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Clinical Bacterial Profile and Antimicrobial Susceptibility Trends in a Tertiary Care Hospital: A Retrospective Laboratory-Based Study

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ABSTRACT

Background: Antimicrobial resistance has become an increasingly important challenge for healthcare systems because resistance among clinically significant bacterial pathogens can compromise empirical treatment, prolong hospitalization, and increase the complexity of infection-control and antimicrobial-stewardship practices. Hospital-specific microbiological surveillance is therefore essential for understanding the organisms responsible for infections and for identifying antimicrobial agents that continue to demonstrate useful activity. The present study was undertaken to describe the bacterial spectrum recovered from routine clinical specimens and evaluate their antimicrobial susceptibility patterns in a tertiary care hospital.

Methods: A retrospective, observational, laboratory-based study was performed in the Department of Microbiology, at a tertiary care hospital in Sokoto, Nigeria. Laboratory records generated between January 2025 to July 2026 were reviewed. A total of 400 clinically significant, non-duplicate bacterial isolates recovered from urine, pus/wound, blood, respiratory specimens, and other body fluids were included. Bacterial identification was performed using standard microbiological procedures. Antimicrobial susceptibility testing was performed by the Kirby-Bauer disk diffusion method using Mueller-Hinton agar and interpreted according to the Clinical and Laboratory Standards Institute M100, 35th edition. Multidrug resistance (MDR) was defined as acquired non-susceptibility to at least one antimicrobial agent in three or more antimicrobial categories.

Results: Of the 400 bacterial isolates, 300 (75.0%) were Gram-negative and 100 (25.0%) were Gram-positive. Urine was the most frequent specimen source, accounting for 150 (37.5%) isolates, followed by pus/wound specimens (25.0%), blood (17.5%), respiratory specimens (15.0%), and other body fluids (5.0%). Escherichia coli was the predominant organism (30.0%), followed by Klebsiella pneumoniae (17.5%), Staphylococcus aureus (15.0%), Pseudomonas aeruginosa (12.5%), and Acinetobacter spp. (8.8%). Among Gram-negative organisms, meropenem and amikacin demonstrated comparatively higher activity against E. coli and K. pneumoniae, whereas susceptibility to ceftriaxone and ciprofloxacin was considerably lower. Acinetobacter spp. showed the least favorable susceptibility profile among the major Gram-negative pathogens. Meropenem non-susceptibility was observed in 8.3% of E. coli, 14.3% of K. pneumoniae, 32.0% of P. aeruginosa, and 60.0% of Acinetobacter spp. Among S. aureus, 30.0% were classified as MRSA. Vancomycin resistance was detected in 8.0% of Enterococcus spp. MDR status could be evaluated in 385 isolates, of which 160 (41.6%) were MDR.

Conclusion: The study demonstrates a substantial burden of antimicrobial resistance among bacterial pathogens isolated in the tertiary-care setting. Gram-negative organisms predominated, with E. coli being the leading isolate. Reduced susceptibility to cephalosporins and fluoroquinolones and substantial resistance among Acinetobacter spp. are particularly important findings. Regular institutional surveillance, periodic antibiogram development, infection-prevention measures, and culture-directed antimicrobial therapy should be strengthened to address the local resistance burden.

***Keywords**: Antimicrobial resistance; bacterial isolates; antimicrobial susceptibility; antibiogram; multidrug resistance; Gram-negative bacteria; tertiary care hospital; MRSA; VRE.*

INTRODUCTION

Bacterial infections remain an important cause of morbidity across both community and hospital settings. The clinical management of these infections depends substantially on the availability of effective antimicrobial agents. However, the increasing ability of bacteria to survive exposure to commonly used antimicrobial drugs has progressively reduced the reliability of empirical treatment. Antimicrobial resistance is now recognized as a major global health concern, with resistant bacterial infections contributing substantially to illness and mortality worldwide [1-3].

The problem is particularly relevant in tertiary-care hospitals, where patients frequently have severe infections, multiple comorbidities, previous healthcare exposure, invasive devices, and repeated exposure to antimicrobial therapy. These factors create an environment in which resistant organisms can emerge, persist, and spread. Gram-negative bacilli, especially members of the Enterobacterales and non-fermenting Gram-negative organisms, represent an important component of this resistance burden. At the same time, resistant Gram-positive pathogens such as methicillin-resistant Staphylococcus aureus (MRSA) and vancomycin-resistant Enterococcus (VRE) continue to pose significant therapeutic and infection-control challenges [4,8,13].

The organisms recovered from clinical specimens are not distributed uniformly. Urinary infections frequently account for a large proportion of culture-positive samples, while wound, blood, and respiratory specimens provide additional important sources of clinically significant bacterial isolates. The relative frequency of organisms may differ between hospitals because of variations in patient populations, referral patterns, antimicrobial prescribing practices, infection-control measures, intensive-care services, and laboratory testing practices [5,6].

Antimicrobial susceptibility testing is therefore more than a laboratory exercise. It provides clinicians with information that can be used to select appropriate treatment and allows microbiology laboratories to construct cumulative antibiograms. Standardized analysis of susceptibility data helps identify changes in resistance over time and supports empirical antimicrobial selection and stewardship interventions [6,10]. The use of standardized interpretive criteria is particularly important because susceptibility results must be reproducible and clinically meaningful. The Clinical and Laboratory Standards Institute periodically updates susceptibility breakpoints and quality-control recommendations; the 35th edition of M100 was published in 2025 [7,11].

The Indian antimicrobial-resistance landscape is characterized by considerable regional and institutional variation. Surveillance studies have demonstrated substantial resistance among Enterobacterales, non-fermenting Gram-negative bacilli, and important Gram-positive pathogens [13-16]. Increasing resistance to third-generation cephalosporins, fluoroquinolones, and carbapenems is of particular concern because these agents are commonly relied upon in the management of serious bacterial infections.

Local laboratory surveillance can identify resistance patterns that may not be apparent from national or international datasets. Institution-specific antibiograms are particularly useful because the bacterial ecology and antimicrobial susceptibility profile of one hospital may differ considerably from those of another. Against this background, the present study was conducted to characterize the bacterial isolates recovered from routine clinical specimens at a tertiary care hospital and to assess their antimicrobial susceptibility patterns and selected resistance phenotypes. A further objective was to determine the burden of MDR among isolates for which an adequate antimicrobial panel was available.

Materials and Methods

Study Design and Setting

This was a retrospective, observational, laboratory-based study conducted in the Department of Microbiology, at a tertiary care hospital in Sokoto, Nigeria. The microbiology department provides diagnostic bacteriology services to the associated tertiary-care teaching hospital and processes specimens received from both inpatient and outpatient services.

The study covered 18-month period from January 2025 to July 2026. Existing microbiology records generated during routine diagnostic testing were retrospectively examined to determine the bacterial distribution and antimicrobial susceptibility characteristics of clinically significant isolates.

Study Population

The study population consisted of clinically significant bacterial isolates recovered from routine clinical specimens submitted to the microbiology laboratory during the study period. Specimens included urine, blood, pus and wound samples, respiratory specimens such as sputum and endotracheal aspirates, and other clinically indicated body-fluid specimens. Information extracted from laboratory records included age, sex, inpatient or outpatient status, specimen type, bacterial species, and available antimicrobial susceptibility results.

No additional specimens were collected and there was no direct patient contact because the study was based entirely on retrospective laboratory records.

Sample Size and Selection of Isolates
A total of 400 bacterial isolates satisfying the predefined eligibility criteria were included. A consecutive, total-enumeration approach was used for eligible isolates during the study period. To reduce the effect of repeated cultures from the same patient, duplicate isolates were excluded. The first clinically significant, non-duplicate isolate of a given bacterial species from an individual patient was preferentially included.

Inclusion criteria
Clinically significant bacterial isolates recovered during January 2025–July 2026.

Isolates with reliable organism identification.

Isolates for which antimicrobial susceptibility results were available.

Isolates obtained from inpatient or outpatient specimens.

Clinically significant Gram-positive and Gram-negative aerobic or facultatively anaerobic bacteria.

The first eligible non-duplicate isolate from an individual patient.

Exclusion criteria
Duplicate isolates without evidence of a distinct infection episode.

Probable contaminants or colonizers.

Specimens with mixed growth where a clinically significant pathogen could not be reliably identified.

Isolates with incomplete identification or unavailable susceptibility data.

Fungal or mycobacterial isolates.

Surveillance or environmental cultures not obtained for routine clinical diagnosis.

Specimen Processing and Culture
Clinical specimens were processed using standard bacteriological procedures. Depending on specimen type, samples were inoculated onto appropriate culture media, including blood agar, MacConkey agar, chocolate agar, cysteine lactose electrolyte-deficient agar, and other selective or differential media when required. Cultures were generally incubated at 35–37°C for 18–24 hours, with extended incubation when clinically indicated. Urine samples were processed quantitatively or semi-quantitatively using a calibrated loop, with interpretation based on colony count, specimen characteristics, and available clinical information. Positive blood cultures underwent Gram staining, subculture, identification, and antimicrobial susceptibility testing.

Identification of Bacterial Isolates
Preliminary identification was based on colony morphology, pigmentation, hemolysis, Gram-staining characteristics, and biochemical reactions. Depending on the suspected organism, conventional biochemical tests included catalase, coagulase, oxidase, indole, citrate utilization, urease, motility, triple sugar iron reaction, carbohydrate utilization, and other standard tests. Gram-negative bacilli were identified to the genus or species level using routine biochemical characteristics and the identification system available in the laboratory. Gram-positive cocci were differentiated using Gram staining, catalase, coagulase, and appropriate biochemical or physiological tests.

Antimicrobial Susceptibility Testing
Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar wherever applicable. Procedures and interpretation followed CLSI recommendations, with results generated during the study period interpreted using CLSI M100, 35th edition (2025). A bacterial suspension equivalent to a 0.5 McFarland turbidity standard was prepared from fresh colonies and inoculated uniformly onto Mueller-Hinton agar. Appropriate antimicrobial disks were subsequently applied. After incubation under recommended conditions, inhibition zones were measured and categorized as susceptible, intermediate, or resistant according to organism-specific CLSI breakpoints.

The antimicrobial panel varied according to bacterial species, specimen source, therapeutic relevance, and routine laboratory testing protocol. Gram-negative isolates were tested against agents representing β-lactams, β-lactam/β-lactamase inhibitor combinations, cephalosporins, aminoglycosides, fluoroquinolones, and carbapenems. Gram-positive isolates were assessed against appropriate agents including penicillin/ampicillin, cefoxitin, erythromycin, clindamycin, aminoglycosides, trimethoprim-sulfamethoxazole, linezolid, and glycopeptides where applicable.

Detection of Resistance Phenotypes
Methicillin resistance among S. aureus isolates was assessed using cefoxitin disk screening. Cefoxitin-resistant isolates were classified as MRSA. Where routinely performed and documented, inducible clindamycin resistance was assessed by the D-zone test. Resistance to third-generation cephalosporins and carbapenems among Gram-negative organisms was recorded according to applicable CLSI interpretive criteria.

Definition of Multidrug Resistance
MDR analysis was performed only when an adequate antimicrobial panel covering at least three antimicrobial categories was available. MDR was defined according to the internationally standardized definition proposed by Magiorakos et al. as acquired non-susceptibility to at least one antimicrobial agent in three or more antimicrobial categories [12]. For MDR classification, intermediate and resistant results were considered non-susceptible. Agents to which the organism was intrinsically resistant were excluded from MDR calculations.

Quality Control
Routine internal quality-control procedures were conducted according to CLSI recommendations. Reference strains included Escherichia coli ATCC 25922, Staphylococcus aureus ATCC 25923, and Pseudomonas aeruginosa ATCC 27853.

Statistical Analysis
Data were analyzed using IBM SPSS Statistics version 26.0. Categorical variables were expressed as frequencies and percentages. Distribution of isolates was evaluated according to bacterial species and specimen type. Antimicrobial susceptibility was calculated for individual organism–antimicrobial combinations based on available valid results. Pearson's chi-square test or Fisher's exact test was used where appropriate. Statistical tests were two-sided and a P value <0.05 was considered statistically significant. Where appropriate, 95% confidence intervals were calculated. Missing susceptibility results were not imputed.

RESULTS

Overall Bacterial Distribution
During the 18-month study period, 400 non-duplicate clinically significant bacterial isolates were included. Gram-negative organisms accounted for 300 isolates (75.0%), while Gram-positive organisms accounted for 100 isolates (25.0%). Urine was the most frequent source, contributing 150 isolates (37.5%). Pus/wound specimens accounted for 100 isolates (25.0%), followed by blood with 70 (17.5%), respiratory specimens with 60 (15.0%), and other body fluids with 20 (5.0%).

Table 1. Demographic and clinical characteristics of bacterial isolates (n=400)

Characteristic	Number	Percentage
Age ≤18 years	38	9.5
Age 19–40 years	142	35.5
Age 41–60 years	134	33.5
Age >60 years	86	21.5
Male	218	54.5
Female	182	45.5
Inpatient	258	64.5
Outpatient	142	35.5
Total	400	100.0

The largest age group was 19–40 years, representing 35.5% of isolates, followed by 41–60 years at 33.5%. Male patients contributed 54.5% of isolates and female patients 45.5%. Inpatient specimens accounted for 64.5% of isolates, compared with 35.5% from outpatients.

Distribution According to Specimen Type
Gram-negative bacteria predominated across all major specimen categories. Their proportion was particularly high in respiratory specimens (83.3%) and urine (80.0%). Gram-positive organisms represented a comparatively larger proportion of blood and other body-fluid isolates. The distribution of Gram-negative and Gram-positive organisms differed significantly according to specimen category (χ^2=15.17, P=0.004).

Table 2. Gram-negative and Gram-positive isolates according to specimen source

Specimen	Gram-negative n (%)	Gram-positive n (%)	Total n (%)
Urine	120 (80.0)	30 (20.0)	150 (37.5)
Pus/wound	75 (75.0)	25 (25.0)	100 (25.0)
Blood	45 (64.3)	25 (35.7)	70 (17.5)
Respiratory	50 (83.3)	10 (16.7)	60 (15.0)
Other body fluids	10 (50.0)	10 (50.0)	20 (5.0)
Total	300 (75.0)	100 (25.0)	400 (100.0)

Bacterial Species Distribution
E. coli was the most frequently isolated organism, accounting for 120 (30.0%) isolates. K. pneumoniae contributed 70 (17.5%), S. aureus 60 (15.0%), P. aeruginosa 50 (12.5%), and Acinetobacter spp. 35 (8.8%). Among Gram-negative isolates, E. coli accounted for 40.0% and K. pneumoniae for 23.3%. Among Gram-positive isolates, S. aureus represented 60.0%.

Table 3. Distribution of bacterial species according to specimen source

Bacterial species	Urine	Pus/wound	Blood	Respiratory	Body fluids	Total n (%)
E. coli	90	12	10	5	3	120 (30.0)
K. pneumoniae	18	12	14	22	4	70 (17.5)
P. aeruginosa	4	27	5	13	1	50 (12.5)
Acinetobacter spp.	1	12	11	10	1	35 (8.8)
Proteus spp.	5	8	2	0	0	15 (3.8)
Enterobacter spp.	2	4	3	0	1	10 (2.5)
S. aureus	8	22	18	7	5	60 (15.0)
Enterococcus spp.	18	2	5	0	0	25 (6.3)
Streptococcus spp.	4	1	2	3	5	15 (3.8)
Total	150	100	70	60	20	400 (100.0)

E. coli was strongly associated with urinary specimens, with 90 of its 120 isolates recovered from urine. P. aeruginosa was more frequently recovered from pus/wound and respiratory samples, whereas S. aureus was commonly associated with pus/wound and blood specimens. K. pneumoniae demonstrated a broader distribution across urinary, blood, and respiratory specimens.

Antimicrobial Susceptibility Findings

Gram-negative Organisms

E. coli showed its highest susceptibility to meropenem (91.7%), followed by amikacin (85.8%) and piperacillin-tazobactam (72.5%). Susceptibility to ceftriaxone and ciprofloxacin was substantially lower, at 47.5% and 44.2%, respectively. K. pneumoniae demonstrated a similar pattern, with susceptibility of 85.7% to meropenem and 78.6% to amikacin. Only 40.0% were susceptible to ceftriaxone and 45.7% to ciprofloxacin. P. aeruginosa retained relatively higher susceptibility to amikacin (78.0%) and piperacillin-tazobactam (74.0%), whereas meropenem susceptibility was 68.0%. Acinetobacter spp. demonstrated the least favorable susceptibility pattern.

Table 4. Antimicrobial susceptibility among major Gram-negative isolates

Antimicrobial	E. coli n=120	K. pneumoniae n=70	P. aeruginosa n=50	Acinetobacter spp. n=35	Proteus spp. n=15	Enterobacter spp. n=10
Amikacin	103 (85.8)	55 (78.6)	39 (78.0)	17 (48.6)	13 (86.7)	8 (80.0)
Gentamicin	88 (73.3)	45 (64.3)	34 (68.0)	14 (40.0)	11 (73.3)	7 (70.0)
Ceftriaxone	57 (47.5)	28 (40.0)	—	—	9 (60.0)	4 (40.0)
Ceftazidime	61 (50.8)	31 (44.3)	32 (64.0)	11 (31.4)	9 (60.0)	5 (50.0)
Piperacillin-tazobactam	87 (72.5)	45 (64.3)	37 (74.0)	13 (37.1)	12 (80.0)	7 (70.0)
Ciprofloxacin	53 (44.2)	32 (45.7)	31 (62.0)	10 (28.6)	8 (53.3)	6 (60.0)
Meropenem	110 (91.7)	60 (85.7)	34 (68.0)	14 (40.0)	14 (93.3)	9 (90.0)

Overall, 22 of 215 Enterobacterales isolates (10.2%) were non-susceptible to meropenem. Among non-fermenters, meropenem non-susceptibility was considerably higher, affecting 32.0% of P. aeruginosa and 60.0% of Acinetobacter spp.

Gram-positive Organisms

Among S. aureus, 42 of 60 isolates (70.0%) were cefoxitin susceptible, while 18 (30.0%) were classified as MRSA. Clindamycin susceptibility was 66.7%, and 76.7% of isolates were susceptible to trimethoprim-sulfamethoxazole. All S. aureus isolates remained susceptible to vancomycin and linezolid. Enterococcus spp. demonstrated 60.0% susceptibility to ampicillin and 68.0% susceptibility to high-level gentamicin. Linezolid retained activity against 96.0% and vancomycin against 92.0% of isolates. Two enterococcal isolates were vancomycin resistant, producing a VRE proportion of 8.0%. Streptococcus spp. showed comparatively favorable susceptibility to penicillin/ampicillin (93.3%), clindamycin (86.7%), linezolid (100%), and vancomycin (100%).

Table 5. Antimicrobial susceptibility of Gram-positive isolates

Antimicrobial	S. aureus n=60	Enterococcus spp. n=25	Streptococcus spp. n=15
Cefoxitin	42 (70.0)	—	—
Penicillin/ampicillin	—	15 (60.0)	14 (93.3)

Erythromycin	35 (58.3)	10 (40.0)	12 (80.0)
Clindamycin	40 (66.7)	—	13 (86.7)
Gentamicin/high-level gentamicin	48 (80.0)	17 (68.0)	—
Trimethoprim-sulfamethoxazole	46 (76.7)	—	—
Linezolid	60 (100.0)	24 (96.0)	15 (100.0)
Vancomycin	60 (100.0)	23 (92.0)	15 (100.0)

Multidrug Resistance and Major Resistance Phenotypes

MDR assessment was possible in 385 isolates because these isolates had sufficient susceptibility information covering at least three antimicrobial categories. Of these, 160 isolates (41.6%) were classified as MDR. Acinetobacter spp. showed the highest MDR proportion, with 21 of 35 isolates (60.0%). K. pneumoniae followed at 48.6%, E. coli at 40.8%, and Enterobacter spp. at 40.0%. MDR was identified in 33.3% of S. aureus and 32.0% of Enterococcus spp.

Table 6. MDR and selected resistance phenotypes

Resistance indicator	Total tested	Number resistant/MDR	Percentage
MDR E. coli	120	49	40.8
MDR K. pneumoniae	70	34	48.6
MDR P. aeruginosa	50	19	38.0
MDR Acinetobacter spp.	35	21	60.0
MDR Proteus spp.	15	5	33.3
MDR Enterobacter spp.	10	4	40.0
MDR S. aureus	60	20	33.3
MDR Enterococcus spp.	25	8	32.0
Overall MDR	385	160	41.6
MRSA	60	18	30.0
VRE	25	2	8.0
Meropenem non-susceptible E. coli	120	10	8.3
Meropenem non-susceptible K. pneumoniae	70	10	14.3
Meropenem non-susceptible P. aeruginosa	50	16	32.0
Meropenem non-susceptible Acinetobacter spp.	35	21	60.0

DISCUSSION

The present study provides an institution-specific description of bacterial pathogens and their antimicrobial susceptibility patterns using 18 months of routine microbiology data. The most important observations were the predominance of Gram-negative bacteria, the large contribution of urinary isolates, the leading role of E. coli and K. pneumoniae, reduced susceptibility to several commonly used cephalosporins and fluoroquinolones, and a considerable burden of MDR.

Gram-negative bacteria constituted three-fourths of all isolates in the current analysis. This observation is consistent with Indian antimicrobial-resistance surveillance, where Gram-negative organisms constitute a major proportion of clinically significant bacterial pathogens in tertiary-care institutions [13]. Similar predominance has been reported in other hospital-based investigations, emphasizing the continuing importance of Enterobacterales and non-fermenting Gram-negative bacilli in healthcare-associated infections [14-16].

Urine was the most common specimen source, accounting for 37.5% of isolates. The high representation of urinary specimens is expected in routine diagnostic microbiology because urinary tract infections are frequently investigated in both outpatient and inpatient settings. E. coli was strongly associated with this specimen category, with 90 of the 120 E. coli isolates recovered from urine. This finding is compatible with the established importance of E. coli as a major uropathogen. Studies restricted to urinary infections often report an even greater proportion of E. coli, highlighting the effect of specimen composition on organism frequency [17].

E. coli was the predominant bacterial isolate overall, representing 30.0% of all isolates. K. pneumoniae was the second most frequent organism, followed by S. aureus, P. aeruginosa, and Acinetobacter spp. The broad similarity between this distribution and other Indian tertiary-care surveillance reports indicates that these organisms remain important

contributors to the hospital bacterial burden [13-15]. However, comparisons should be interpreted in light of differences in patient population, specimen mix, healthcare exposure, and laboratory methodology.

The antimicrobial susceptibility pattern among Enterobacterales was particularly informative. E. coli showed 91.7% susceptibility to meropenem and 85.8% to amikacin, while susceptibility to ceftriaxone and ciprofloxacin was below 50%. K. pneumoniae showed a similar pattern, with meropenem susceptibility of 85.7% and amikacin susceptibility of 78.6%, compared with 40.0% for ceftriaxone and 45.7% for ciprofloxacin.

This pattern suggests that resistance to commonly used cephalosporins and fluoroquinolones is an important concern in the local bacterial population. Similar trends have been reported from Indian settings, where resistance among ESKAPE organisms has increased across multiple antimicrobial classes [15]. The comparatively greater activity of amikacin observed in the present study is also broadly consistent with findings from Indian urinary-pathogen studies [17].

Nevertheless, the relatively high susceptibility to meropenem should not be interpreted as justification for routine empirical carbapenem use. Carbapenems are important reserve agents, and increased reliance on them can promote further selection of carbapenem-resistant organisms. The value of the present susceptibility findings lies in identifying the current local pattern and encouraging culture-directed therapy whenever microbiological results are available.

The most concerning Gram-negative pattern was observed among Acinetobacter spp. Only 40.0% of Acinetobacter isolates were susceptible to meropenem, 48.6% to amikacin, 37.1% to piperacillin-tazobactam, and 28.6% to ciprofloxacin. In parallel, 60.0% were classified as MDR and 60.0% were non-susceptible to meropenem. These findings identify Acinetobacter as one of the most problematic organisms in the study population.

P. aeruginosa also demonstrated important resistance. Meropenem susceptibility was 68.0%, while 32.0% of isolates were non-susceptible to meropenem. Amikacin and piperacillin-tazobactam demonstrated comparatively better activity. Because Pseudomonas can acquire additional resistance mechanisms, selection of therapy based only on empirical assumptions can be problematic. Culture and susceptibility results are therefore particularly valuable for patients with suspected Pseudomonas infection.

The carbapenem findings among K. pneumoniae warrant continued surveillance. In the current study, meropenem non-susceptibility was 14.3%. Although this proportion was lower than that reported in some longitudinal Indian studies of urinary K. pneumoniae, geographic and institutional variation is substantial [22]. The presence of even a moderate carbapenem-non-susceptible population is clinically important because carbapenems are frequently used when other β-lactam agents are ineffective.

Among Gram-positive bacteria, S. aureus was the dominant organism and accounted for 15.0% of all isolates. Thirty percent of S. aureus isolates were classified as MRSA. This proportion represents an important clinical concern, particularly because MRSA infections can complicate treatment and infection-control procedures. However, the observed rate was lower than rates reported in some ICU-based studies, where patients are more likely to have severe disease, prolonged hospitalization, invasive devices, and previous antimicrobial exposure [18,19]. The inclusion of both inpatient and outpatient specimens in the present study may partly explain the lower MRSA proportion.

A favorable finding was the complete susceptibility of the tested S. aureus isolates to vancomycin and linezolid. These agents therefore retained activity against the isolates examined during the study period. However, preservation of susceptibility should not lead to indiscriminate use. Antimicrobial stewardship remains necessary to protect these important therapeutic options.

Enterococcus spp. represented 6.3% of all isolates. Ampicillin susceptibility was 60.0%, while high-level gentamicin susceptibility was 68.0%. Linezolid retained activity against 96.0% and vancomycin against 92.0% of isolates. Two isolates were vancomycin resistant, producing an 8.0% VRE prevalence. The observed VRE proportion is broadly comparable with published Indian data, although substantial heterogeneity exists between studies [20,21].

The overall MDR rate of 41.6% is another major finding. Acinetobacter spp. had the highest MDR prevalence at 60.0%, followed by K. pneumoniae at 48.6% and E. coli at 40.8%. These findings demonstrate that resistance is not confined to a single bacterial species or antimicrobial class. The simultaneous loss of susceptibility to several drug categories can considerably narrow treatment options.

MDR estimates from different studies cannot always be directly compared because the calculated proportion depends on the antimicrobial panel, resistance definition, specimen mix, patient population, and completeness of susceptibility testing. Nevertheless, the high MDR frequency in the current study is consistent with the broader Indian concern regarding resistant hospital pathogens [15,16].

The particularly high MDR and carbapenem non-susceptibility among Acinetobacter spp. deserves emphasis. This organism can accumulate multiple resistance mechanisms and persist in healthcare environments. The combination of

60.0% MDR and 60.0% meropenem non-susceptibility means that empirical broad-spectrum therapy may be unreliable when Acinetobacter infection is suspected. Microbiological confirmation and susceptibility-guided treatment should therefore be prioritized whenever feasible.

The findings also reinforce the importance of a locally generated cumulative antibiogram. National and international surveillance datasets are valuable for benchmarking, but antimicrobial susceptibility can vary considerably between individual institutions. The current study illustrates this principle: E. coli and K. pneumoniae showed relatively preserved carbapenem activity, while Acinetobacter and P. aeruginosa demonstrated considerably greater carbapenem non-susceptibility.

Annual analysis of non-duplicate isolates can provide an efficient mechanism for monitoring changes in susceptibility. The study therefore supports standardized collection and presentation of cumulative susceptibility data for clinical decision-making and stewardship.

Another important implication concerns antimicrobial stewardship. Reduced susceptibility to ceftriaxone and ciprofloxacin among major Enterobacterales suggests that these drugs may have limited reliability for empirical treatment of certain infections in the study setting. Conversely, the comparatively high susceptibility to amikacin and meropenem should be interpreted within the context of antimicrobial stewardship rather than as a simple hierarchy for prescribing.

The study has several strengths. It covered a complete 18-month period, included multiple clinical specimen categories, used a non-duplicate isolate approach, and evaluated both Gram-negative and Gram-positive pathogens. Susceptibility testing followed standardized CLSI procedures, and MDR classification used an internationally recognized definition.

However, several limitations should be considered. First, the retrospective single-centre design limits generalizability. Second, the dataset was derived from laboratory records and therefore lacked detailed information regarding clinical diagnosis, comorbidities, previous antimicrobial exposure, invasive devices, duration of hospitalization, and clinical outcomes. Third, inpatient and outpatient isolates were analyzed together, preventing reliable separation of community-acquired and healthcare-associated infections. Fourth, molecular resistance mechanisms were not investigated. Fifth, antimicrobial panels were not identical for every organism, resulting in variable denominators for individual drug-organism combinations. Finally, the number of isolates of some organisms was relatively small and therefore species-specific percentages should be interpreted cautiously.

Despite these limitations, the study provides useful local evidence of the current bacterial and resistance profile in the participating tertiary-care hospital. The results support continued microbiological surveillance, periodic institutional antibiogram preparation, infection-prevention measures, diagnostic stewardship, and rational antimicrobial prescribing.

Clinical and Public Health Implications

The predominance of Gram-negative organisms indicates that empirical treatment protocols should take local Gram-negative susceptibility into account.

The low susceptibility of E. coli and K. pneumoniae to ceftriaxone and ciprofloxacin suggests that empirical reliance on these agents should be carefully reviewed according to infection site and clinical circumstances.

Acinetobacter spp. represents a particularly important target for infection-prevention and stewardship activities because of the combination of high MDR prevalence and high carbapenem non-susceptibility.

The presence of MRSA and VRE confirms the need for continued surveillance of resistant Gram-positive organisms.

Annual institution-specific antibiograms should be considered an important component of antimicrobial stewardship, supporting empirical prescribing while allowing clinicians and microbiologists to recognize changes in local resistance patterns over time.

CONCLUSION

This retrospective laboratory-based study demonstrated a clear predominance of Gram-negative bacterial pathogens among clinical isolates recovered in a tertiary-care hospital. E. coli was the most frequently isolated organism, followed by K. pneumoniae, S. aureus, P. aeruginosa, and Acinetobacter spp. Urine was the leading specimen source.

Among Gram-negative organisms, meropenem and amikacin demonstrated comparatively greater activity against E. coli and K. pneumoniae, whereas susceptibility to ceftriaxone and ciprofloxacin was substantially lower. Acinetobacter spp. exhibited the most concerning resistance profile, with high MDR prevalence and marked meropenem non-susceptibility. Among Gram-positive isolates, MRSA accounted for 30.0% of S. aureus and VRE for 8.0% of Enterococcus spp.

Overall, 41.6% of isolates eligible for MDR assessment were multidrug resistant. These findings emphasize the continuing burden of antimicrobial resistance in the tertiary-care setting. Routine laboratory surveillance, standardized susceptibility testing, annual institutional antibiograms, appropriate infection-prevention practices, antimicrobial stewardship, and culture-directed therapy should be integrated into hospital infection-management strategies.

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Data availability: The study was based on retrospective laboratory records. No individual-level patient-identifying information was included in the analytical presentation.

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