveillance, and inappropriate antibiotic use contribute to elevated rates of resistant infections compared to high-income countries (HICs) [11]. A global study conducted in 76 countries reported a 65% increase in total antibiotic consumption between 2000 and 2015, with consumption rates rising by 39% overall and being driven primarily by low- and middle-income countries [12]. Bangladesh, a lower-middle-income country in South Asia, represents one of the most critical hotspots of AMR in the region. Recent reports reveal alarmingly high resistance rates among major bacterial pathogens, posing a direct threat to both national and regional health security [13].

A nationwide surveillance conducted between 2017 and 2020, identified *E. coli* as the predominant pathogen (32.5%), followed by *Klebsiella* spp. (15.5%) and *Pseudomonas* spp. (10.6%) [14].In a tertiary hospital in Mymensingh District, Bangladesh, analyses of 4,403 bacterial isolates (2017–2020) showed increasing resistance over time among commonly prescribed antibiotics, with *E. coli* dominating among Gram-negative pathogens and *S. aureus* being the most prevalent Gram-

positive species [15]. Hospital wastewater isolates in Dhaka showed that 87% of bacteria were resistant to at least three antibiotic classes, with β-lactam and macrolide resistance particularly common [16]. A recent study by A. Rahman et al. (2025) found about 62.9% of *E. coli* isolates from clinical specimens were resistant to third-generation cephalosporins, and around 42% of *S. aureus* isolates were methicillin-resistant (MRSA) [14].A major driver of AMR in Bangladesh is the rampant and unregulated access to antibiotics. It is common for individuals to purchase antibiotics from informal drug sellers or pharmacies without a doctor's prescription, often for conditions like the common cold where antibiotics are ineffective. This is compounded by a lack of awareness among the general population, who may not understand the importance of completing the full course of antibiotics or the risks of self-medication[17]. A survey conducted across three cities in the Jessore district of Bangladesh found that 35.8% of patients failed to complete their prescribed antibiotic courses [18]. Beyond human misuse, the agricultural and aquaculture sectors in Bangladesh further exacerbate the problem, where antibiotics are frequently administered to promote animal growth and prevent disease, thereby creating reservoirs of resistance that can spread to humans and the environment [19].

Given the escalating threat of AMR, particularly in low- and middle-income countries like Bangladesh, comprehensive and up-to-date insights into the local resistance landscape are crucial for guiding effective public health interventions [20]. Although multiple studies have reported antibiotic resistance trends in Bangladesh, most remain fragmented and lack systematic synthesis. Given the rapid escalation of resistance, a unified assessment is crucial to provide an overall picture of the resistance burden in clinically important pathogens. Such evidence not only supports healthcare professionals in clinical decision-making but also alerts policymakers and the public to the urgent need for coordinated action. Therefore, this systematic review and meta-analysis was undertaken to determine the prevalence and antimicrobial resistance patterns of major bacterial pathogens in Bangladesh between 2019 and 2024. This study also aimed to identify surveillance gaps and propose evidence-based recommendations. The findings are intended to serve as a reference for future research and to help policymakers and healthcare providers develop optimal strategies to mitigate antibiotic resistance and its associated problems.

Methods

Study Design and Search Strategy

This systematic review and meta-analysis followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) guidelines [21]. A comprehensive and systematic literature search was conducted across multiple electronic databases, including PubMed, Google Scholar, ResearchGate, and DOAJ, to identify relevant studies on antimicrobial resistance (AMR) in Bangladesh published from January 1, 2019, to December 31, 2024. To ensure broad coverage, only studies published in English were included. The search strategy utilized a combination of keywords and Boolean operators (AND/OR) to ensure a thorough and inclusive retrieval of

relevant articles. Key search terms included “antimicrobial resistance,” “antibiotic susceptibility,” “drug-resistant bacteria,” and specific pathogen names, combined with “Bangladesh.” Following the database searches, titles and abstracts were screened to identify potentially relevant publications. Duplicate records were removed using the reference management software Zotero, and full-text articles of the selected studies were reviewed in detail to assess eligibility based on predefined inclusion and exclusion criteria.

Inclusion and Exclusion Criteria

To ensure a careful and unbiased selection of studies for this systematic review and meta-analysis, strict inclusion and exclusion criteria were set. These criteria were designed to identify original research articles that focused on antibiotic resistance in human samples from Bangladesh, published within a specific time period, and with clear methods and data reporting. Two independent investigators conducted a manual screening of studies identified by the search. Where discrepancies arose between the two investigators, resolution was achieved through discussion and consensus or by consulting a third investigator. The process for study inclusion is shown in a PRISMA flow diagram (Figure 1). A detailed summary of the inclusion and exclusion criteria applied during screening and selection is presented in Table 1.

Table 1. Inclusion and exclusion criteria for studies on antibiotic resistance in Bangladesh (2019–2024).

Inclusion Criteria	**Exclusion Criteria**
Studies published between January 2019 and December 2024	Studies published before 2019 or after 2024
Original research reporting on antibiotic resistance in humans	Studies on non-human subjects or environmental samples
Studies presenting clear methodologies, sampling procedures, and reporting a minimum of 10 bacterial isolates.	Studies presenting insufficient or unclear methodology, or incomplete outcome data.
Studies reporting occurrence, prevalence, and antimicrobial resistance (AMR) patterns of bacterial pathogens	Studies lacking data on antibiotic resistance or susceptibility patterns
Full-text availability of chosen studies	Abstract-only or inaccessible full-text articles

Inclusion Criteria	Exclusion Criteria
Studies published in the English language	Articles in languages other than English

Data extraction

Data extraction was carried out using Microsoft Excel 365 to organize and manage information from the selected studies. The extracted information encompassed key study characteristics such as year of publication, study location, origin of infection, patient category or classification, methods of susceptibility testing, standards for resistance testing, gender, source of infection, and medical condition or illness category. To ensure accuracy and minimize errors, data extraction was performed independently by three reviewers.

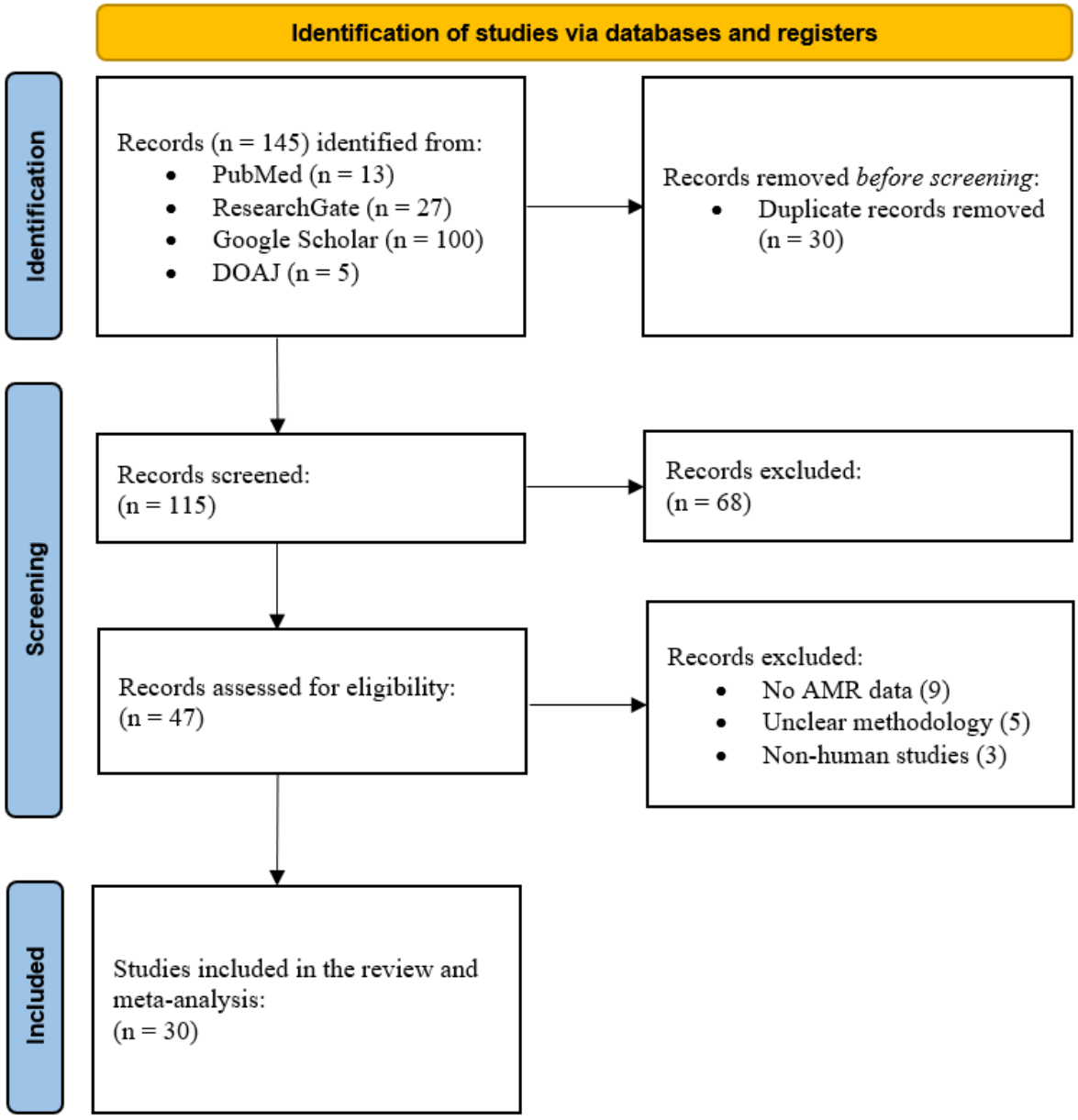


Figure 1: The PRISMA flow diagram of the methodological workflow.

Meta Analysis

Publication bias was assessed using funnel plots, Begg's rank correlation test, and Egger's regression test. Heterogeneity among studies was evaluated with Cochran's Q and Higgins' I^2 statistics [22], with values exceeding 75% considered indicative of high heterogeneity [23]. The prevalence and resistance patterns of each bacterium against different antibiotics was analyzed by

pooling data from individual studies. Since most of the included studies did not provide detailed information on the origin of infection (e.g., hospital-acquired or community-acquired) or patient demographics such as gender, the antibiotic resistance (ABR) data from all studies were combined for this analysis. The resistance for each antibiotic is summarized using the median resistance (MR) along with the interquartile range (IQR). To handle the anticipated high level of heterogeneity among studies, we used a random-effects model. To stabilize the variances of proportions, the inverse variance model [24] and the Freeman–Tukey double arcsine transformation was applied [25], [26]. The pooled prevalence and antibiotic resistance for each pathogen, along with their 95% confidence interval (CI) and 95% prediction interval (PI), are visually represented in forest plots. All statistical analyses were conducted using the R statistical platform with the meta and metafor packages.

Results

Search Results and Study Characteristics

Of the 150 records identified through database searches, 30 studies met the inclusion criteria for this systematic review and meta-analysis. The included studies were published between 2019 and 2024, with the highest proportion in 2024 (10/30, 33.3%), followed by 2020 (7/30, 23.3%), 2021 (6/30, 20.0%), 2019 (3/30, 10.0%), 2023 (3/30, 10.0%), and 2022 (1/30, 3.3%). Geographically, most investigations were conducted within Dhaka (22/30, 73.33%), while the remainder originated from outside Dhaka (8/30, 26.67%). With respect to clinical sources, urinary tract infections were represented in 6 studies (20%), urine samples without specific UTI diagnosis in 2 studies (6.66%), bloodstream infections in 6 studies (20%), Pus sample in 2 studies (6.66%) and stool, sputum and tracheal sample in 1 study each (3.33%), while almost half of the studies (11/30, 36.66%) included multiple sample types. One-third of the studies focused on in-patients (9/30, 30.0%), whereas none involved out-patients, 9 (30.0%) included both categories, and 12 (40.0%) did not specify patient classification. In terms of infection origin, hospital-acquired cases were reported in 3 studies (10%), community-acquired in 1 (3.33%), none involved both and 26 (86.66%) did not specify. Gender distribution was reported in 15 studies (50.0%), while the remaining 15 (50.0%) did not provide this information. Antimicrobial susceptibility testing relied almost exclusively on disk diffusion (29/30, 96.67%), with no study applying dilution methods and one study not reporting the technique. The majority (27/30, 90.0%) adhered to Clinical and Laboratory Standards Institute (CLSI) guidelines, none followed NCCLS standards, and 3 studies (10.0%) did not specify the interpretive criteria. A summary of the characteristics of the studies included in this review is given in Table 2.

Table 2: Key Characteristics of included studies

Variable	**Categories**	**Number (Total =30)**	**Percentage (%)**	**Reference**
Year of publication	2019	3	10.0	[27], [28], [29]

	2020	7	23.3	[30], [31], [32], [33], [34], [35], [36]
	2021	6	20	[37], [38], [39], [40], [41], [42]
	2022	1	3.3	[43]
	2023	3	10.0	[44], [45], [46]
	2024	10	33.3	[47], [48], [49], [50], [51], [52], [53], [54], [55], [56]
Origin of infection	Community-acquired	1	3.33	[45]
	Hospital-acquired	3	10	[33], [46], [52]
	Both	0	0.00	
	Unknown	26	86.66	[27], [28], [29], [30], [31], [32], [34], [35], [36], [37], [38], [39], [40], [41], [42], [43], [44], [47], [48], [49], [50], [51], [53], [54], [55], [56]
Patient category or classification	In-patient	9	30	[31], [33], [41], [42], [46], [47], [48], [49], [55]
	Out-patient	0	0.00	
	Inpatient and outpatient	9	30	[28], [29], [32], [34], [37], [38], [43], [45], [52]
	Did not mention	12	40	[27], [30], [35], [36], [39], [40], [44], [50], [51], [53], [54], [56]
Methods for testing resistance	Disk diffusion	29	96.66	[27], [28], [29], [30], [31], [32], [33], [34], [35], [36], [37], [38], [39], [40], [41], [42], [43], [44], [46], [47], [48], [49], [50], [51], [52], [53], [54], [55], [56]
	Dilution	0	00.00	
	Not mention	1	3.33	[45]

Standard for resistance testing	CLSI	27	90	[28], [29], [30], [31], [32], [33], [34], [35], [36], [37], [38], [39], [40], [41], [42], [43], [44], [46], [47], [49], [50], [51], [52], [53], [54], [55], [56]
	NCCLS	0	00.00	
	Did not mention	3	10	[27], [45], [48]
Location	Within Dhaka	22	73.33	[29], [30], [31], [32], [34], [36], [37], [38], [39], [40], [41], [42], [44], [45], [46], [47], [49], [50], [52], [53], [55], [56]
	Outside of Dhaka	8	26.66	[27], [28], [33], [35], [43], [48], [51], [54]
Gender	Both (male and female)	15	50	[27], [29], [30], [32], [33], [34], [35], [37], [41], [43], [44], [45], [48], [53], [55]
	Unavailable	15	50	[28], [31], [36], [38], [39], [40], [42], [46], [47], [49], [50], [51], [52], [54], [56]
Medical condition or illness category	Urinary tract infection	6	20	[28], [29], [30], [31], [32], [35], [43]
	stool samples	1	3.66	[35]
	Urine sample	2	6.66	[27], [37]
	Blood sample	6	20	[34], [41], [44], [47], [48], [50], [54]
	Pus sample	2	6.66	[53], [54]
	Sputum samples	1	3.33	[45]
	Multiple samples/infection	11	36.66	[33], [36], [38], [39], [40], [42], [46], [49], [51], [52], [56]
	Tracheal Sample	1	3.33	[55]

Pooled Prevalence of Bacterial Pathogens

The pooled prevalence of major bacterial pathogens in Bangladesh was estimated through a random-effects meta-analysis of 30 studies conducted between 2019 and 2024, encompassing more than 270,000 clinical specimens collected from diverse patient populations across the country. The analysis focused on eight major bacterial groups: *Acinetobacter* spp., *Klebsiella* spp., *Pseudomonas* spp., *E. coli*, *Proteus* spp., *S. aureus*, *Enterococcus* spp., and *Enterobacter* spp. Among these, *E. coli* exhibited the highest pooled prevalence at 12% (95% CI: 8–16%; I^2 = 98.9%), followed by *Klebsiella* spp. (8%; 95% CI: 4–12%; I^2 = 98.3%) and *Pseudomonas* spp. (7%; 95% CI: 3–13%; I^2 = 99.5%). *Acinetobacter* spp. accounted for 6% (95% CI: 2–12%; I^2 = 98.8%), while *S. aureus* contributed 5% (95% CI: 2–8%; I^2 = 98.2%). *Proteus* spp. and *Enterobacter* spp. were less common, each at 3% (95% CI: 1–6% and 0–7%, respectively). *Enterococcus* spp. was the least prevalent at 2% (95% CI: 0–4%; I^2 = 97.5%).Prediction intervals were wide for all pathogens, with *E. coli* ranging from 1 to 34 percent and *Pseudomonas* spp. from 0 to 45 percent, reflecting substantial between-study variability and suggesting that prevalence in individual settings may deviate considerably from the pooled estimates. The consistently high heterogeneity, with I^2 values exceeding 96 percent for all organisms, is likely driven by differences in patient populations, specimen types such as blood, urine, respiratory, and wound samples, diagnostic methodologies, and study periods, which highlights the need for context-specific interpretation.

Notably, Gram-negative organisms dominated the bacterial landscape, with *E. coli* and *Klebsiella* spp. together comprising more than half of all reported isolates. This underscores their clinical significance, particularly in bloodstream and urinary tract infections, and their role as key targets for antimicrobial stewardship and infection prevention programs in Bangladesh.

Forest plots summarizing the pooled prevalence for each organism are presented in Supplementary Figures (S1–S8). Regression tests and rank correlation tests indicated evidence of publication bias for several pathogens (Table 3). Significant heterogeneity was confirmed using Cochrane's Q and I^2 statistics, while Baujat plots were utilized to identify the studies contributing most to heterogeneity. Results of influential study analyses are also reported in Table 3.

Table 3: Meta-Analysis of Pooled Prevalence of Bacterial Pathogens in Clinical Samples,

Pathogen	Overall Percent Pooled Prevalence (95%CI)	Influential Studies	Percent Pooled Prevalence After Removal of the Influential Study (95%CI)	Heterog-eneity (I2)	Between Study Variance (τ^2)	Overall Regression Test (p Value)	Overall Rank Cor-relation Test (p Value)
Klebsiella spp.	8% (4%; 12%)	Haque et al. (2024)	6.69% (3.61%; 10.60%)	0.98	0.024052	0.0001	0.0908
Pseudomonas spp.	7% (3%; 13%)	Kabir et al. (2024)	6.09% (2.66%; 10.75%)	0.99	0.046805	0.0064	0.0201
E. coli	12% (8%;16%)	R. Saha et al. (2024)	12.82% (9.54%; 16.49%)	0.99	0.015799	0.4146	0.6504
Acinetobacter spp.	6% (2%; 12%)	Haque et al. (2024)	4.90% (1.57%; 9.82%)	0.99	0.046318	0.0009	0.1073

S. aureus	5% (2%; 8%)	Safain et al. (2021)	3.92% (1.50%; 7.33%)	0.98	0.021825	0.0015	0.0251
Proteus spp.	3% (1%; 6%)	Baral et al. (2024)	1.92% (0.55%; 4.05%)	0.99	0.016359	0.0085	0.0758
Enterococcus spp.	2% (0%; 4%)	Nobel et al. (2024)	1.29% (0.40%; 2.65%)	0.97	0.008643	0.3706	0.5322
Enterobacter spp.	3% (0%; 7%)	T. Rahman et al. (2021)	1.93% (0.13%; 5.42%)	0.96	0.021651	0.1704	0.3918

Pooled Resistance of Bacterial Pathogens

The overall resistance burden of each bacterial species across all antibiotic classes was estimated using a random-effects meta-analysis, yielding pooled resistance proportions with 95% confidence intervals. Forest plots illustrated the distribution of resistance across studies, with estimates clustering near 0% or 100%, and the pooled effect sizes represented by diamonds. Individual forest plots for each organism are presented in Figures 2–9. Substantial heterogeneity was observed (I^2 = 99.99%, $p < 0.001$), reflecting variability in study populations, methodologies, and geographic settings.

The pooled resistance proportions were 41% for *Klebsiella* spp. (95% CI: 0.340–0.496, I^2 = 99.71%), 56.% for *Pseudomonas* spp. (95% CI: 0.483–0.636, I^2 = 99.85%), 46% for *E. coli* (95% CI: 0.387–0.548, I^2 = 99.90%), 53% for *Acinetobacter* spp. (95% CI: 0.459–0.596, I^2 = 97.99%), 43% for *S. aureus* (95% CI: 0.344–0.533, I^2 = 99.89%), 44% for *Proteus* spp. (95% CI: 0.323–0.561, I^2 = 99.99%), 70% for *Enterococcus* spp. (95% CI: 0.554–0.770, I^2 = 99.65%), and 40% for *Enterobacter* spp. (95% CI: 0.334–0.531, I^2 = 99.98%).

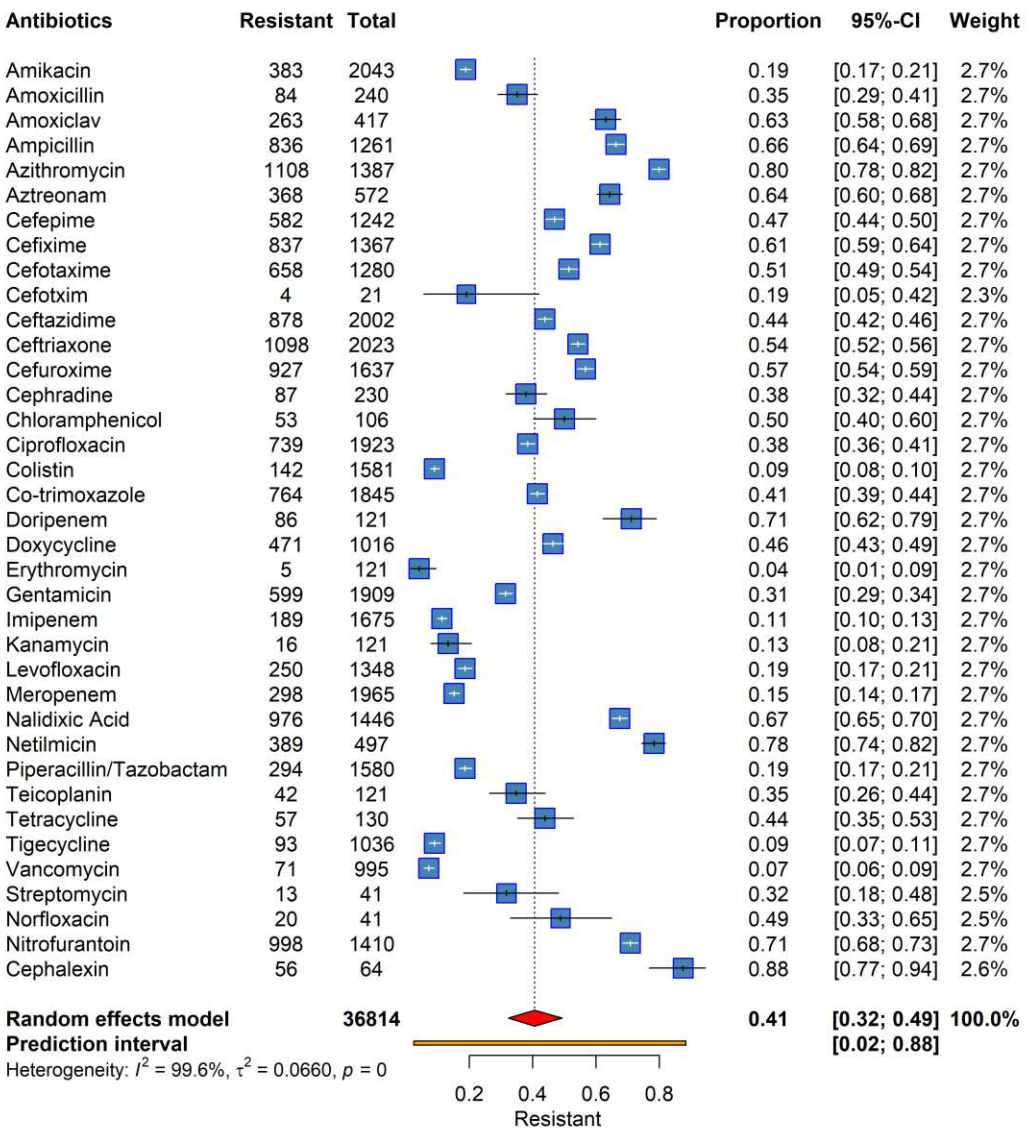


Figure 2: Forest plot depicting the pooled resistance of *Klebsiella* spp. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

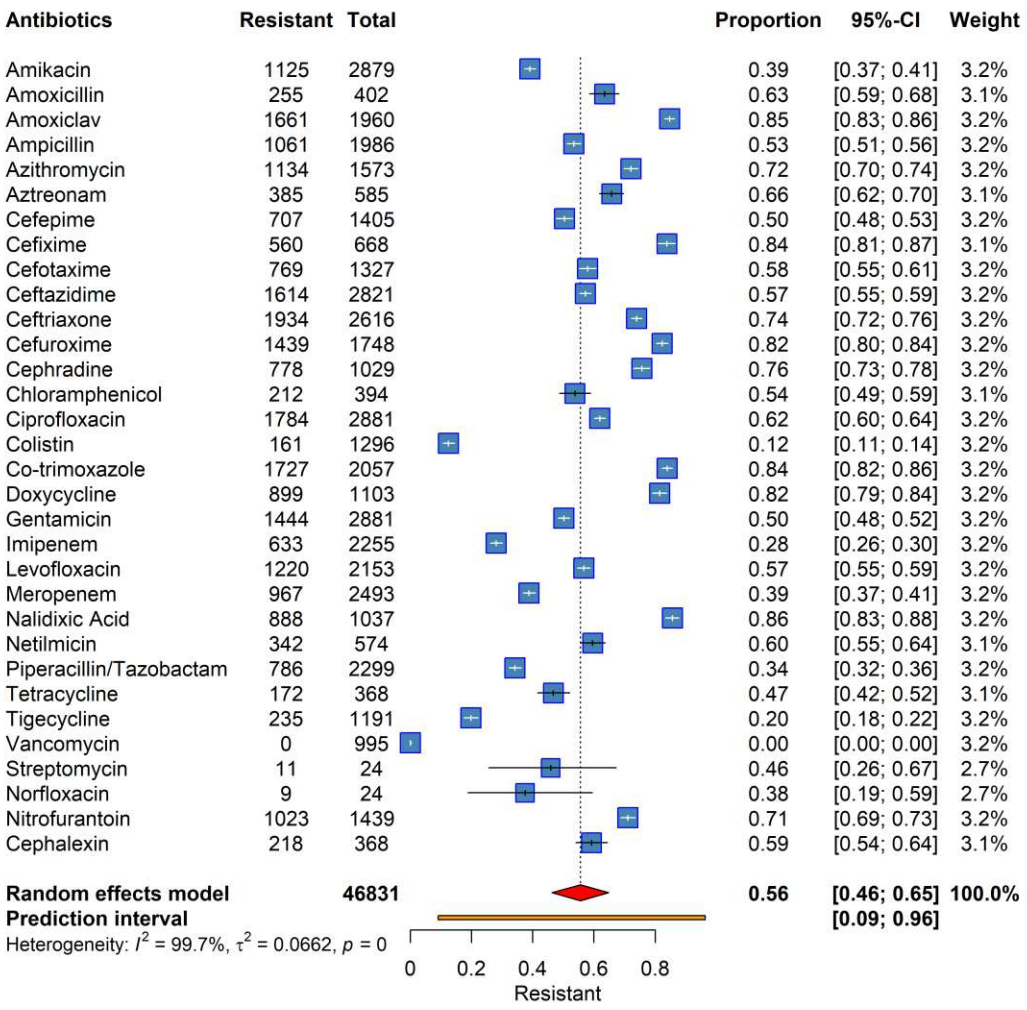


Figure 3. Forest plot depicting the pooled resistance of *Pseudomonas* spp. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

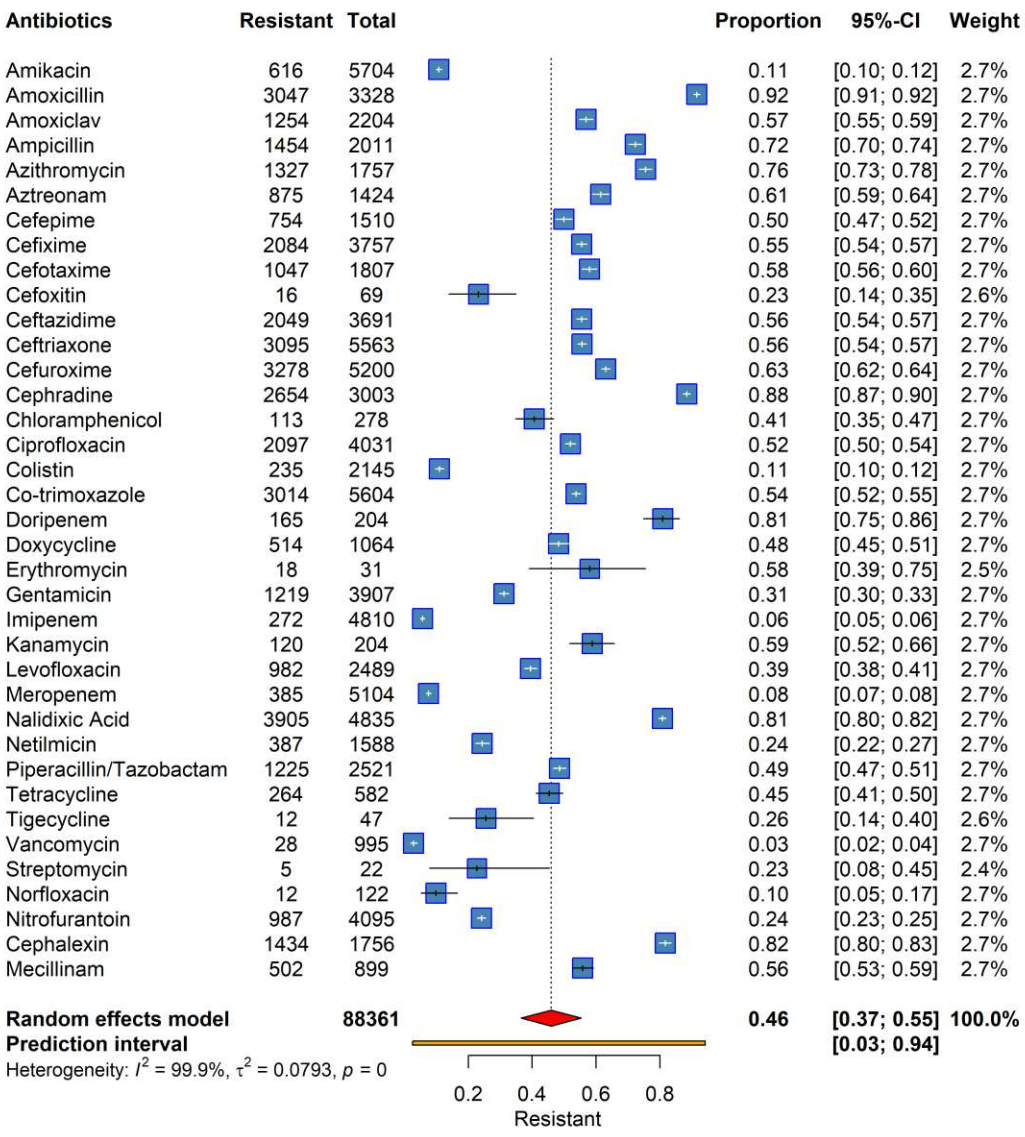


Figure 4: Forest plot depicting the pooled resistance of *E. coli*. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

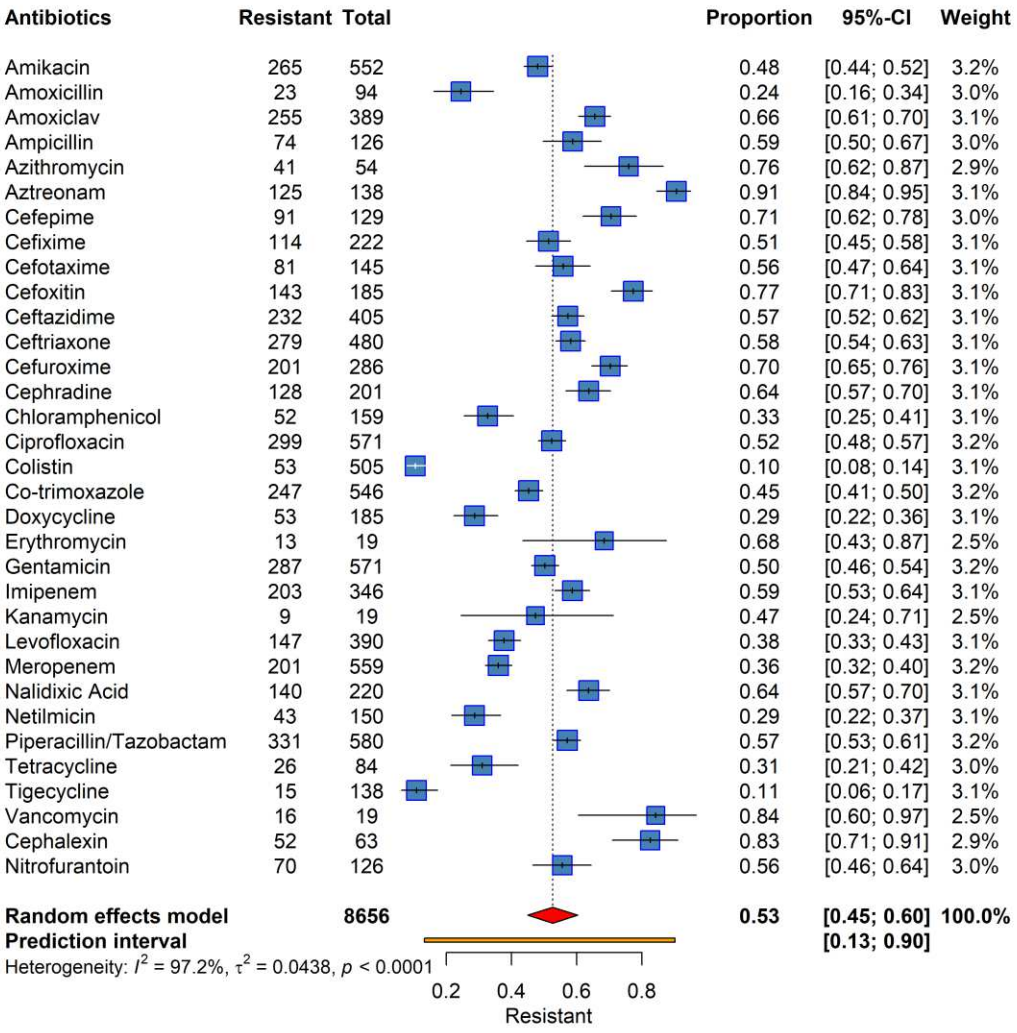


Figure 5: Forest plot depicting the pooled resistance of *Acinetobacter* spp. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

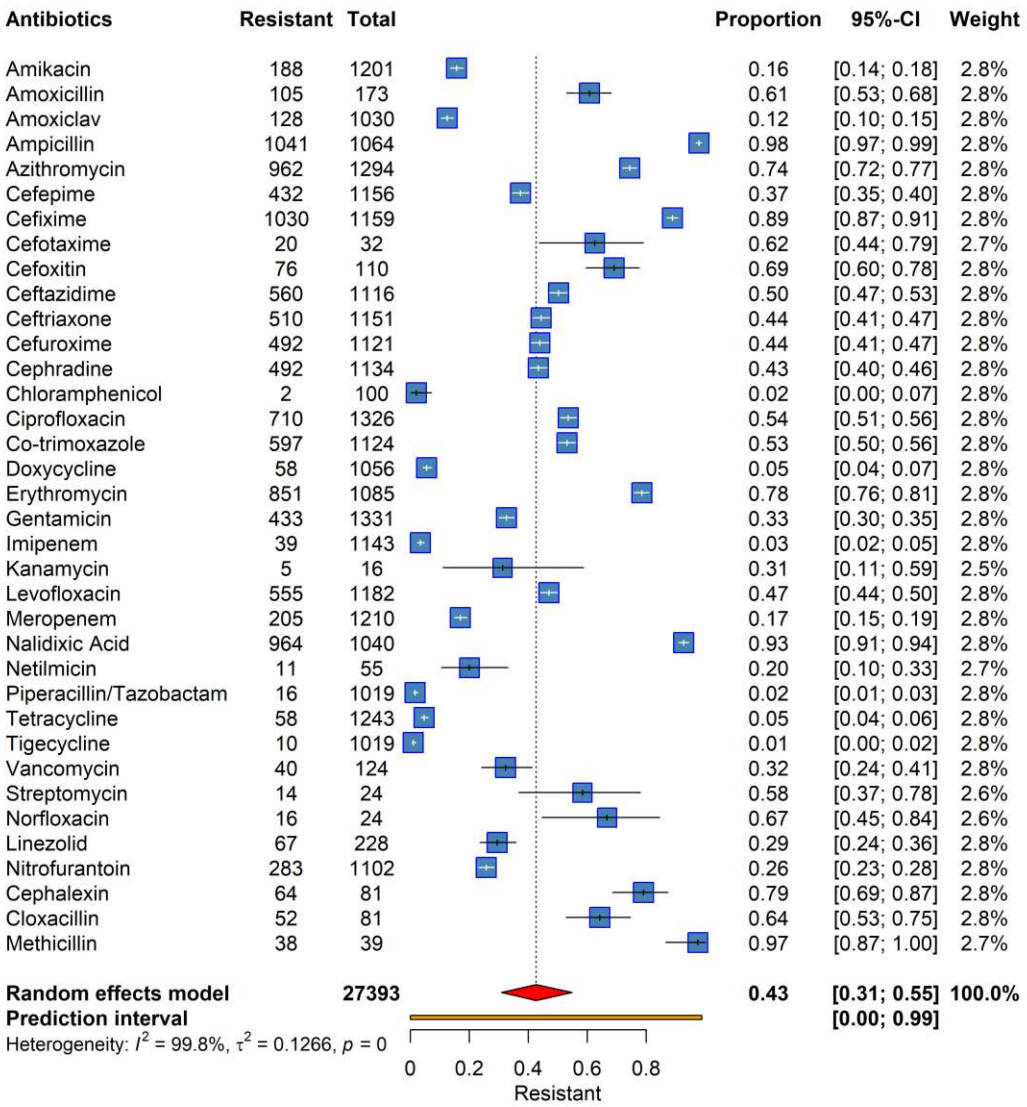


Figure 6: Forest plot depicting the pooled resistance of *S. aureus*. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

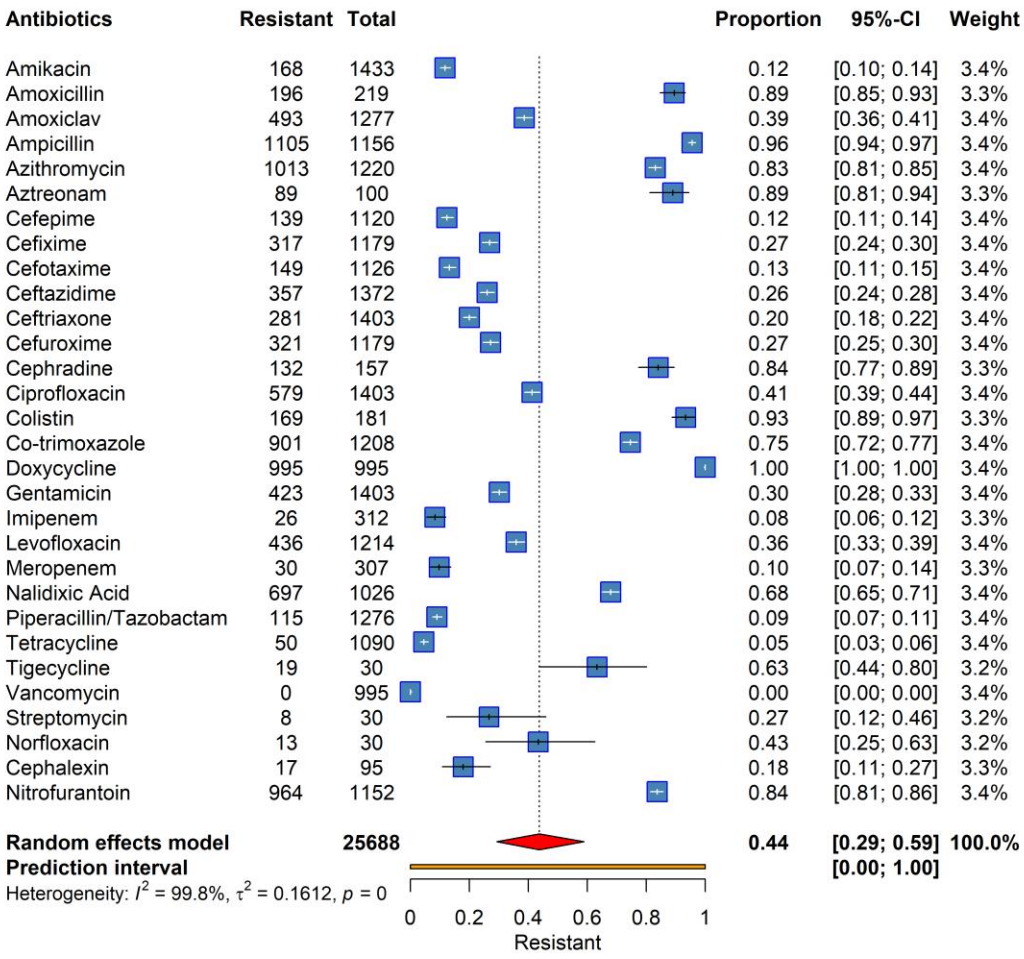


Figure 7: Forest plot depicting the pooled resistance of *Proteus* spp. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

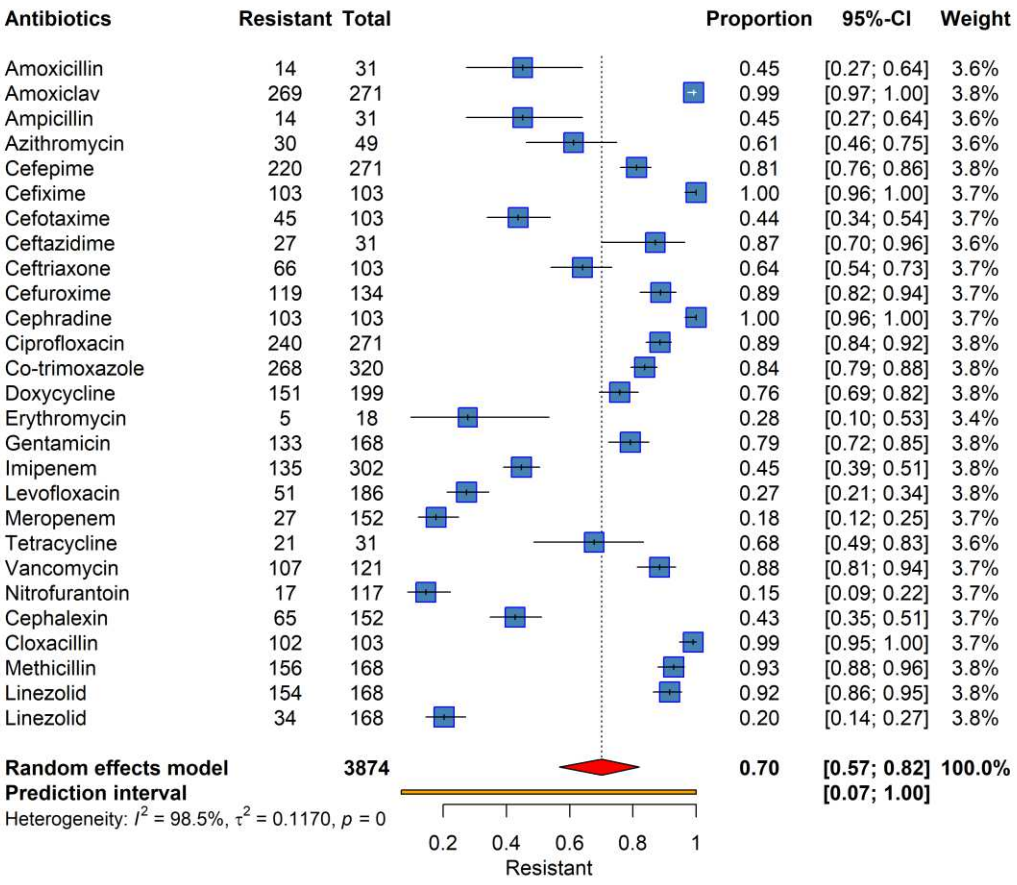


Figure 8: Forest plot depicting the pooled resistance of *Enterococcus* spp. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

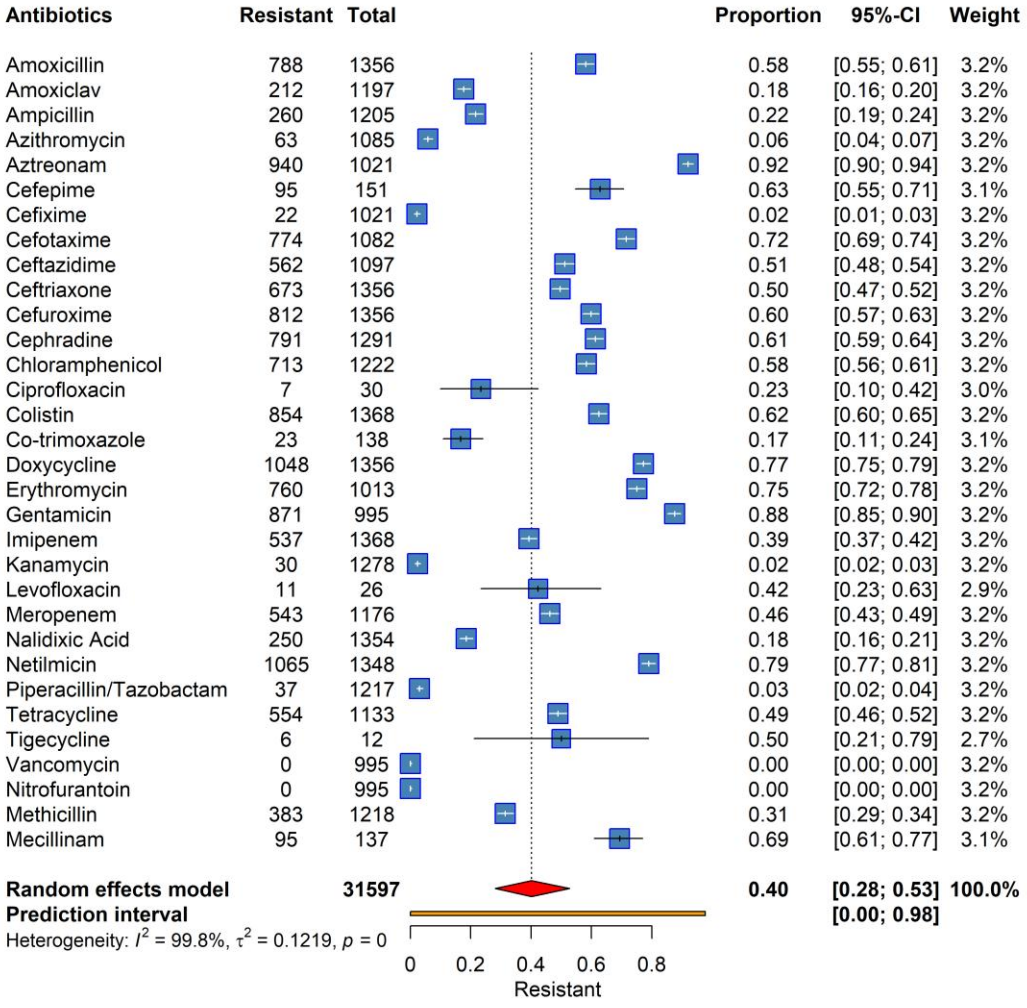


Figure 9: Forest plot depicting the pooled resistance of *Enterobacter* spp. Squares represent study-specific estimates weighted by sample size, horizontal lines show 95% confidence intervals, and the red diamond indicates the overall pooled estimate.

Antibiotic-wise Resistance Patterns

Resistance levels across bacterial species were also evaluated by calculating the median resistance rate (MR) and interquartile range (IQR) for each antibiotic–organism pair. Among the 30 studies reviewed, *Klebsiella* spp. were reported in 17 studies. These isolates showed high resistance to Ampicillin 82.37% (IQR 70.51-88.09%), Cephalexin 87.5% (IQR 87.5-87.5%) and low resistance to Colistin 2.12% (IQR 0.60-27.12%), Erythromycin 4.13% (IQR 4.13-4.13%), Tigecycline 10% (IQR 8.06-36.70%), Vancomycin 7.14% (IQR 7.14-7.14%). The *Acinetobacter* spp. Were reported in 12 studies showing that high resistance Amoxiclav 80.49% (IQR 67.73-83.23%), Aztreonam 87.28% (IQR 82.53-92.02%), Vancomycin 84.21% (IQR 84.21-84.21%), Cefepime 95.56% (IQR 70.09-97.78%), Cefoxitin 97.33% (IQR 67.89-98.67%). However low resistance to Colistin 8.24% (IQR 4.88-19.51%), Tigecycline 10.36% (IQR 9.62-11.09%). From 18 studies, *Pseudomonas* spp. showed high resistance to Amoxiclav, Ampicillin, Cefuroxime, Cephradine, Co-trimoxazole, Doxycycline, Nalidixic Acid, which are 87.67% (IQR 79.16-93.14%), 82.53% (IQR 58.17-96.87%), 87.13% (IQR 61.90-98.41%), 84.54% (IQR 79.75-89.33%), 83.33% (IQR 75-87.03%), 87.69% (IQR 83.84-91.53%),84.53% (IQR 83.93-85.12) individually. No resistance showed Vancomycin 0% (IQR 0-0%). Individually, another 18 studies reported that, *E. coli.* showed high resistance in Amoxicillin, Ampicillin, Cephradine, Doripenem, Doxycycline which are 92.44% (IQR 88.47-95.84%), 82.58% (IQR 74.78-92.33%), 89.93% (IQR 88.20-91.30%), 80.88% (IQR 80.88-80.88%), 80.29% (IQR 80.29-80.29%) respectively, and show low resistance to Imipenem 10.36% (IQR 2.56-41%), Vancomycin 0% (IQR 0-0%). *Proteus* spp. were reported in 8 study showing high resistance to Amoxicillin, Aztreonam, Cephradine, Colistin, Nitrofurantoin which are 92.47% (IQR 88.86-93%), 89% (IQR 89-89%), 83.15% (IQR 80.28-88.34%), 95.69% (IQR 87.84-96.12%), 84.22% (IQR 81.58-85.66%) respectively, low resistance show Imipenem 10.75% (IQR 1.72-33.33%), Meropenem 6.45% (IQR 1.72-19.35%), Tetracycline 5.36% (IQR 4.89-5.83%) and Vancomycin 0%(IQR 0-0%) most effective drug against *proteus* spp. *S. aureus* was reported in 12 study showing that high resistance to Ampicillin 83.33% (IQR 10.52-92.30%), Mecillinam 97.43% (67.72-97.43%) and low resistance to Chloramphenicol, Imipenem, Piperacillin/Tazobactam, Tigecycline, Vancomycin which are 0% (IQR 0-6.25%), 3.64% (IQR 2.56-33.37%), 0% (IQR 0-33.33%), 0% (IQR 0-20.83%), 7.41% (IQR 5.12-18.74%) respectively. *Enterococcus* spp. was reported in 4 study showing that high resistance to Amoxicillin, Cefepime, Cefuroxime, Cephradine, Cephalexin, Mecillinam, Cloxacillin which are 99.4% (IQR 99.1-99.7%), 100% (IQR 100-100%), 100% (IQR 100-100%), 90.58% (IQR 86.36-94.80%), 99.02% (IQR 99.02-99.02%), 91.66% (IQR 91.66-91.66%), 98.21% (IQR 98.21-98.21%) respectively. *Enterobacter* spp. was reported in 8 study showing that high resistance in Nalidixic Acid 80.55% (IQR 57.72-83.73%) and show low resistance Colistin, Imipenem, Ampicillin, Tigecycline which are 5.45% (IQR 4.26-52.73%), 10.69% (IQR 7.27-14.59%), 11.11% (IQR 5.55-47.91%), 0% (IQR 0-0%). The detailed pooled resistance estimates for each pathogen–antibiotic pair, expressed as median resistance (MR) with interquartile range (IQR), are presented in Tables 4 and 5.

Table 4: Median resistance (MR) with interquartile range (IQR) and number of isolates (n) for selected bacterial pathogens across included studies.

Antibiotics	***Klebsiella* spp.**		***Acinetobacter* spp.**		***Pseudomonas* spp.**		***E. coli***	
	MR % (IQR)	**n**	**MR % (IQR)**	**n**	**MR % (IQR)**	**n**	**MR % (IQR)**	**n**
Amikacin	22.73 (13.67-52.70)	2043	46.15 (41.46-82.67)	552	37.05 (19.01-53.76)	2879	16.45 (10.61-25.75)	5704
Amoxicillin	56.47 (32.41-78.93)	240	44.80 (27.74-61.87))	94	78.69 (69.50-87.87)	402	92.44 (88.47-95.84)	3328
Amoxiclav	75 (53.25-78.18)	417	80.49 (67.73-83.23)	389	87.67 (79.16-93.14)	1960	78.23 (70.78-83.31)	2204
Ampicillin	82.37 (70.51-88.09)	1261	58.73 (58.73-58.73)	126	82.53 (58.17-96.87)	1986	82.58 (74.78-92.33)	2011
Azithromycin	58.54 (45.24-68.89)	1387	57.89 (28.95-65.53)	54	66.66 (41.88-74.57)	1573	62.87 (53.94-75.62)	1757
Aztreonam	67.72 (41.18-85.28)	572	87.28 (82.53-92.02)	138	57.77 (48.88-71.71)	585	67 (47.82-68.96)	1424
Cefepime	47.11 (43.82-68.29)	1242	95.56 (70.09-97.78)	129	42.01 (35.29-58.64)	1405	58 (18-330)	1510
Cefixime	61.16 (59.45-72.99)	1367	37.02 (27.12-40.15)	222	79.61 (70.83-82.35)	668	71.01 (49.74-73.97)	3757
Cefotaxime	52.40 (40.96-64.10)	1280	70.13 (60.46-79.80)	145	52.66 (37.33-74.39)	1327	53 (52.83-53.19)	1807
Cefoxitin	19.05 (19.05-19,05)	21	97.33 (67.89-98.67)	185			23.18 (23.18-23.18)	69
Ceftazidime	42.45 (23.08-70.57)	2002	57.94 (47.73-90.25)	405	53.52 (38.30-62.90)	2821	60 (39.84-66.28)	3691
Ceftriaxone	55.10 (44.77-66.70)	2023	55.56 (35-87.80)	480	72.22 (42.30-88.63)	2616	64.85 (50.91-69.67)	5563
Cefuroxime	56.01 (51.52-73.90)	1637	61.94 (43.08-79.68)	286	87.13 (61.90-98.41)	1748	71.78 (57.69-74.77)	5200
Cephradine	76.19 (4524-78.42)	230	54.84 (37.42-72.26)	201	84.54 (79.75-89.33)	1029	89.93 (88.20-91.30)	3003
Chloramphenicol	44.05 (30.91-57.18)	106	19.8 (8.88-32.24)	159	37.74 (28.48-46.99)	394	40 (23.50-56.02)	278
Ciprofloxacin	43.20 (26.81-71.90)	1923	42.11 (36.56-76.22)	571	55.31 (32.35-71.11)	2881	53 (36.48-60.72)	4031
Colistin	2.12 (0.60-27.12)	1581	8.24 (4.88-19.51)	505	14.48 (6.04-34.37)	1296	24.38 (1.44-42.63)	2145
Co-trimoxazole	51.36 (33.39-57.95)	1845	56 (40.70-58.37)	546	83.33 (75-87.03)	2057	60.62 (47.08-64.63)	5604
Doripenem	71.07	121					80.88	204

	(71.07-71.07)						(80.88-80.88)	
Doxycycline	53.97 (50.01-57.94)	1016	46.60 (37.15-49.97)	185	87.69 (83.84-91.53)	1103	80.29 (80.29-80.29)	1064
Erythromycin	4.13 (4.13-4.13)	121	68.42 (68.42-68.42)	19			58.06 (58.06-58.06)	31
Gentamicin	40 (22.58-51.02))	1909	54.80 (35.79-73.50)	571	61.55 (33.61-76.95)	2881	37.23 (29.03-40.12)	3907
Imipenem	14.29 (7.93-43.29)	1675	56.10 (26.75-75.70)	346	32.49 (27.25-41.82)	2255	10.36 (2.56-41)	4810
Kanamycin	13.22 (13.22-13.22)	121	50 (50-50)	19			58.82 (58.82-58.82)	204
Levofloxacin	27.02 (17.86-32.67)	1348	34.09 (26.66-48.12)	390	55.17 (26.05-66.55)	2153	52.26 (29.55-55.84)	2489
Meropenem	13.64 (6.45-52.07)	1965	20.51 (17.69-46.43)	559	32 (17.18-159)	2493	15.64 (6.49-21.81)	5104
Nalidixic Acid	77.42 (49.95-82.31)	1446	45.33 (43.72-61.55)	220	84.53 (83.93-85.12)	1037	78.71 (70.80-86.97)	4835
Netilmicin	31.40 (19.05-56.10)	497	12.90 (10.81-31.07)	150	68.89 (34.52-73.73)	574	18.12 (15.94)	1588
Piperacillin/Tazobactam	23.41 (9.39-49.59)	1580	65 (38.46-92)	580	27 (23.14-42.91)	2299	44.10 (21.40-61.50)	2521
Teicoplanin	19.57 (12.01-27.14)	121						
Tetracycline	63.77 (62.83-63.77)	130	27.69 (13.85-34.90)	84	46.73 (46.43-46.43)	368	57.60 (35.44-65.86)	582
Tigecycline	10 (8.06-36.70)	1036	10.36 (9.62-11.09)	138	62.50 (30.76-71.05)	1191	12 (10.77-40.90)	47
Vancomycin	7.14 (7.14-7.14)	995	84.21 (84.21-84.21)	19	0 (0-0)	995	0 (0-0)	995
Streptomycin	31.71 (31.71-31.71)	41			45.83 (45.83-45.83)	24	22.72 (22.72-22.72)	22
Norfloxacin	48.78 (48.78-48.78)	41			37.5 (37.5-37.5)	24	46.77 (42.88-50.66)	122
Nitrofurantoin	49.70 (33.70-72.47)	1410	70 (70-70)	126	68.52 (58.01-74.36)	1439	21.31 (14.76-41.54)	4095
Cephalexin	87.5 (87.5-87.5)	64			59.23 (59.23-59.23)	368	61.38 (50.04-72.72)	1756
Mecillinam							55.83 (55.83-55.83)	899

Table 5: Median resistance (MR) with interquartile range (IQR) and number of isolates (n) for selected bacterial pathogens across included studies.

Antibiotics	***Proteus* SPP.**		***S. aureus***		***Enterococcus* SPP.**		***Enterobacter* SPP.**	
	MR % (IQR)	**n**	**MR % (IQR)**	n	**MR % (IQR)**	***n***	**MR % (IQR)**	***n***
Amikacin	20.96 (9.38-38.27)	1433	31.83 (9.67-63.98)	1201	45.16 (45.16-45.16)	31	24.04 (20.88-58.57)	1356
Amoxicillin	92.47 (88.86-93)	219	73.36 (40.71-94.87)	173	99.4 (99.1-99.7)	271	59.44 (39-74.53)	1197
Amoxiclav	77.41 (58.62-83)	1277	21.15 (8.28-40.54)	1030	45.16 (45.16-15.16)	31	69.44 (66.66-89.23)	1205
Ampicillin	77.09 (61.48-85)	1156	83.33 (10.52-92.30)	1064	50.72 (30.91-70.52)	49	11.11 (5.55-47.91)	1085
Azithromycin	59.33 (41.10-73.44)	1220	63.10 (46.42-79.14)	1294	77.68 (70.39-84.94)	271	64.28 (61.30-78.57)	1021
Aztreonam	89 (89-89)	100					59.85 (51.85-76.35)	151
Cefepime	36.66 (20.69-60.96)	1120	60.49 (33.92-71.22)	1156	100 (100-100)	103	71.42 (35.71-85.71)	1021
Cefixime	33.39 (43.26-64.53)	1179	63.63 (41.73-76.23)	1159	43.68 (43.68-43.68)	103	74.51 (68.11-82.11)	1082
Cefotaxime	32.25 (19.93-47.62)	1126	43.45 (21.88-62.50)	32	87.09 (87.09-87.09)	31	60.41 (57.27-68.75)	1097
Cefoxitin			23.07 (11.54-53.20)	110				
Ceftazidime	54.77 (33.41-76.23)	1372	45.45 (31.03-49.94)	1116	64.05 (64.05-64.05)	103	63.48 (44.56-75.48)	1356
Ceftriaxone	54.83 (44.46-74.25)	1403	42.21 (23.92-58.84)	1151	75.81 (63.71-87.90)	134	63.33 (47.35-69.54)	1356
Cefuroxime	60.17 (45.67-71.50)	1179	42.82 (23.07-52.63)	1121	100 (100-100)	103	61.11 (56.19-76.50)	1291
Cephradine	83.15 (80.28-88.34)	157	46.44 (26.19-51.28)	1134	90.58 (86.36-94.80)	271	55.61 (54.07-75.91)	1222
Chloramphenicol			0 (0-6.25)	100			22.21 (19.44-24.99)	30
Ciprofloxacin	64 (32.70-70.19)	1403	53.60 (51.39-58.77)	1326	68.36 (47.04-88.83)	320	55.55 (47.44-71.42)	1368
Colistin	95.69 (87.84-96.12)	181					5.45 (4.26-52.73)	138
Co-trimoxazole	64.51 (58.06-72.41)	1208	48.55 (28.20-57.62)	1124	71.24 (67.88-74.61)	199	56.26 (49.03-63.10)	1356
Doxycycline	76.58 (76.58-76.58)	995	50 (2.21-57.89)	1056	27.27 (27.27-27.27)	18	60.01 (52.22-67.79)	1013

Erythromycin			68.75 (43.42-74.35)	1085	79.16 (79.16-79.16)	168	60.43 (46.88-73.98)	995
Gentamicin	51.72 (32.91-61.28)	1403	33.97 (26-46.12)	1331	61.29 (31.13-64.87)	302	37.78 (27.77-64.28)	1368
Imipenem	10.75 (1.72-33.33)	312	3.64 (2.56-33.37)	1143	20.14 (15.62-24.65)	186	10.69 (7.27-14.59)	1278
Kanamycin			15.62 (7.8-23.43)	16			42.26 (41.96 -42.55)	26
Levofloxacin	27.86 (16.09-43.95)	1214	39.49 (13.47-52.93)	1182	33.33 (17.64-47.31)	152	53.27 (40.52-62.58)	1176
Meropenem	6.45 (1.72-19.35)	307	16.28 (8.64-35.90)	1210	38.70 (24.91-50.90)	117	14.43 (6.85-19.59)	1354
Nalidixic Acid	60.02 (55.82-64.23)	1026	75.75 (51.56-85.40)	1040	67.74 (67.74-67.74)	31	80.55 (57.72-83.73)	1348
Netilmicin			11.53 (5.76-19.55)	55			21.42 (19.80-23.11)	1217
Piperacillin/Tazobactam	20 (6.89-21.50)	1276	0 (0-33.33)	1019			50.90 (34.68-72.67)	1133
Tetracycline	5.36 (4.89-5.83)	1090	30.95 (11.11-37.50)	1243	63.15 (45.21-81.08)	121	50 (50-50)	12
Tigecycline	63.33 (63.33-63.33)	30	0 (0-20.83)	1019			0 (0-0)	995
Vancomycin	0 (0-0)	995	7.41 (5.12-18.74)	124	11.11 (8.53-13.70)	117	20.83 (10.41-31.25)	995
Streptomycin	26.66 (26.66-26.66)	30	29.16 (14.58-43.75)	24				
Norfloxacin	43.33 (43.33-43.33)	30	33.33 (16.66-49.99)	24				
Nitrofurantoin	84.22 (81.58-85.66)	1152	16.31 (11.54-19.59)	45	42.71 (26.91-52)	152	47.59 (25.52-51.38)	1218
Cephalexin	17.89 (17.89-17.89)	95	41.35 (20.68-62.03)	39	99.02 (99.02-99.02)	103		
Mecillinam			97.43 (67.72-97.43)	39	91.66 (91.66-91.66)	168	60.07 (55.44-64.70)	137
Linezolid					20.38 (20.38-20.38)	168		
Cloxacillin					98.21 (98.21-98.21)	168		

Significant AMR Findings and Graphical Overview

In addition to pooled prevalence and antibiotic-wise resistance patterns, the most significant antimicrobial resistance findings across all study pathogens are summarized in Table 6. This table

consolidates the most critical resistance profiles reported in the included studies, allowing a focused overview of key resistance patterns. Furthermore, a graphical overview based on pooled raw counts of resistant versus susceptible isolates across all studies was generated in Figure 10. This visualization provides a clear, integrated picture of the total resistance burden by directly aggregating the raw counts of resistant and susceptible isolates for each pathogen–antibiotic pair from all studies.

Table 6. Significant antimicrobial resistance profiles in clinical isolates from selected studies

Author and year	No. of Isolates	Significant Findings (Resistance %)	Remarks	Reference
Khatun et al. (2019)	304	Detection rate of ESBL production among *Pseudomonas* spp. were (91.67 %), *Klebsiella* spp. (83.33 %), *Proteus* spp. (69.49%), *E. coli (*64.42 %).	High ESBL resistance was observed across multiple pathogens, with aztreonam, ampicillin, amoxyclav, and piperacillin showing higher resistance.	[27]
Saha et al. (2019)	1664	Gram-negative isolates exhibited substantial resistance to ampicillin (58-84%), cephradine (80-94%), and amoxiclav (53-77%). Conversely, Gram-positive isolates demonstrated markedly elevated resistance rates to nalidixic acid (70–95%) and erythromycin (68–90%).	Gram-positive and Gram-negative organisms demonstrated markedly elevated resistance to widely prescribed first-line antimicrobial agents, most notably amoxiclav, cephalosporins, and nalidixic acid.	[28]
Afroz et al. (2019)	430	Isolated uropathogens showed highest resistance for Amoxycillin (86-97%) and Cefracin (71-100%). High resistance was also observed for Cefixime (52-85%), Ceftriaxone (50-71%), Ciprofloxacin (50-88%), Cotrimoxazole (50-75%), Gentamicin (57-75%) and Nitrofurantoin (43-100%). Uropathogens were least resistant to Imipenem (0-15%) and Amikacin (0-29%).	A high degree of resistance was observed against commonly prescribed antimicrobials for urinary tract infections, with amoxicillin and cefradine exhibiting the highest resistance rates, whereas imipenem and amikacin demonstrated the lowest.	[29]
Hossain et al. (2020)	1663	*E. coli* isolates demonstrated low resistance to imipenem (1.9%), meropenem (2.8%), amikacin (2.8%), and colistin (2.9%) and nitrofurantoin (15.8%). Resistance trends varied by demographics: amikacin resistance was more frequent in older patients, nitrofurantoin resistance was	Resistance was lowest to carbapenems, aminoglycosides, and colistin, while nitrofurantoin showed comparatively higher resistance. Resistance patterns varied with age and gender, indicating	[30]

		higher in males, and imipenem resistance increased in isolates from adults >40 years.	emerging risks in specific patient groups.	
Dasgupta et al. (2020)	537	The prevalence of multi-drug resistant uropathogens was 77.6% for *E. coli*, 71.9% for *Klebsiella* spp., 90.5% for *Pseudomonas* spp., 86.2% for *S. aureus* and 92.9% for *Enterobacter* spp.	There is a very high prevalence of multidrug-resistant uropathogens among hospitalized patients. The emergence of carbapenem resistance, particularly in *Enterobacter* spp., poses a serious therapeutic challenge.	[31]
Rahman et al. (2020)	1452	*E. coli* showed high rates of sensitivity to nitrofurantoin 79.76%, gentamicin 75.31%, amikacin 88.65%, imipenem 97.89%, and meropenem 80.87%. *Pseudomonas species* showed a high rate of sensitivity to imipenem (70.45%). *Enterococcus species* showed a high rate of sensitivity to vancomycin 94.05%, imipenem 70.83%, and linezolid 79.76%.	Although carbapenems and some aminoglycosides still show good activity, the overall antimicrobial resistance is rising, highlighting the need for careful antibiotic use.	[32]
Nusrat et al. (2020)	95	*Acinetobacter* spp. showed high resistance with 92.7% to gentamicin and 87.8% to ceftriaxone. *Klebsiella* spp. had 83.3% resistance to ceftriaxone. *Pseudomonas* spp. showed 88.8% resistance to ciprofloxacin and 72.2% to ceftriaxone. *E. coli* isolates were 100% resistant to ceftriaxone and ciprofloxacin, while *Proteus* spp. 100% were resistant to ceftriaxone.	Pathogens in ICU patients show alarmingly high resistance, especially against ceftriaxone, ciprofloxacin, and gentamicin, leaving limited therapeutic options.	[33]
M. H. Rahman et al. (2020)	158	*E. coli* showed very high resistance to ampicillin (95.6%), cephradine (91.3%), and doxycycline (81.2%). *Klebsiella* had 85.7% resistance to ampicillin, while *Acinetobacter* and *Pseudomonas* exhibited >70% resistance to fluoroquinolones and cephalosporins. *Proteus* was 100% resistant to ampicillin, cephradine, and fluoroquinolones. Among Gram-positives, *Staphylococcus* showed	Resistance to common first-line drugs is widespread, especially in *E. coli* and *Klebsiella*, limiting treatment options. Carbapenems retain high effectiveness against Gram-negatives, while Gram-positive organisms remain susceptible to linezolid and vancomycin.	[34]

		92.3% resistance to ampicillin and >50% to fluoroquinolones, whereas *Enterococcus* had moderate fluoroquinolone resistance but no resistance to vancomycin/linezolid.		
M. M. Rahman et al. (2020)	31	*Enterotoxigenic E. coli* (ETEC) strains showed resistance to amoxicillin–clavulanic acid (82.6%), tetracycline (65.21%), nalidixic acid (73.91%), azithromycin (78.26%), ciprofloxacin (47.82%), ampicillin (60.86%), and erythromycin (47.82%). *Enteropathogenic E. coli* (EPEC) strains showed resistance to amoxicillin–clavulanic acid, ampicillin, and erythromycin (87.5% each), and 75% resistance to tetracycline and nalidixic acid.	Both ETEC and EPEC strains exhibited multidrug resistance with high resistance rates to commonly used antibiotics, limiting therapeutic options and indicating a need for cautious antimicrobial use.	[35]
Alam et al. (2020)	1266	The percentage of MDR among gram-positive and gram-negative bacterial isolates was 68.8% and 66.0%, respectively. About 82% of *Enterococcus* spp. and 76% of *Proteus* spp. were MDR.	High burden of MDR pathogens in wound infections, especially in *Enterococcus* and *Proteus*. Effective options remain limited to last-line drugs such as vancomycin, linezolid, colistin, and carbapenems.	[57]
Sharmin et al. (2021)	1337	Among the collected samples, *Pseudomonas aeruginosa* isolation increased from 4% (2019) to 6% (2020). Resistance remained high against ceftriaxone (87–88%), gentamicin (70–87%), and netilmicin (70–80%).	The rising prevalence of *P. aeruginosa* in UTIs and its widespread multidrug resistance pose serious therapeutic challenges.	[37]
Jobayer et al. (2021)	1231	Among the Gram-negative bacteria, 14.9% were identified as extended-spectrum β-lactamase (ESBL)-producing organisms. Gram-negative isolates exhibited high resistance to amoxicillin (80–100%), co-trimoxazole (55–80%), fluoroquinolones (60–80%), and cephalosporins (>60%).	The presence of ESBL-producing Gram-negative organisms and their high resistance rates indicate a serious therapeutic challenge in clinical management.	[38]

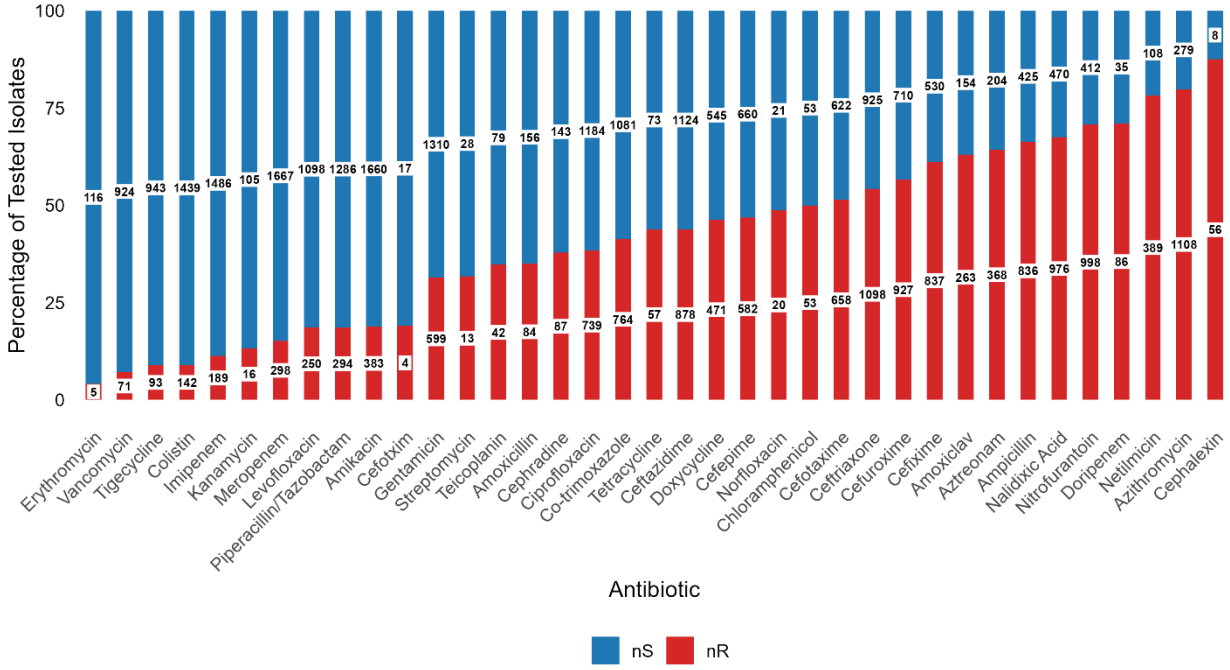
Aminul et al. (2021)	123	The majority of *Klebsiella pneumoniae* isolates were multi-drug resistant (82%), 16.6% were ESBL producers. Among β-lactamase genes, NDM was most prevalent (23.3%), followed by OXA-48 (8%) and KPC (7.3%), while VIM and IMP were absent.	The high burden of multidrug resistance in *Klebsiella pneumoniae*, along with the notable presence of carbapenemase genes highlights an alarming resistance pattern that may compromise available treatment choices and worsen patient outcomes.	[39]
Jain et al. (2021)	100	98% of the *E. coli* isolates were multidrug-resistant (MDR). The AmpC gene was detected in 68% of the isolates, while 32% was tetC positive. Notably, 34% of the isolates were resistant to carbapenem.	Multidrug-resistance is alarmingly increasing in *E. coli*. The high rate of resistance to carbapenem and the presence of genes like AmpC and tetC critically limit treatment options against infections.	[40]
T. Rahman et al. (2021)	64	All isolated *S. aureus, Coagulase negative Staphylococcus*, Group-B *Streptococcus* and *Micrococcus* showed 100% resistance to ceftriaxone, cefotaxime and ceftazidime. All isolated *Enterobacter* spp., *Pseudomonas aeruginosa* and *Citrobacter* spp. showed 100% resistance to amoxiclav, amikacin, ceftriaxone, cefixime, and ceftazidime.	The universal resistance to third-generation cephalosporins and aminoglycosides in both Gram-positive and Gram-negative isolates is alarming.	[41]
Safain et al. (2021)	430	53% of isolates were multidrug-resistant (MDR), including 97% of *E. coli*. The CTX-M-I gene was the most prevalent (63%), followed by NDM-I (22%). The ermB (55%) and aac(6')-Ib (35%) genes were the most frequently detected macrolide and aminoglycoside resistance genes. There was a twofold increase in MDR strains isolated between 2015 and 2019.	A high prevalence of multidrug resistance was observed among clinical isolates, with *E. coli* identified as a principal reservoir of resistance determinants. The predominance of CTX-M-1 and NDM-1 denotes extensive β-lactam resistance, whereas the detection of macrolide and aminoglycoside resistance genes indicates a concerning escalation in resistance trends.	[42]
Majumder et al. (2022)	995	Across three study phases (2011, 2016, 2021), *E. coli*	A high and rising rate of resistance among	[43]

		remained the predominant uropathogen (62% in 2021, 86% in 2016, 76% in 2011), followed by *Klebsiella* spp. (≈10–11%). Gram-negative organisms showed >50% resistance to most tested antibiotics. Very high resistance (66.7–93.8%) was observed to cotrimoxazole, ciprofloxacin, cefuroxime, cephradine, amoxicillin, and nalidixic acid.	uropathogens was observed against conventional antibiotics used for urinary tract infections. Nitrofurantoin demonstrated the lowest resistance, whereas resistance to other commonly used agents, including carbapenems and aminoglycosides, has increased significantly.	
Begum et al. (2023)	85	*S. aureus* showed 100% sensitivity to linezolid and vancomycin, indicating no resistance. *Klebsiella* spp. showed 13% resistance to meropenem, while *E. coli* showed 20% resistance. *Acinetobacter* spp. exhibited significant resistance, with only 70% sensitive to colistin. *Pseudomonas* spp. retained good activity against meropenem and piperacillin-tazobactam (100%), but resistance was seen in 18% to amikacin and ceftazidime.	Bloodstream pathogens showed varying resistance patterns, with high resistance in *Acinetobacter* and moderate resistance in *Klebsiella* and *E. coli*. While last-line agents like vancomycin, linezolid, carbapenems, and piperacillin-tazobactam remain effective, rising resistance in Gram-negatives is concerning.	[44]
Ahmed et al. (2023)	46	*Klebsiella* showed poor sensitivity to ceftriaxone (57.1%), ceftazidime (14.2%), cefixime (28.5%), and amoxicillin (21.4%). *S. pneumoniae* isolates also demonstrated resistance, with sensitivity to ceftriaxone (45.5%), ceftazidime (54.5%), cefixime (36.3%), and no sensitivity to amoxicillin (0%). Most bacterial isolates were recovered from patients with uncontrolled diabetes.	The predominance of resistant *Klebsiella pneumoniae* and *Streptococcus pneumoniae*, along with the absence of amoxicillin activity against *S. pneumoniae*, indicates reduced therapeutic value of β-lactam agents in community-acquired pneumonia among diabetic patients.	[45]
P. Saha et al. (2023)	108	The overall frequency of drug resistance for *Pseudomonas aeruginosa* was very high (53.7% - 98.1%) to all 14 regularly used antibiotics tested. Isolates showed the highest resistance (98.1%) to aztreonam, followed by doxycycline (95.4%), ceftriaxone (94.4%), and amoxiclav (93.5%).	Multidrug resistance in *P. aeruginosa* was alarmingly high, with most common antibiotics including β-lactams, tetracyclines, and β-lactamase inhibitor combinations showing poor activity.	[46]

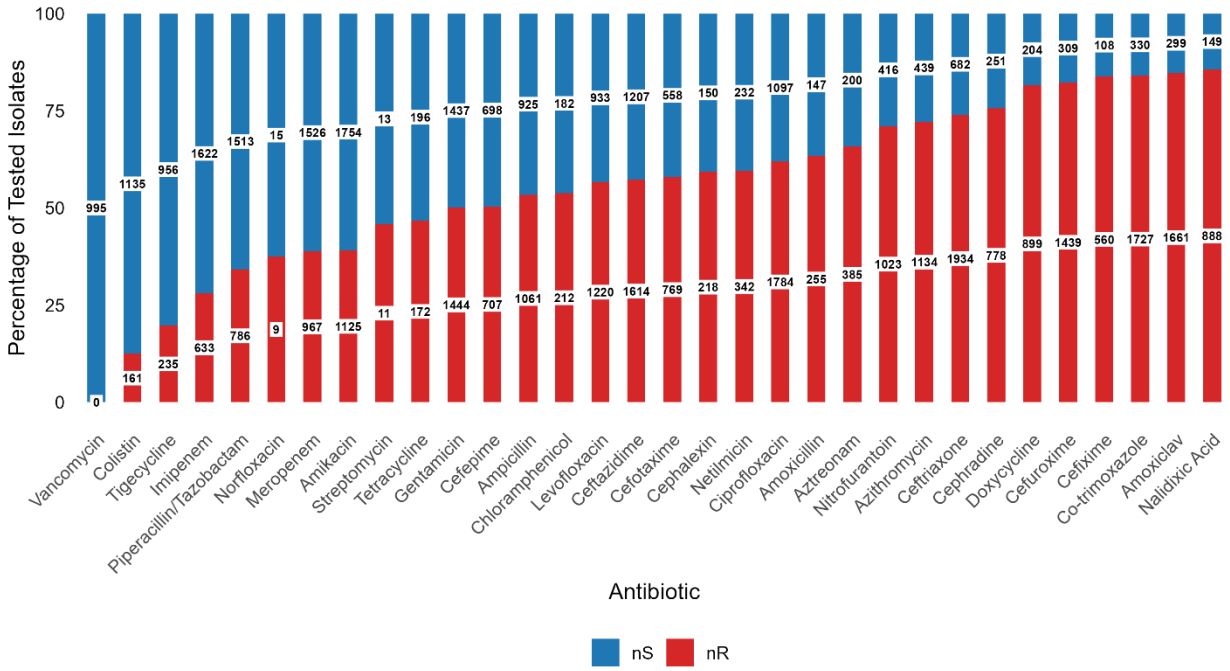
R. Saha et al. (2024)	313	Coagulase-negative *Staphylococci* (CoNS) showed high resistance to ampicillin, cephradine, and erythromycin, with 47% methicillin resistance and 10% vancomycin resistance. *S. aureus* also showed 31.5% methicillin resistance. *Acinetobacter* spp. exhibited very high resistance to ampicillin (90%), cephradine (80%), and cefuroxime (90%).	High rates of methicillin resistance in staphylococci and multidrug resistance in *Acinetobacter* spp. pose major therapeutic challenges.	[47]
Siam et al. (2024)	34	Gram-positive isolates showed high resistance to ampicillin (100%), while Gram-negatives also demonstrated complete resistance to ampicillin and high resistance to ceftazidime (40%).	The universal resistance to ampicillin and reduced activity of cephalosporins highlight the limited usefulness of conventional therapies.	[48]
Salam et al. (2024)	85	The most frequent isolates from ICU patients were *Pseudomonas* spp. (30.59%), *E. coli* (24.71%), *Acinetobacter* spp. (20%), and *Klebsiella* spp. (14.12%). High resistance was observed to ciprofloxacin (78.82%), gentamicin (82.35%), ceftazidime (75.29%), levofloxacin (68.24%), amikacin (64.71%), and meropenem (49.41%).	Most ICU pathogens exhibited multidrug resistance, with fluoroquinolones, aminoglycosides, and cephalosporins showing poor activity.	[49]
Asaduzzaman et al. (2024)	573	*Acinetobacter* showed moderate to high resistance to aminoglycosides (45–53%), cephalosporins (28–45%), fluoroquinolones (28–39%), and carbapenems (17–19%). Among these, 66.7% were MDR, 13.6% XDR, and 2.3% pan-drug resistant (PDR).	The prevalence of multi-drug resistant and extensively drug-resistant *Acinetobacter* spp. is a major concern, as is the emergence of pan-drug-resistant strains.	[50]
Meghla et al. (2024)	47	All isolates were multidrug resistant, showing resistance to at least four antibiotics. The highest resistance was observed to cefepime (100%) and cefotaxime (87%).	The predominance of MDR *Acinetobacter baumannii*, *Enterobacter hormaechei*, and *Staphylococcus pasteuri*highlights the severity of pediatric pneumonia cases.	[51]
N. Sharmin et al. (2024)	338	62.22% of isolates were multidrug resistant (MDR) and 28.89% were extensively drug resistant (XDR).	The high proportion of MDR and XDR strains presents a severe therapeutic challenge,	[52]

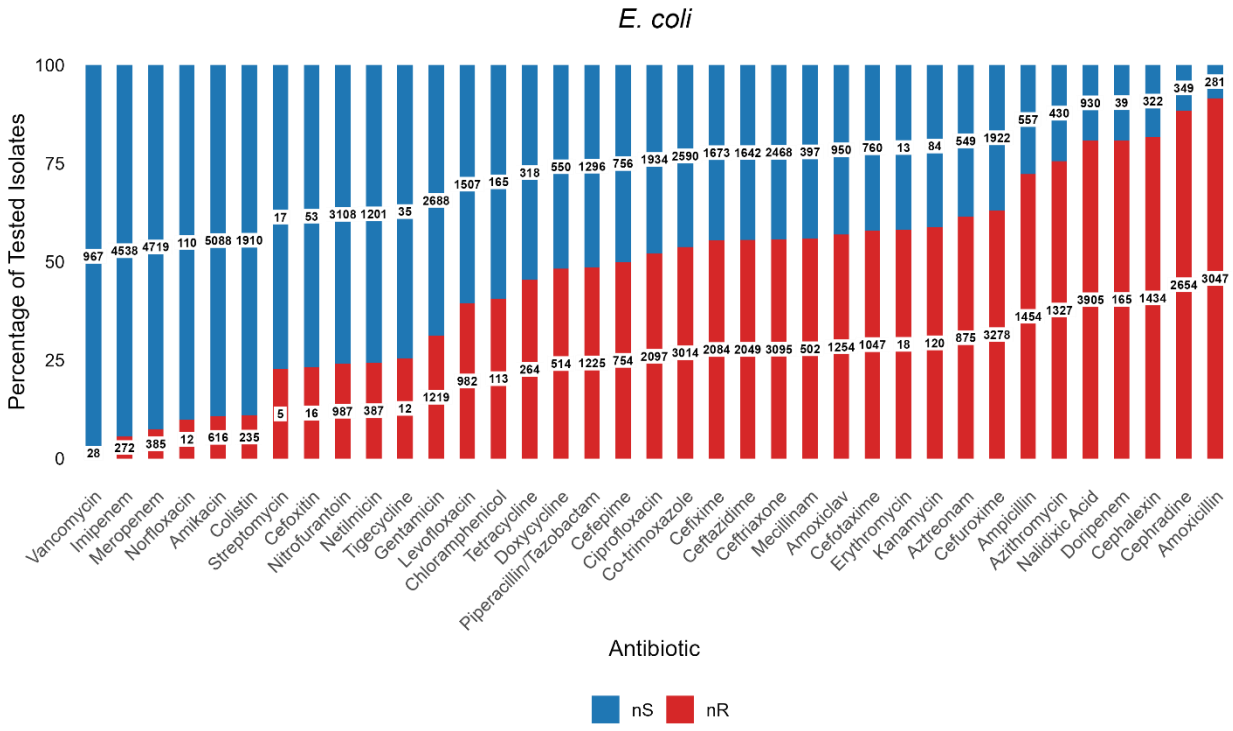
			emphasizing the urgent need for effective antimicrobial stewardship.	
Baral et al. (2024)	141	About 61.3% of ulcers were polybacterial. *E. coli* showed the highest multidrug resistance (81.8%), and most Gram-negative isolates were resistant to ampicillin.	High multidrug resistance, especially in *E. coli*, poses a major therapeutic challenge in diabetic foot ulcer.	[53]
Nobel et al. (2024)	891	The cumulative multidrug resistance (MDR) rate among Gram-negative bacteria was 92.9%, while Gram-positive bacteria also demonstrated an alarming MDR rate of 87.5%.	Both Gram-negative and Gram-positive bacteria, particularly *E. coli*, *Pseudomonas* spp., *S. aureus*, and *Enterococcus faecalis*, showed a high prevalence of multi-drug resistance, posing a significant challenge to public health.	[54]
Haque et al. (2024)	273	Among isolates from ICU patients, 81% were Gram-negative bacteria. Except for *S. aureus*, around 90% of the prevalent bacteria were multidrug-resistant, while 60% of *Acinetobacter* spp. and *Pseudomonas* spp. were extensively drug-resistant.	High prevalence of MDR and XDR gram-negative pathogens in ICU patients poses serious treatment challenges.	[55]
Kabir et al. (2024)	232	Biofilm-forming *Pseudomonas aeruginosa* strains were significantly resistant to colistin. Among biofilm-specific antibiotic resistance genes, 16.67% were *ndvB*, and 8.33% were *PA1874* and *PA1877*.	The presence of biofilm-associated and resistance genes in *P. aeruginosa* highlights their role in persistent infections and colistin resistance, complicating treatment of chronic and device-related infections.	[56]

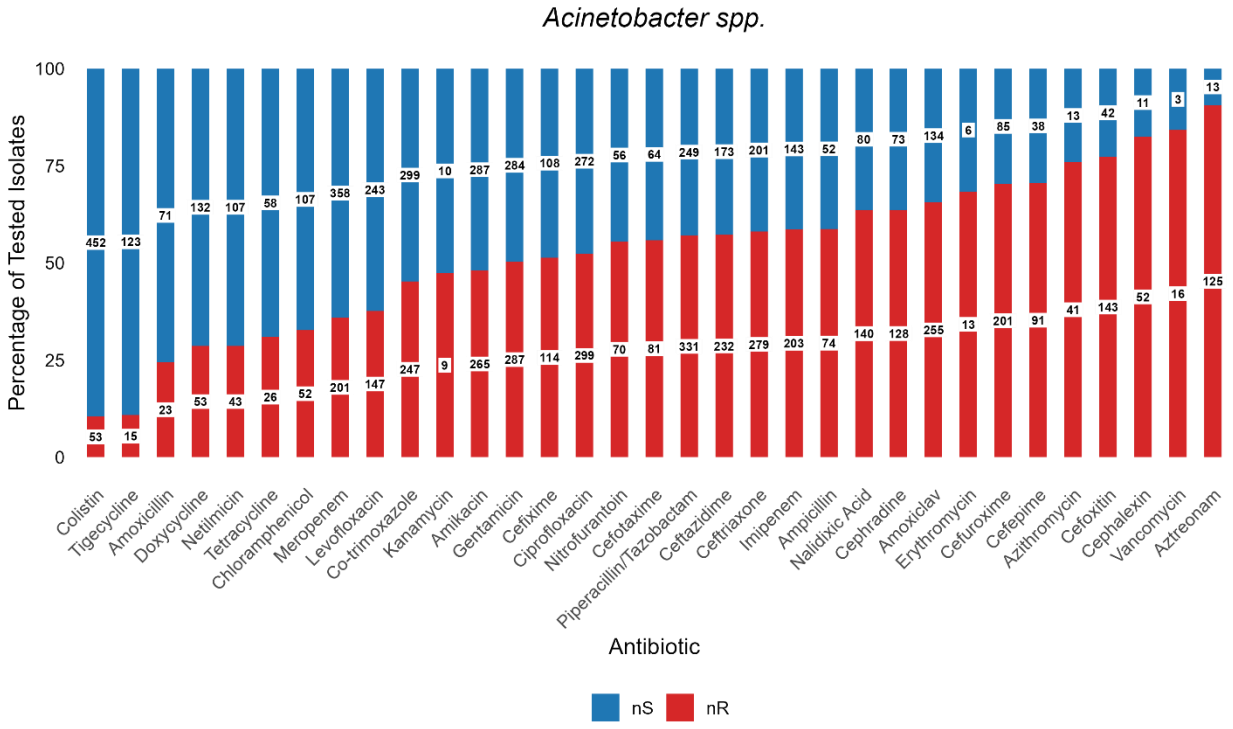
Klebsiella spp.

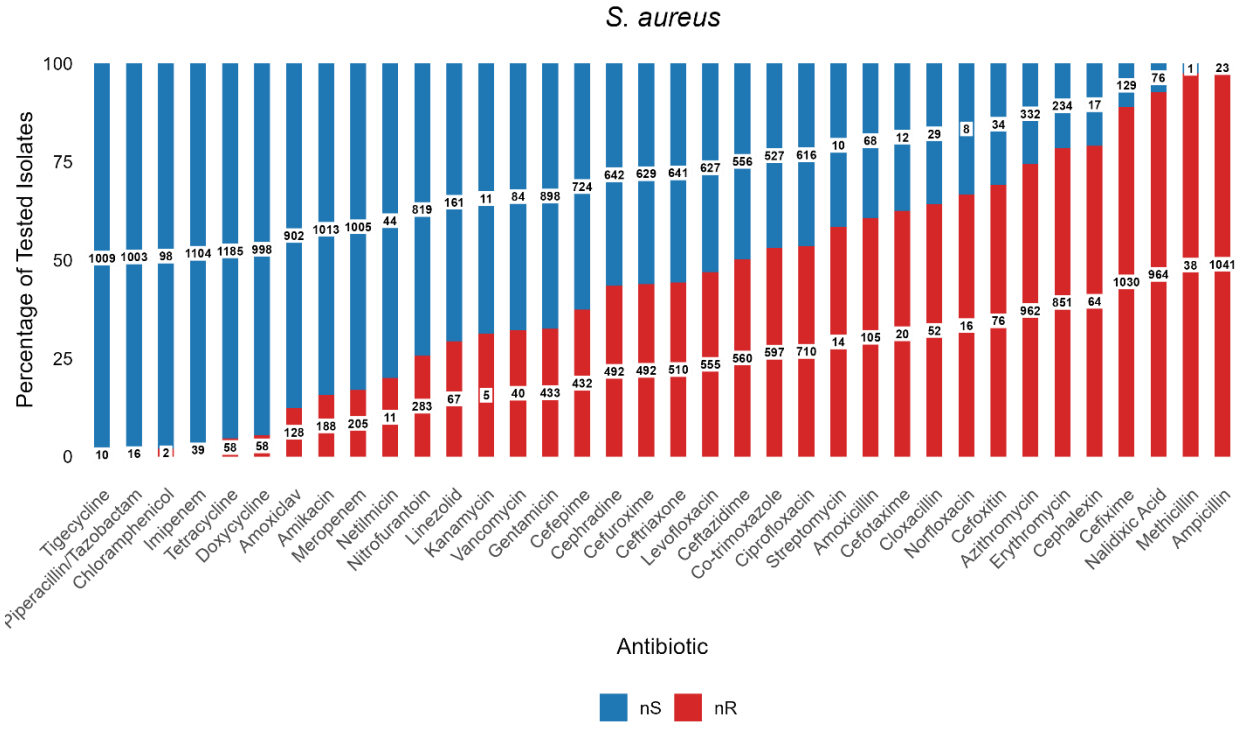


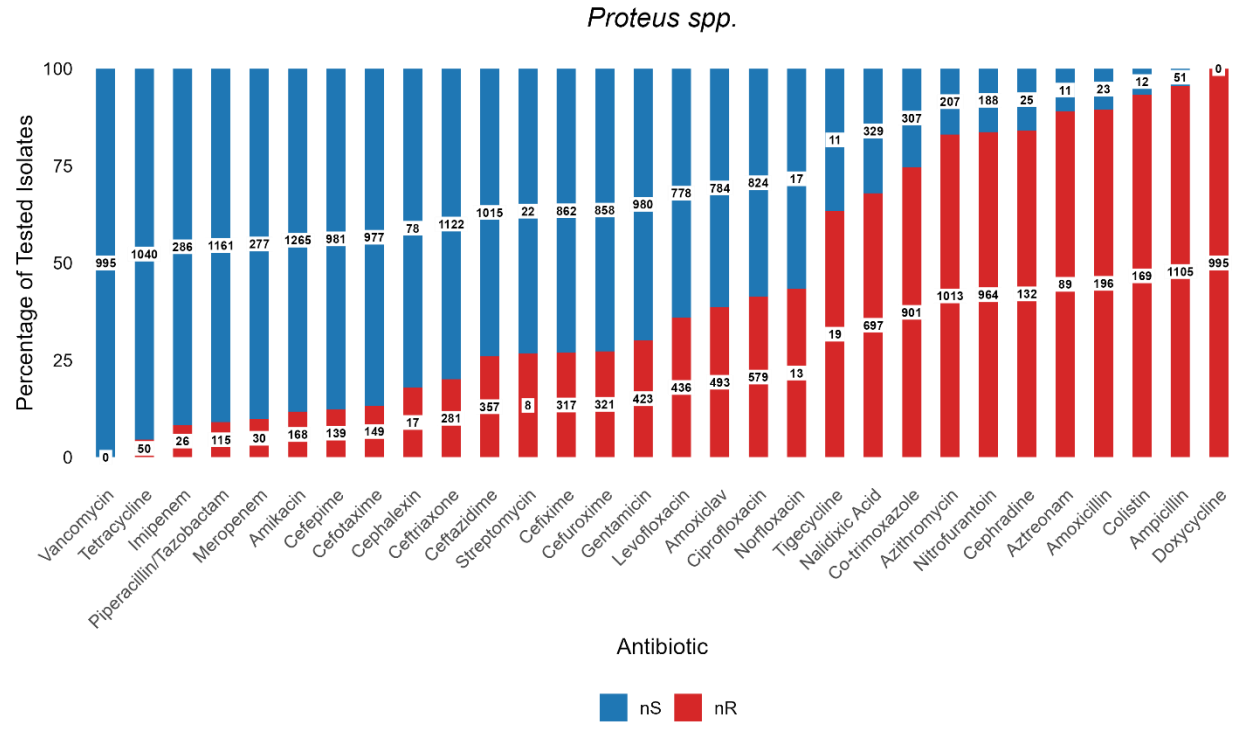
Pseudomonas spp.




E. coli
Percentage of Tested Isolates
100
75
50
25
0
967 4538 4719 110 5088 1910 17 53 3108 1201 35 2688 1507 165 318 550 1296 756 1934 2590 1673 1642 2468 397 950 760 13 84 549 1922 557 430 930 39 322 349 281
28 272 385 12 616 235 5 16 987 387 12 1219 982 113 264 514 1225 754 2097 3014 2084 2049 3095 502 1254 1047 18 120 875 3278 1454 1327 3905 165 1434 2654 3047
Vancomycin
Imipenem
Meropenem
Norfloxacin
Amikacin
Colistin
Streptomycin
Cefoxitin
Nitrofurantoin
Netilmicin
Tigecycline
Gentamicin
Levofloxacin
Chloramphenicol
Tetracycline
Doxycycline
Piperacillin/Tazobactam
Cefepime
Ciprofloxacin
Co-trimoxazole
Ceftixime
Ceftazidime
Ceftriaxone
Mecillinam
Amoxiclav
Cefotaxime
Erythromycin
Kanamycin
Aztreonam
Cefuroxime
Ampicillin
Azithromycin
Nalidixic Acid
Doripenem
Cephalexin
Cephradine
Amoxicillin
Antibiotic
nS
nR


Acinetobacter spp.
Percentage of Tested Isolates
100
75
50
25
0
452 123 71 132 107 58 107 358 243 299 10 287 284 108 272 56 64 249 173 201 143 52 80 73 134 6 85 38 13 42 11 3 13
53 15 23 53 43 26 52 201 147 247 9 265 287 114 299 70 81 331 232 279 203 74 140 128 255 13 201 91 41 143 52 16 125
Colistin
Tigecycline
Amoxicillin
Doxycycline
Netilmicin
Tetracycline
Chloramphenicol
Meropenem
Levofloxacin
Co-trimoxazole
Kanamycin
Amikacin
Gentamicin
Ceftixime
Ciprofloxacin
Nitrofurantoin
Cefotaxime
Piperacillin/Tazobactam
Ceftazidime
Ceftriaxone
Imipenem
Ampicillin
Nalidixic Acid
Cephradine
Amoxiclav
Erythromycin
Cefuroxime
Cefepime
Azithromycin
Cefoxitin
Cephalexin
Vancomycin
Aztreonam
Antibiotic
nS
nR


S. aureus
Percentage of Tested Isolates
100
75
50
25
0
1009 1003 98 1104 1185 998 902 1013 1005 819 161 11 84 898 724 642 629 641 627 556 527 616 10 68 12 29 8 34 332 234 17 129 76 1 23
10 16 2 39 58 58 128 188 205 11 283 67 5 40 433 432 492 492 510 555 560 597 710 14 105 20 52 16 76 962 851 64 1030 964 38 1041
Tigecycline
Piperacillin/Tazobactam
Chloramphenicol
Imipenem
Tetracycline
Doxycycline
Amoxiclav
Amikacin
Meropenem
Netilmicin
Nitrofurantoin
Linezolid
Kanamycin
Vancomycin
Gentamicin
Cefepime
Cephradine
Cefuroxime
Ceftriaxone
Levofloxacin
Ceftazidime
Co-trimoxazole
Ciprofloxacin
Streptomycin
Amoxicillin
Cefotaxime
Cloxacillin
Norfloxacin
Cefoxitin
Azithromycin
Erythromycin
Cephalexin
Cefixime
Nalidixic Acid
Methicillin
Ampicillin
Antibiotic
nS
nR


Proteus spp.
Percentage of Tested Isolates
100
75
50
25
0
995 1040 286 1161 277 1265 981 977 78 1122 1015 22 862 858 980 778 784 824 17 11 329 307 207 188 25 11 23 12 51 0
0 50 26 115 30 168 139 149 17 281 357 8 317 321 423 436 493 579 13 19 697 901 1013 964 132 89 196 169 1105 995
Vancomycin
Tetracycline
Imipenem
Piperacillin/Tazobactam
Meropenem
Amikacin
Cefepime
Cefotaxime
Cephalexin
Ceftriaxone
Ceftazidime
Streptomycin
Cefixime
Cefuroxime
Gentamicin
Levofloxacin
Amoxiclav
Ciprofloxacin
Norfloxacin
Tigecycline
Nalidixic Acid
Co-trimoxazole
Azithromycin
Nitrofurantoin
Cephradine
Aztreonam
Amoxicillin
Colistin
Ampicillin
Doxycycline
Antibiotic
nS
nR

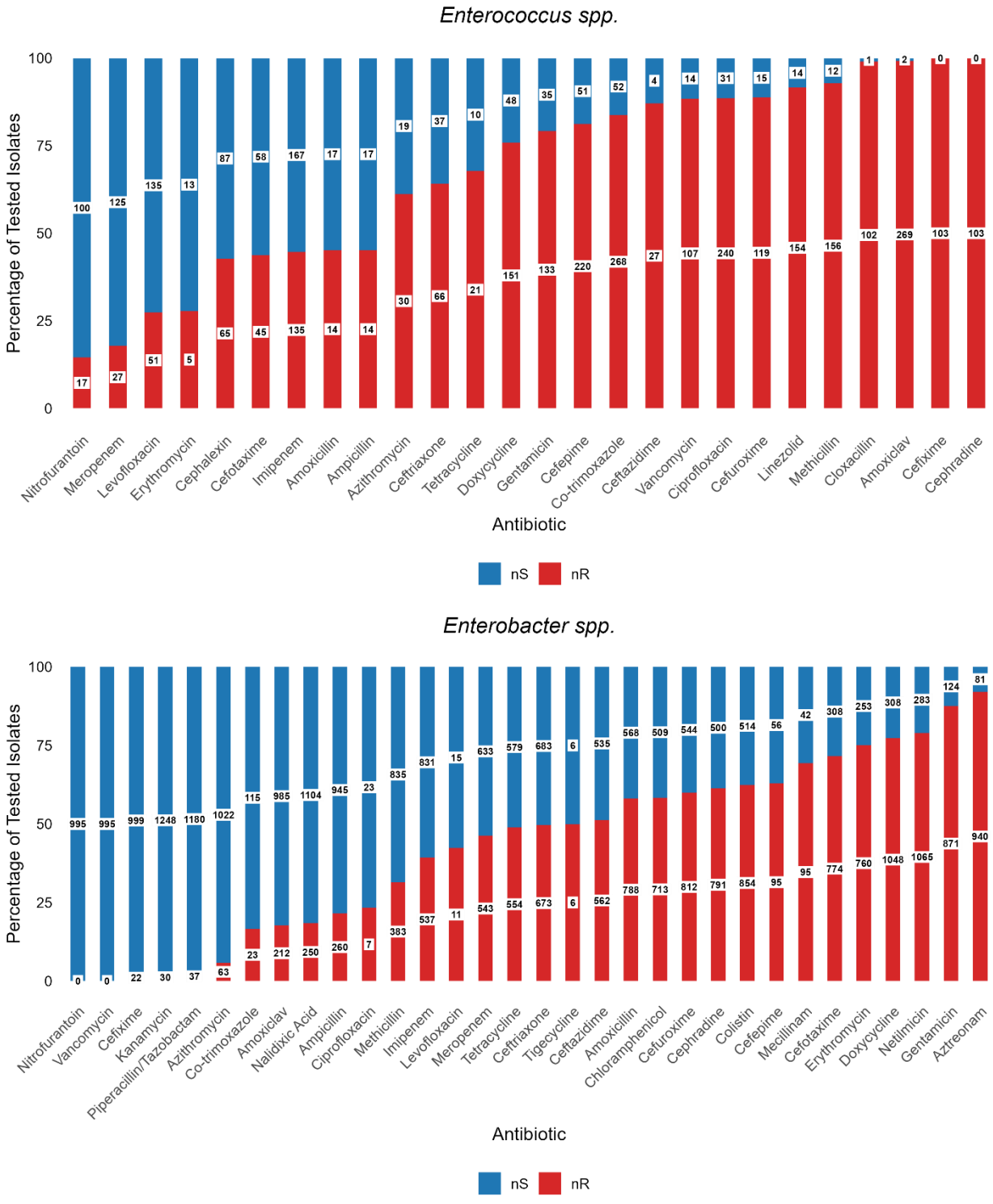


Figure 10: Graphical overview of antimicrobial resistance profiles based on pooled raw counts of resistant and susceptible isolates across all included studies. nR = No. of resistant isolates, nS = No. of non-resistant isolates.

Discussion

Antimicrobial resistance (AMR) remains a critical public health threat in low- and middle-income countries, largely driven by deficiencies in healthcare infrastructure, inadequate sanitation, and the pervasive misuse and self-medication of antibiotics [3]. In Bangladesh, these challenges are particularly acute, yet evidence on the national resistance landscape has remained fragmented. To address this gap, the present study provides the first systematic review and meta-analysis from Bangladesh synthesizing data published between 2019 and 2024, and it provides a comprehensive overview of both pathogen prevalence and resistance patterns. By pooling evidence from over 270,000 clinical specimens, this work highlights the dual challenge of a heavy infectious disease burden and rising resistance in Bangladesh.

E. coli is the most frequently isolated pathogen from diverse clinical specimens in Bangladesh and is often used as a sentinel organism to monitor antimicrobial resistance trends in healthcare settings [59]. Beyond being a commensal of the gastrointestinal tract, pathogenic strains of *E. coli*are major causative agents of urinary tract infections, bloodstream infections, and neonatal sepsis, often presenting with multidrug-resistant (MDR) profiles that severely limit therapeutic options. Our systematic review and meta-analysis demonstrates a pooled prevalence of 12% for *E. coli* among clinical samples, with very high resistance to commonly prescribed β-lactams, including 92.44% to amoxicillin and 82.58% to ampicillin. Resistance to third-generation cephalosporins such as cephradine (89.93%), cefuroxime (71.78%) and cefixime (71.78%) further indicates the dissemination of extended-spectrum β-lactamase (ESBL)–producing *E. coli* in the clinical setting. These findings are consistent with the IEDCR National AMR Surveillance Report [60], which identified *E. coli* as the leading Gram-negative pathogen in clinical settings, with high resistance to β-lactams and cephalosporins, and only partial susceptibility retained to aminoglycosides and carbapenems [59].

Klebsiella spp. accounted for a pooled prevalence of 8% and demonstrated a high level of pooled antibiotic resistance (41%). It demonstrated markedly elevated resistance to cephalexin (87.5%), ampicillin (82.37%), cephradine (76.19%), and doripenem (71.07%). Reports from regions with limited access to healthcare resources, including South Asia, the Middle East, and parts of Africa, similarly indicate a higher prevalence and resistance rate of multidrug-resistant (MDR) *Klebsiella* infections [61]. A 2024 systematic review of hospital-acquired infections estimated a global CRKP prevalence of 28.7%, with South Asia highest at 66% [62]. Mortality associated with CRKP infections is also alarmingly high, reaching up to 50% in bloodstream infections [63].

A similar trend was observed for *Pseudomonas* spp., which accounted for a pooled prevalence of 7% and demonstrated 56% pooled resistance in clinical isolates. The resistance profile of *Pseudomonas* spp. revealed alarmingly high rates across multiple antibiotic classes, with the greatest resistance observed against doxycycline (87.69%), amoxiclav (87.67%), cefuroxime (87.13%), nalidixic acid (84.53%), cephradine (84.54%), co-trimoxazole (83.33%), and ampicillin (82.53%). These findings indicate limited efficacy of tetracyclines, β-lactams, and

fluoroquinolones. Most concerningly, *Pseudomonas* spp. also exhibited substantial resistance to carbapenems, including imipenem (32.49%) and meropenem (32.00%), which are widely regarded as the last line of defense against multidrug-resistant Gram-negative bacterial infections. Research by Zhao et al. (2025) similarly documented the alarming prevalence of carbapenem-resistant *Pseudomonas aeruginosa* (CRPA), with its rising detection rates associated with increased morbidity and mortality in China [64].

Acinetobacter spp. demonstrated a pooled antibiotic resistance rate of 53%. Extremely high resistance was observed among cephalosporins, with Cefoxitin (97.33%) and Cefepime (95.56%) showing almost complete loss of activity, while Aztreonam (87.28%) also exhibited alarmingly high resistance. Resistance to carbapenems was highly concerning, with imipenem showing a resistance rate of 56.1% and meropenem 20.5%. This growing resistance is driven by several bacterial defense mechanisms, including the natural and acquired production of β-lactamases, such as metallo-β-lactamases and carbapenem-hydrolyzing oxacillinases (CHDLs). The bacteria also defend themselves by losing their outer membrane porin proteins, which prevents the drug from entering, and sometimes by modifying their penicillin-binding proteins [65], [66] This remarkable adaptability has become a critical clinical challenge, severely restricting therapeutic options for patients, particularly in intensive care unit (ICU) settings [66]. Similar high rates of antibiotic resistance in *Acinetobacter* spp. have been documented in studies from various countries, including Bangladesh, India, and Nepal [66], [67], [68], [69], [70].The pooled analysis of antibiotic resistance in *Proteus* spp. isolates revealed a resistance rate of 58.81% to the tested antibiotics. High resistance rates were observed against ciprofloxacin (64 %), ceftazidime (54.77 %), cotrimoxazole (49 %), and cefuroxime (60.17 %). These findings are largely consistent with a study conducted in South India, which reported resistance rates of 58 % to ciprofloxacin, 50 % to ceftazidime, and 49 % to cotrimoxazole [71].*Enterobacter* spp. exhibited an overall pooled antibiotic resistance rate of 40%. The most alarming resistance was detected among the fluoroquinolones, with Nalidixic Acid demonstrating 80.55% resistance, underscoring the diminishing clinical utility of this widely prescribed class. Similarly, elevated resistance was observed among the cephalosporins, particularly Cefixime (74.51%) and Cefepime (71.42%), while the β-lactam/β-lactamase inhibitor combination Amoxiclav also showed high resistance (69.44%), reflecting substantial therapeutic limitations across multiple antibiotic classes.

Among the Gram-positive organisms, *S. aureus* exhibited an overall pooled antibiotic resistance rate of 43% in Bangladesh. This widespread resistance, particularly to commonly used first-line drugs, is a major clinical concern. The most alarming finding was the near-complete loss of efficacy for Mecillinam, which showed an exceptionally high resistance rate of 97.43%. Resistance was also substantial within the penicillin group, with Ampicillin at 83.33% and Amoxicillin at 73.36%. Similarly, fluoroquinolones demonstrated considerable resistance, as evidenced by a 75.75% resistance rate for Nalidixic Acid. The high prevalence of resistant *S. aureus* in the community poses a significant public health threat, as these bacteria may act as reservoirs for Methicillin-resistant *S. aureus* (MRSA), increasing the risk of community-acquired MRSA

infections [72]. This observation is supported by a study from Vietnam (2014–2021), which reported very high resistance to azithromycin (82.28%), erythromycin (82.82%), and clindamycin (82.32%), demonstrating the continued clinical challenge posed by resistant strains [73]. The emergence of multidrug-resistant MRSA has also been well-documented in research from Nepal, Iran and other regions globally [74], [75]. *Enterococcus* spp. demonstrated a high pooled prevalence of antibiotic resistance at 70%. The highest resistance was observed against Nalidixic Acid (80.55%). Resistance to β-lactams was also pronounced, with Cefixime (74.51%) and Cefepime (71.42%). This finding is consistent with research by Colak and Asgin (2021), who documented high rates of third-generation cephalosporin resistance in *Enterobacter cloacae* complex. Additionally, resistance to Amoxiclav (69.44%) and to macrolides, such as Azithromycin (64.28%), further highlights the multidrug-resistant profile of this pathogen. Previous studies have shown that *Enterococcus* spp. possess multiple mechanisms of macrolide resistance, including efflux pumps and ribosomal modification, which further complicate treatment [76].

This review is subject to several limitations inherent in the available literature. The included studies were heterogeneous in design, setting, and sample size, which likely contributed to the very high statistical heterogeneity ($I^2 > 97\%$) observed in the pooled estimates. Most studies relied on disk diffusion for antimicrobial susceptibility testing, with limited use of broth microdilution or molecular methods, raising concerns about methodological consistency and comparability. Moreover, the majority of the studies were conducted in the Dhaka division, which may not fully capture the national landscape of antibiotic resistance in Bangladesh and limits the generalizability of the findings. The analysis was also constrained by inconsistently reported data on key variables such as infection origin (community-acquired versus hospital-acquired), patient demographics, and specific clinical specimen types. This scarcity of detailed data hindered a more granular assessment of resistance patterns across clinical contexts and patient groups. Finally, although a comprehensive search was performed across major databases, our synthesis is based solely on published studies. This reliance may introduce publication bias and could overlook relevant unpublished or gray literature sources.

Despite the alarming resistance trends highlighted in this review, several antibiotics still demonstrate relatively low resistance and therefore remain clinically useful against major pathogens in Bangladesh. Notably, carbapenems (imipenem, meropenem) show consistently low resistance across multiple Gram-negative pathogens, including *E. coli* (10-15%), *Klebsiella* spp. (13-14%), *Enterobacter* Spp. (10-14%) and *Proteus* spp. (6-10%). Similarly, colistin demonstrates exceptionally low resistance, particularly in *Klebsiella* spp. (2.12%), and remains a valuable agent for *Enterobacter* (5.45%), *Acinetobacter* spp. (8.24%) and *Pseudomonas* (14.48%). Tigecycline also showed consistently low resistance, particularly in *E. coli* (12%), *Klebsiella* spp. (10%), *Acinetobacter* spp. (10.36%), and *S. aureus* (0%), making it a valuable option for both Gram-negative and Gram-positive infections. Aminoglycosides such as netilmicin and amikacin retained favorable activity against several pathogens. *E. coli* (16–18%), *Acinetobacter* spp. (12.9% for netilmicin) and *S. aureus* (11.53% for netilmicin, 15.62% for kanamycin) all showed lower

resistance levels, suggesting they remain useful in selected clinical contexts. Vancomycin remains highly effective against Gram-positive pathogens, with low resistance in *S. aureus* (7.41%) and *Enterococcus* spp. (11.11%).

Given the global shortage of new antibiotics, it is imperative that existing agents are used judiciously. Evidence indicates that controlled and reduced use of antibiotics can mitigate resistance [77], which can be achieved through a multi-pronged approach. This includes implementing stricter regulations on antibiotic use and educating both healthcare professionals and the public, as irrational antibiotic use is common in Bangladesh through both prescription and self-medication [18], [78]. A robust national antimicrobial stewardship program (ASP) should be institutionalized across all public and private hospitals, with dedicated committees, treatment guidelines, and regular audits of antibiotic prescribing practices. However, evidence from tertiary hospitals in Bangladesh shows that awareness of ASPs is low, and none had functioning stewardship initiatives [79]. To obtain more comparable and high-quality data, strengthening laboratory capacity is also critical. Faster, accurate diagnostics will allow prescribers to move from empiric broad-spectrum therapy to more targeted treatment, reducing unnecessary exposure to high-resistance drugs [80]. Implementation of the AWaRe framework (WHO's Access, Watch, Reserve classification) in national guidelines and hospital formularies would further help steer antibiotic use towards more appropriate agents and preserve last-line options. Beyond healthcare facilities, community engagement, especially in rural areas, should be expanded. Protocols such as the Community Dialogue Approach (CDA) have been proposed to raise awareness and change antibiotic usage behavior at the community level in Bangladesh [81]. Furthermore, the prioritization of infection prevention and control (IPC) measures in healthcare systems, including improved hygiene, safe water and sanitation, rigorous environmental cleaning, and comprehensive staff training, can substantially reduce infection prevalence and, consequently, antibiotic consumption [82].

Conclusion

This systematic review and meta-analysis provides a comprehensive overview of the antimicrobial resistance patterns of major clinical bacterial isolates in Bangladesh between 2019 and 2024. The findings reveal alarmingly high resistance rates to commonly used first-line antibiotics, including ampicillin, amoxicillin, and third-generation cephalosporins, across both Gram-negative and Gram-positive pathogens. Despite this concerning trend, several antibiotic classes demonstrated comparatively low resistance. Colistin, carbapenems, and vancomycin were found to be the most effective agents against most pathogens. However, the narrow spectrum of remaining effective antibiotics emphasizes the urgent need to preserve their utility through a coordinated national response. Implementing antimicrobial stewardship programs (ASPs), enforcing stricter regulations, and strengthening public awareness initiatives are critical to reducing inappropriate consumption and preventing the further spread of resistant pathogens.

Supplementary Materials

Figure S1: Forest plot showing the pooled prevalence of *Klebsiella* spp.

Figure S2: Forest plot showing the pooled prevalence of *Pseudomonas* spp.

Figure S3: Forest plot showing the pooled prevalence of *Escherichia coli.*

Figure S4: Forest plot showing the pooled prevalence of *Acinetobacter* spp.

Figure S5: Forest plot showing the pooled prevalence of *Staphylococcus aureus.*

Figure S6: Forest plot showing the pooled prevalence of *Proteus* spp.

Figure S7: Forest plot showing the pooled prevalence of *Enterococcus* spp.

Figure S8: Forest plot showing the pooled prevalence of *Enterobacter* spp.

Reference

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