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Assessment of Antimicrobial Susceptibility Patterns and Empirical Therapy Coverage using a Hospital Antibiogram in a Tertiary Care Hospital

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ABSTRACT

Background

Antimicrobial resistance compromises the effectiveness of empirical antibiotic therapy and is one of the most critical global health challenges, particularly for resource-limited hospital settings. Empirical treatment decisions are based on outdated assumptions about susceptibility patterns, often resulting in treatment failure and further propagation of resistance. Hospital antibiograms should be an important input into empirical choices, but most available reports remain simply descriptive in nature and do not examine the adequacy of empirical coverage for prevalent pathogens. Linking susceptibility data to empirical antibiotic adequacy enables a more clinically meaningful tool for antibiotic stewardship.

Objectives

This study aims to describe the distribution and antimicrobial susceptibility of bacterial isolates in a tertiary care hospital and to assess the adequacy of empirical antibiotic coverage based on local susceptibility data.

Materials and Methods

This cross-sectional laboratory-based study was conducted at a tertiary care hospital. It included 837 non-duplicate bacterial isolates collected from various clinical specimens between September 2023 and September 2024. Antimicrobial susceptibility testing was done by the Kirby–Bauer disk diffusion technique and interpreted as per CLSI M39-A5 guidelines. Calculation of empirical coverage was done by mapping each pathogen to its standard first-line empirical regimen as per hospital and national guidelines, and coverage was expressed as a percentage of isolates susceptible to the selected agent.

Results

Gram-negative bacteria constituted the majority (82.3%), with the following leading isolates: Escherichia coli (34.3%), Klebsiella pneumoniae (18.6%), and Klebsiella oxytoca (15.0%). Carbapenems and β-lactam/β-lactamase inhibitor combinations were the most active agents (>90%), while fluoroquinolones had low susceptibility rates (<40%). Empirical coverage analysis revealed ≥95% adequate coverage for Pseudomonas aeruginosa, K. oxytoca, and Proteus mirabilis, whereas Staphylococcus aureus and coagulase-negative staphylococci had lower coverage (74% and 71%, respectively).

Conclusions

Empirical coverage adequacy varied significantly across pathogens and emphasizes updating empirical therapy guidelines in line with local antibiogram data. The inclusion of empirical coverage assessment into routine surveillance can strengthen the role of antimicrobial stewardship toward providing optimal patient outcomes.

Keywords: Antibiogram, Empirical therapy, antimicrobial resistance; Empirical coverage, Bacterial susceptibility, Tertiary care hospital, antimicrobial stewardship, Infection management

1. INTRODUCTION

Bacterial infections remain a major cause of morbidity and mortality in low-resource healthcare settings, where diagnostic delays, constrained formularies, and heterogeneous empiric prescribing patterns complicate timely, effective treatment [1-3]. In India, empiric therapy is often initiated without the advantage of culture and susceptibility results; thus, the concordance between local pathogen epidemiology and first-line regimens represents a critical determinant of clinical outcomes and antimicrobial selection pressure [4-6]. Contemporary reports suggest that gram-negative organisms such as Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Proteus spp are dominant pathogens in many healthcare-associated and community-onset syndromes, while gram-positive pathogens, including Staphylococcus aureus and Enterococcus spp., make important contributions to bloodstream, skin, and soft-tissue infections, in addition to device-related infections [7-10]. However, the distribution of isolates and resistance phenotypes may vary across facilities, levels of care, and patient risk strata; therefore, setting-specific data are needed to inform empiric coverage [11-12].

Resource constraints bear on both access to and stewardship of antimicrobials. Dependence on a limited portfolio of agents, variable adherence to guidelines, and intermittent stock-outs may favour use of broad-spectrum classes, even where resistance undermines their effectiveness [13-15]. Routine escalation to reserve agents is not workable or desirable without evidence of benefit. A pragmatic assessment of pathogen profiles and susceptibility, anchored in the local setting, is thus critical in order to calibrate empiric therapy that maximizes the probability of appropriate initial coverage while minimizing unnecessary exposure to broad-spectrum drugs [16-17].

Optimizing empirical antibiotic choice relies on continued, context-specific pathogen distribution and susceptibility surveillance. Antibiograms are at the heart of this process, but in most settings, they are largely descriptive and do not quantify whether prevailing empirical regimens provide adequate coverage for locally prevalent pathogens [18-19]. Empirical coverage—which refers to the proportion of culture-confirmed infections for which the selected empirical regimen exhibits in vitro activity—provides a practical link between microbiological surveillance and bedside decision-making, thus enhancing the clinical utility of antibiograms for selection of first-line therapy [20].

While numerous studies report on the trends of susceptibility, far fewer describe how their data inform the adequacy of standard empirical regimens at the local level [21]. This research closes that gap by quantifying the coverage of empirical therapies using laboratory susceptibility data, hence operationalizing surveillance findings to support context-specific empirical prescribing and strengthening the integration of microbiological evidence into clinical decision-making [22].

The current study aims to characterize the distribution and antimicrobial susceptibility of bacterial isolates recovered in a tertiary care hospital and to assess the empirical coverage of the most commonly prescribed first-line antibiotics based on local resistance patterns. It also hypothesizes that the adequacy of standard empirical antibiotic coverage differs among the bacterial pathogens, with some first-line regimens showing suboptimal coverage because of emerging resistance. Therefore, the study aims to describe pathogen distribution, analyse antimicrobial susceptibility profiles, and assess the coverage of empirical therapy provided by commonly used antibiotics in a tertiary care hospital.

2. METHODOLOGY

2.1 Study Settings

The study was conducted in India, a country with mixed healthcare system comprising of both Government and Private sector hospitals. The government and insurance hospitals offer free or subsidized healthcare to economically disadvantaged populations. These low – resource settings are vulnerable to inappropriate antimicrobial use due to high patient volumes, a wide spectrum of infections, diagnostic and infection control limitations along with less impactful stewardship practices. The antibiogram was developed in this setting to help uncover these resistance patterns and act as a tool of epidemiological surveillance and for clinical decision making.

2.2 Study Design

This was a cross – sectional retrospective study conducted in a low resource hospital from July 2024 to November 2024.

2.3 Development of Hospital Antibiogram

2.3.1 Collection of Source Data

Antimicrobial susceptibility reports were collected retrospectively from the hospital's microbiology department from September 2023 to September 2024. Data collection yielded 837 isolates from 10

different types of specimens, after screening and filtering according to the CLSI M39 A5 guidelines.

2.3.2 Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing had been performed in the hospital laboratory according to the CLSI M39 A5 guidelines. The Kirby–Bauer disk diffusion method was used on Mueller–Hinton agar with depth of 4 mm. Bacterial inocula were prepared from fresh cultures and adjusted to 0.5 McFarland standard. Antimicrobial disks of standard potency were applied, and plates were incubated at 35 ± 2 °C for 16–18 hours in ambient air. Zone diameters were measured in millimetres and interpreted using the current CLSI breakpoint tables.

Antimicrobial susceptibility results were interpreted according to CLSI M100 (2023–2024). For agents without organism-specific breakpoints, CLSI-recommended surrogate interpretive criteria were applied. Similarly, cefazolin breakpoints for non-CSF isolates were used as surrogates to predict susceptibility to oral first-generation cephalosporins such as cephalexin. Breakpoints for combination antibiotics like Cefaperazone – Sulbactam was interpreted using individual Cefaperazone guidelines. For piperacillin–tazobactam, CLSI breakpoints designated for the combination drug were used, consistent with standard recommendations. No interpretive criteria were assigned for agents without CLSI-approved breakpoints for the tested organism (e.g., metronidazole for aerobic gram-positive or gram-negative bacteria), and such drugs were excluded from the antibiogram analysis.

Antimicrobial susceptibility results were interpreted according to CLSI M100 (2023–2024). For agents without organism-specific breakpoints, CLSI-recommended surrogate interpretive criteria were applied. Similarly, cefazolin breakpoints for non-CSF isolates were used as surrogates to predict susceptibility to oral first-generation cephalosporins such as cephalexin.

2.3.3 Data analysis and Antibiogram development

The data collected was entered and analysed in Microsoft Excel. The different sensitivity and resistance patterns were analysed and sorted according to the classes of antibiotics. The final antibiogram was also developed in Microsoft Excel with conditional formatting to show the different rates of susceptibility and resistance.

2.4 Ethics Statement

The ethics approval was waived as this study only involved retrospective data analysis of the data from patient's laboratory records. The confidentiality of the data was maintained and it was ensured that there were no identifiers.

3. RESULTS

An antibiogram was developed from the antimicrobial susceptibility reports obtained from the hospital's microbiology department. Over 837 isolates were identified from 10 categories of specimen in accordance with the CLSI M39 – A5 guidelines. The 837 isolates were obtained from patients with various different demographics in terms of age.

3.1 Source Demographics

Out of the 837 isolates, the isolates were obtained from a broad range of age groups, as shown in **Table.1 : Age distribution of Source of the isolates**Table. The highest proportion of bacterial isolates were found between ages 50–57 with 231 isolates from that category (27.6%), followed by 42–49 years with 200 isolates from that category (23.9%) and 58–65 years (15.9%) with 133 isolates. The remaining age distribution were as follows : The 34–41 years age group with 69 isolates (8.24%), the 66–73 years group with 66 isolates (7.8%), with 26–33 years with 35 isolates (4.2%), 18–25 years with 21 isolates (2.5%), and below 18 years with 8 isolates (0.95%), with the remaining isolates from patients above 73 and younger than 18.

Table.1 : Age distribution of Source of the isolates

Age	Frequency (n)	Percentage (%)
Below 18	8	0.95
18 – 25	21	2.5
26 – 33	35	4.2
34 – 41	69	8.24
42 – 49	200	23.9
50 – 57	231	27.6
58 - 65	133	15.9
66 – 73	66	7.8
Above 73	74	8.8

Among the 837 isolates, 435 isolates were obtained from males accounting for 52.97% of the isolates and 402 isolates were from females accounting for 47.03% of the isolate, as shown in Table 2.

Table.2 : Gender Distribution

GENDER	Frequency	Percentage
Male	435	52.97%
Female	402	47.03%

3.2 Laboratory Characteristics of the Isolates

3.2.1 Distribution of different specimens isolated

As shown in Table 3, the majority of the isolates were isolated from specimens like urine, blood, tissue, wound swab and pus. A small proportion of isolates are obtained from specimens like rectal swab, E. T. aspiration fluid, sputum, pleural fluid and ascitic fluid which are classified as miscellaneous. Urine sample accounted for 335 isolates (40.02%), followed by blood samples with 246 isolates (29.39%), tissue samples with 104 isolates (12.42%) and pus specimens contributed 81 isolates (9.68%), while the remaining specimens were classified as miscellaneous. Miscellaneous specimens include with samples including wound swabs with 41 isolates (4.9%), sputum with 10 isolates (1.19%), pleural fluid with 8 isolates (0.95%), endotracheal aspiration fluid with 6 isolates (0,71%), rectal swab with 3 isolates (0.35%) and ascitic fluid with 3 isolates (0.35%).

Table.3 : Categorization of different specimens collected

Specimen	Freq (n)	Percentage (%)
Urine	335	40.02
Blood	246	29.39
Tissue	104	12.42
Wound swab	41	4.9
Pus	81	9.68
Rectal swab	3	0.35
Sputum	10	1.19
Pleural fluid	8	0.95
E. T. Aspiration fluid	6	0.71
Ascitic Fluid	3	0.35

3.2.2 Distribution of the Pathogens isolated

On culture testing, a wide range of pathogens were identified of which were 7 were gram negative and 2 were gram positive. The pathogenic distribution as shown in Table 4 was as follows: E.coli was isolated in 287 out of the 837 isolates (34.29%), followed by Klebsiella pneumonia and Klebsiella oxytoca with 156 (18.6%) and 126 (15.05%) isolates, respectively. Staphylococcus aureus was found in 118 isolates (14.1%) and Pseudomonas aeruginosa was found in 96 isolates (11.46%). Proteus mirabilis, Proteus vulgaris, Salmonella typhi and Coagulase negative Staphylococcus were found in less than 30 isolates.

Table.4 : Distribution of Bacterial Pathogens isolated from various clinical specimens

Organism isolated	Frequency	Percentage
E. coli	287	34.29%
S. typhi	17	2.03%
K. pneumoniae	156	18.6%
K. oxytoca	126	15.05%
P. vulgaris	11	1.31%
P. mirabilis	13	1.55%
P. aeruginosa	96	11.46%
S. aureus	118	14.1%
Coagulase -ve Staphylococcus	13	1.55%

Specimen wise distribution as shown in Table 5 reveals that E. coli was found majorly in urine with 52.6% isolates. Klebsiella spp were found predominantly in urine followed by blood with more than 34% percent isolates found in them. P. aeruginosa was found majorly in blood with 42.7% isolates. Gram positive organisms S. aureus and coagulase negative staphylococcus were found majorly in blood with more than 40 percent of isolates.

Organism	Urine (n, %)	Blood (n, %)	Tissue (n, %)	Pus (n, %)	Others (n. %)	Total
E. coli	151 (52.6%)	42 (14.6%)	41(14.2%)	30 (10.4%)	23 (8.01%)	287
S. typhi	06 (35.3%)	11 (64.7%)	0 (0%)	0 (0%)	0 (0%)	17
K. pneumoniae	54 (34.6%)	53 (34%)	22 (14.1%)	16 (10.2%)	09 (5.7%)	156
K. oxytoca	46 (36.5%)	38 (0.3%)	19 (15.07%)	15 (11.9%)	08 (0.06%)	126
P. vulgaris	05 (45.4%)	03 (27.3%)	0 (0%)	0 (0%)	03 (27.3%)	11
P. mirabilis	05 (38.5%)	02 (15.3%)	02 (15.3%)	0 (0%)	04 (30.7%)	13
P. aeruginosa	24 (25%)	41 (42.7%)	12 (12.5 %)	09 (9.37%)	10 (10.41%)	96
S. aureus	41 (34.7%)	48 (40.7%)	08 (6.77%)	11 (9.3%)	10 (8.47%)	118
Coagulase -ve Staphylococcus	03 (23.07%)	06 (46.15%)	0 (0%)	0 (0%)	04 (30.7%)	13
Total	335	246	104	81	71	837

Table.5 : Specimen wise Distribution of Bacterial Isolates

3.3 Susceptibility Rates of Isolated Pathogens

3.3.1 Individual Susceptibility Profile of E. coli

As shown in Table 6, E. coli showed maximum sensitivity to Carbapenems like Meropenem and Imipenem , Cefotaxime and Piperacillin – Tazobactam, followed by Cefaperazone – Sulbactam and Ceftriaxone. It showed moderate sensitivity towards Amoxycillin – Clavulenic acid, whereas it was least sensitive towards Cefuroxime, Ampicillin and Ciprofloxacin.

Table.6 : %Susceptibility of E.coli

Antibiotics	Breakpoints	%S
Amikacin	≤4	84
Gentamicin	≤2	62
Cefotaxime	≤1	100
Cefuroxime	≤8	29
Ceftriaxone	≤1	82
Cef/sulbactam	≤16	88
Ciprofloxacin	≤0.25	33
Amoxy/clav	≤8/4	82
Ampicillin	≤8	30
Pip – taz	≤16/4	100
Meropenem	≤1	100
Imipenem	≤1	96
Nitrofurantoin	≤32	100
Cotrimoxazole	≤2/38	50

3.3.2 Individual Susceptibility Profile of S. typhi

Individual susceptibility profile of S. typhi as shown in Table 7 showed that the organism was most susceptible to Carbapenems and 3rd generation Cephalosporins like Cefotaxime, Cefixime and Ceftriaxone along with Ofloxacin. S. typhi was least susceptible to Cotrimoxazole.

Table.7 : %Susceptibility of S. typhi

Antibiotics	Breakpoints	% S
Cefotaxime	≤1	81
Cefixime	≤1	82
Ceftriaxone	≤1	83
Ofloxacin	≤0.12	93
Meropenem	≤1	92
Imipenem	≤1	94

Cotrimoxazole	≤2/38	40

3.3.3 Individual Susceptibility Profile of K. pneumoniae

K. pneumoniae showed most susceptibility to Carbapenems like Meropenem and Imipenem and Piperacillin – Tazobactam , followed by Cefotaxime and showed least susceptibility to Cefuroxime, as shown in Table 8.

Table.8 : %Susceptibility of K. pneumoniae

Antibiotics	Breakpoints	%S
Amikacin	≤16	45
Gentamicin	≤2	79
Cefotaxime	≤1	82
Cefuroxime	≤8	18
Ceftriaxone	≤1	81
Cef/sulbactam	≤16/8	68
Ciprofloxacin	≤0.25	47
Amoxy/clav	≤8/4	70
Pip – taz	≤16/4	93
Meropenem	≤1	96
Imipenem	≤1	96
Nitrofurantoin	≤32	54
Cotrimoxazole	≤2/38	64
Doxycycline	≤4	70

3.3.4 Individual Susceptibility Profile of K. oxytoca

K. oxytoca had maximum susceptibility to Amikacin, and Carbapenems like Meropenem and Imipenem, as shown in Table 9. Also, it showed least susceptibility to Cotrimoxazole.

Table.9 : %Susceptibility of K. oxytoca

Antibiotics	Breakpoints	%S
Amikacin	≤16	100
Gentamicin	≤2	71
Cefotaxime	≤1	85
Ceftriaxone	≤1	85
Cef/sulbactam	≤ 16	61
Amoxy/clav	≤8/4	72
Pip – taz	≤16/4	96
Meropenem	≤1	100
Imipenem	≤1	100
Cotrimoxazole	≤2/38	32
Doxycycline	≤4	87

3.3.5 Individual Susceptibility Profile of P. vulgaris

P. vulgaris had highest susceptibility to Piperacillin – Tazobactam and Carbapenems – Meropenem and Imipenem and moderate susceptibility to Amikacin, Gentamicin and Cefaperazone – Sulbactam as shown in Table 10.

Table.10 : %Susceptibility of P. vulgaris

Antibiotics	Breakpoints	% S
Amikacin	≤16	41
Gentamicin	≤2	71
Cef/sulbactam	≤ 16	96
Pip – taz	≤16/4	96
Meropenem	≤1	93
Imipenem	≤1	100

3.3.6 Individual Susceptibility Profile of P. mirabilis

As shown in Table 11, P. mirabilis was most susceptibility to Cefaperazone – Sulbactam, Piperacillin – Tazobactam, Meropenem and Imipenem. It showed moderate susceptibility to Amikacin and Gentamicin.

Table.1 : %Susceptibility of P. mirabilis

Antibiotics	Breakpoints	% S
Amikacin	≤4	41
Gentamicin	≤2	71
Cef/sulbactam	≤ 16	96
Pip – taz	≤8/4	96
Meropenem	≤1	93
Imipenem	≤1	100

3.3.7 Individual Susceptibility Profile of P. aeruginosa

Susceptibility profile of P. aeruginosa, as shown in Table 12, shows that that the organism is most susceptible to Piperacillin – Tazobactam and Carbapenems, followed by Cefotaxime and Cefaperazone – Sulbactam and least susceptibility towards Cotrimoxazole.

Table.12 : %Susceptibility of P. aeruginosa

Antibiotics	Breakpoints	% S
Amikacin	≤16	53
Gentamicin	≤2	69
Cefotaxime	≤1	85
Ceftriaxone	≤8	60
Cef/sulbactam	≤16	84
Ciprofloxacin	≤1	40
Levofloxacin	≤ 2	63
Pip – taz	≤16/4	100
Meropenem	≤2	88
Imipenem	≤2	93
Cotrimoxazole	≤2/38	11

3.3.8 Individual Susceptibility Profile of S. aureus

S. aureus showed high susceptibility towards Meropenem and Imipenem followed by Ceftriaxone and Cefotaxime and least susceptibility towards Ciprofloxacin, as shown in Table 13.

Table.2 : %Susceptibility of S. aureus

Antibiotics	Breakpoints	% S
Cefotaxime	≤4	81
Ceftriaxone	≤4	87
Cef/sulbactam	≤16	71
Cephalexin	≤ 2	99
Ciprofloxacin	≤1	34
Levofloxacin	≤ 1	70
Amoxy/clav	≤4/2	74
Pip – taz	≤8/4	72
Meropenem	≤1	92
Imipenem	≤1	94
Cotrimoxazole	≤16	28
Metronidazole	≤16	90
Doxycycline	≤4	79

3.3.9 Individual Susceptibility Profile of Coagulase negative Staphylococci

Coagulase negative Staphylococci showed high susceptibility towards Metronidazole, followed Piperacillin – Tazobactam and Ceftriaxone. It showed moderate susceptibility towards Ciprofloxacin, Meropenem and Amoxycillin – Clavulenic acid.

Table.14 : %Susceptibility of Coagulase negative Staphylococci

Antibiotics	Breakpoints	% S
Ceftriaxone	≤4	83
Ciprofloxacin	≤1	57
Amoxy/clav	≤4/2	71
Pip – taz	≤8/4	83
Meropenem	≤1	72

3.4 Cumulative Hospital Antibiogram (September 2023–September 2024)

A cumulative antibiogram was developed using 837 non-duplicate clinical isolates in accordance with CLSI M39-A5 guidelines. The antibiogram summarizes the percentage susceptibility of the major gram-negative and gram-positive organisms to commonly tested antibiotics. Overall, carbapenems and β-lactam/β-lactamase inhibitor combinations demonstrated the highest activity across gram-negative isolates, whereas fluoroquinolones and older cephalosporins showed markedly reduced susceptibility. Among gram-positive isolates, Staphylococcus aureus exhibited good susceptibility to third-generation cephalosporins and carbapenems but poor response to fluoroquinolones and cotrimoxazole. The cumulative antibiogram provides a consolidated overview of local susceptibility trends and forms the basis for evaluating empirical antibiotic coverage for commonly isolated organisms in this hospital setting.

3.4 Evaluation of Empirical Antibiotic Coverage among Clinical Isolates

Empirical coverage was assessed by mapping each pathogen to its standard first-line empirical antibiotic, based on both hospital protocols and guideline recommendations.

As shown in Table 14, Empirical agents assigned against P. aeruginosa and K. pneumonia showed 100% coverage against these organisms, followed Piperacillin/Tazobactam showing 96% coverage against Proteus Mirabilis. All other organisms were moderately covered (74 – 83%) by their assigned empirical agents, with Amoxicillin/ Clavulanic acid showing least coverage against Coagulase negative S. aureus.

Antibiotic Susceptibility Patterns of Commonly Isolated Bacteria for 2024

Numbers below represent **percent of susceptible isolates**

Organisms		No of Strains	Amikacin	Gentamicin	Cefotaxime	Cefixime	Cefuroxime	Ceftriaxone	Cefoperazone-Sulbactam	Cephalexin	Ciprofloxacin	Levofloxacin	Ofloxacin	Amoxicillin-Clavulanic Acid	Ampicillin	Piperacillin-tazobactam	Meropenem	Imipenem	Nitrofurantoin	Cotrimoxazole	Metronidazole	Doxycycline
Gram Negative	*Eshcerichia coli*	287	84	62	100		29	82	88		33			82	30	100	100	96	100	50	71	
	Salmonella typhi	17			81	82		83					93				92	94		40		
	Klebsiella pneumoniae	156	45	79	82		18	81	68		47			70		93	95	96	54	64		70
	Klebsiella oxytoca	126	100	71	85			85	61					72		96	100	100		32		87
	Proteus vulgaris	11	92	62	83			80			17	29				82	96	100	11	18		
	Proteus mirabilis	13	41	71					96							96	93	100				
	Pseudomonas aeruginosa	96	53	69	85			60	84	52	40	63			30	100	88	93		11		
Gram Positive	*Staphylococcus aureus*	118			81			87	71	99	34	70		74		72	92	94		28	90	79
	Coagulase(-) staphylococcus	13						83			57			71		83	72				92	

Legend: Green shades indicate higher susceptibility; yellow–orange indicate moderate to low susceptibility; red indicates very low susceptibility / high resistance. Grey indicates not tested.

0 25 50 75 100 Not tested

Figure.1 - Heatmap-Style Cumulative Antibiogram (2023–2024)

Heatmap showing the percentage susceptibility of major clinical isolates to commonly used antibiotics. Colour scale: dark green = 100%, light green = 75–99%, yellow = 50–74%, orange = 25–49%, red = 0–24%, and grey = not tested. Higher susceptibility is represented by greener shades and increasing resistance by warmer colours.

Table.15 – Percentage of isolates susceptible to standard empirical antibiotics with corresponding MDR rates

Organisms	No of Isolates	Assigned Empirical Drug	# Tested (for the drug)	# S %	Coverage (n/N) %	MDR%
E. coli	287	Ceftriaxone	287	235	82%	18%
S. typhi	17	Ceftriaxone	17	14	83%	17%
K. pneumoniae	156	Ceftriaxone	156	126	81%	19%
K. oxytoca	126	Meropenem	126	126	100%	0%
P. vulgaris	11	Piperacillin/ Tazobactam	11	9	82%	18%
P. mirabilis	13	Cefaperazone/ Sulbactam	13	12	96%	4%
P. aeruginosa	96	Piperacillin/ Tazobactam	96	96	100%	0%
S. aureus	118	Amoxicillin Clavulanic acid	118	88	74%	26%
Coagulase -ve Staphylococcus	13	Amoxicillin Clavulanic acid	13	9	71%	29%

4. DISCUSSION

Gram-negative organisms predominated in our study, with Escherichia coli and Klebsiella spp. being the most common, constituting the major share of isolates. This pattern is in concordance with findings from the 10-year analysis by Singh et al., where, among bloodstream infections at a tertiary care centre, K. pneumoniae (21.9%) and E. coli (19.1%) were the most frequent Enterobacteriaceae isolates and showed rising resistance to cefotaxime, carbapenems, and piperacillin-tazobactam[23].

A cross-sectional study conducted in Gujarat by Patel et al. found that E. coli dominated urinary tract isolates and K. pneumoniae was more frequent in ICU/respiratory samples; more than one-fourth of the isolates exhibited carbapenem resistance, and over half were ESBL-producers. These Indian data support our findings and reinforce the fact that Enterobacteriaceae remain important pathogens in tertiary-care settings in India[24].

Regarding antimicrobial susceptibility, our results of higher activity among carbapenems and β-lactam/β-lactamase inhibitor combinations but reduced sensitivity to third-generation cephalosporins and fluoroquinolones are consistent with national trends. Such resistance may arise due to prolonged exposure to broad-spectrum antibiotics, inadequate de-escalation, and incomplete adherence to principles of stewardship, as discussed by Gandra et al. (2021) and Holmes et al. (2016) [4,16]. However, these classes remain valuable as empiric options in high-risk settings, especially where gram-negative organisms dominate. The retrospective Indian multicentred study, conducted between 2017 and 2022 by the Indian Council of Medical Research-AMRSN network, reported a significant rise in imipenem and meropenem resistance for Klebsiella and E. coli bloodstream isolates[25]. In a rural Karnataka study, Markos Mardourian et al. found that Enterobacteriaceae from urine and blood showed a resistance of over 45% to quinolones and cephalosporins and over 25% to carbapenems[26]. International experts described a "continual evolution" of carbapenemase-producing Enterobacterales, now generally known as CREs; carbapenem resistance is no longer limited to K. pneumoniae but is widespread among Enterobacterales worldwide[27]. The implications of our findings thus reinforce that third-generation cephalosporins and fluoroquinolones may no longer serve reliably as empirical treatments in our setting without input from local susceptibility data. Additionally, stewardship programs should emphasize restricted carbapenem use to preserve efficacy, particularly against emerging carbapenemase producers.

When we assessed empirical coverage of first-line antimicrobials, adequacy was heterogeneous across pathogens; though most gram-negatives were well covered with β-lactam/β-lactamase inhibitor

combinations and carbapenems, coverage of some gram-positive isolates was poorer. This points to the fact that empirical regimens cannot presume uniform efficacy across all organisms. The Gujarat study by Patel et al. showed that almost a quarter of E. coli/K. pneumoniae strains were carbapenem-resistant, and over half of them were ESBL-producers, thus limiting empirical options[24]. Similarly, the ICMR-AMRSN multicentre data reported that resistance in hospital-acquired bloodstream infection preceded community-acquired ones and highlighted the need for tailored empirical policies[25]. These findings therefore, highlight the importance of calculating empirical coverage percentages along with cumulative antibiogram data, thereby transforming what had been 'surveillance summaries' into actionable decision tools.

Beyond organism-level data, these findings have broader implications for antimicrobial stewardship. Integration of antibiogram data with clinical outcomes can strengthen institutional antibiotic guidelines and enable periodic re-evaluation of empirical policies. Data-driven stewardship interventions, such as cumulative antibiogram review, feedback to prescribers, and local formulary update, have shown measurable reductions in broad-spectrum antibiotic use and infection recurrence rates, as studied by Karanika et al and Dik et al[28,6]. The development of hospital-specific antibiograms, as implemented in this study, represents a practical measure for the optimization of empiric therapy in low-resource settings. Regular updating every 6–12 months will allow tracking of evolving resistance, guide formulary decisions, and limit the use of reserve antibiotics.

5. LIMITATIONS

This was a single tertiary care hospital-based study, and it may not be representative. Molecular typing and genotypic confirmation of resistance mechanisms were not done. Furthermore, clinical outcomes and antibiotic consumption data were not correlated with microbiological results, which could provide further insights. Future multicentric and longitudinal studies integrating molecular surveillance and outcome measures are warranted to strengthen these findings.

6. CONCLUSION

Gram-negative bacteria, particularly E. coli and Klebsiella species, were the most commonly isolated pathogens. Carbapenems and β-lactam/β-lactamase inhibitor combinations showed the greatest susceptibility, whereas decreased sensitivity to third-generation cephalosporins and fluoroquinolones indicates persistent resistance patterns.Empirical coverage analysis showed that, while most first-line regimens remain effective, coverage varied between organisms, particularly among gram-positive isolates. These findings underscore the need for regular, data-driven revision of empirical antibiotic guidelines. Routine development of hospital-specific antibiograms with a combined coverage assessment can promote more rational antibiotic use and strengthen stewardship programs in tertiary care settings.

7. DECLARATION BY THE AUTHORS

7.1 Consent for Publication

Informed consent was waived as data was obtained from the hospital's microbiology department and electronic health records. It was ensured that there were no identifiers and confidentiality was maintained.

7.2 Availability of data and materials

All the data and supporting information are enclosed within the article.

7.3 Funding

No external funding was received.

7.4 Contribution of Authors

All the authors contributed equally in the study

7.5 Conflict of Interest

The authors declare no conflict of interest.

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