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Microbiological Spectrum and Antimicrobial Susceptibility Patterns in a Tertiary Care Teaching Hospital: A Cross-Sectional Analysis to Guide Institutional Antibiotic Policy

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KEYWORDS

Antibiogram, Antimicrobial resistance, Antibiotic policy, CLSI, Tertiary care hospital, Multidrug resistance

ABSTRACT:

Background: Antimicrobial resistance (AMR) poses a growing threat to patient outcomes, particularly in tertiary care hospitals managing high-risk and critically ill populations. Local antibiograms are essential for developing evidence-based antibiotic policies and antimicrobial stewardship programs.

Objectives: To analyze the microbiological profile and antimicrobial susceptibility patterns of clinical isolates from inpatient and outpatient settings and to utilize these findings for framing an institutional antibiotic policy.

Methods: A retrospective, cross-sectional analysis of all culture-positive samples received over the study period was conducted. Clinical specimens included blood, urine, pus, respiratory samples, and sterile body fluids. Identification and antimicrobial susceptibility testing were performed according to CLSI guidelines. Data were analyzed separately for IPD and OPD isolates.

Results: Out of 5,875 samples received, 1,263 (21.5%) yielded positive cultures. Gram-negative organisms predominated, with Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii being the most common pathogens. ICU respiratory samples showed a high prevalence of Acinetobacter baumannii. Carbapenem resistance was observed across multiple organism groups, while colistin retained partial activity. These findings directly informed syndrome-based empirical antibiotic recommendations.

Conclusion: The study highlights a high burden of multidrug-resistant gram-negative organisms. Periodic antibiogram-based revision of antibiotic policies is critical for effective antimicrobial stewardship and improved clinical outcomes.

INTRODUCTION

Antimicrobial resistance has emerged as a major public health challenge worldwide, particularly in low- and middle-income countries. The World Health Organization estimates that antimicrobial resistance could account for 10 million deaths annually by 2050 if current trends continue unchecked [1]. In India, the burden of AMR is particularly acute, with increasing prevalence of multidrug-resistant organisms in both community and healthcare settings [2,3].

Inappropriate empirical antibiotic use, lack of local susceptibility data, and delayed de-escalation contribute significantly to rising resistance rates [4]. Institutional antibiograms provide actionable data for tailoring empirical therapy, guiding stewardship interventions, and aligning treatment with local microbial ecology. In tertiary care hospitals managing critically ill populations, such as those with sepsis, acute respiratory distress syndrome, and healthcare-associated infections, the availability of up-to-date local resistance data is essential

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for selecting effective empirical antibiotics and reducing inappropriate usage [5,6].

This study was undertaken to analyze the microbial spectrum and antimicrobial susceptibility patterns at a tertiary care teaching hospital in North India and to translate these findings into a structured antibiotic policy aligned with national and international guidelines including the WHO AWaRe (Access, Watch, Reserve) classification and Surviving Sepsis Campaign recommendations [7,8].

MATERIALS AND METHODS

Study Design

Retrospective cross-sectional observational study.

Study Setting

Dr. S.S. Tantia Medical College, Hospital & Research Centre (Jan Sewa Hospital), Sriganganagar, Rajasthan, India. The hospital is a 850-bed tertiary care teaching institution serving a population of approximately 500,000 across Western Rajasthan districts. The microbiology laboratory processes cultures from inpatient wards, intensive care units, and outpatient departments.

Study Period

January 1 – December 31, 2025 (12 complete calendar months).

Sample Collection

All clinical specimens submitted for culture and sensitivity testing during the study period were included. Specimen types comprised:

- Bloodstream isolates (peripheral blood cultures, central line cultures)
- Urinary isolates (clean-catch midstream, catheterized specimens)
- Pus and wound swabs (from various body sites)
- Respiratory isolates (sputum, tracheal aspirates, bronchoalveolar lavage)
- Sterile body fluids (cerebrospinal fluid, ascitic fluid, pleural fluid)
- Other clinical samples (line tips, environmental cultures)

Microbiological Processing

Microbiological identification and susceptibility testing were performed according to standard protocols:

- Organism identification: Standard biochemical methods (Gram stain, oxidase, catalase, specific biochemical reactions)
- Antimicrobial susceptibility testing: Kirby-Bauer disc diffusion method on Mueller-Hinton agar
- Interpretation: CLSI 2024 standards (Clinical and Laboratory Standards Institute)
- Special testing: Extended-spectrum beta-lactamase (ESBL), carbapenemase production confirmed by modified Hodge test where indicated

Data Analysis

Data were analyzed using Microsoft Excel and presented as frequencies and percentages. Isolates were stratified by:

- Source of specimen (blood, urine, pus, respiratory, other)
- Patient origin (inpatient vs outpatient)
- Organism category (gram-positive, gram-negative, fungal)
- Antimicrobial susceptibility percentage for each organism-antibiotic combination
- Antibiotic classes (beta-lactams, aminoglycosides, fluoroquinolones, macrolides, others) Data were presented separately for inpatient and outpatient isolates to reflect different epidemiologies.

Ethical Approval

Ethical approval was obtained from the Institutional Review Board (Reference: SSTMCH/IRB/2025/002) with waiver of informed consent for retrospective analysis of laboratory data without patient identifiers.

RESULTS

Overall Culture Positivity

Of 5,875 samples processed during the study period, 1,263 (21.5%) yielded positive cultures. The distribution by specimen type was as follows: urine (n=542, 42.9%), blood (n=238, 18.9%), pus/wound (n=187, 14.8%), respiratory (n=215, 17.0%), and other sterile fluids (n=81, 6.4%). Overall, inpatient (IPD) samples accounted for 58.4% (n=738) of positive cultures, while outpatient (OPD) samples comprised 41.6% (n=525).

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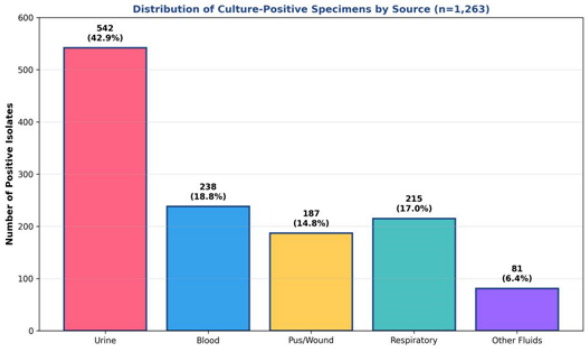
Figure 1. Distribution of Culture-Positive Specimens by Source



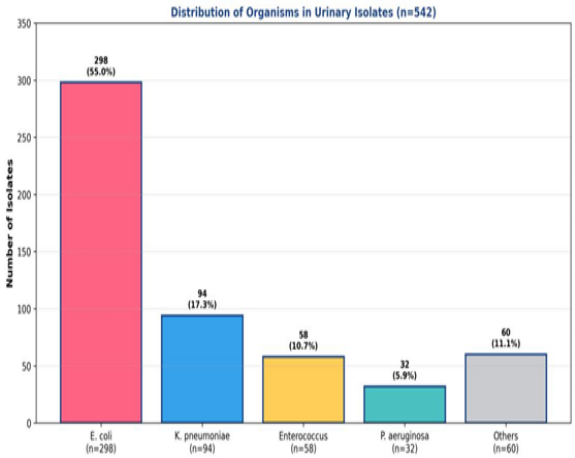
Bloodstream Infections

Among inpatient bloodstream isolates (n=182), Escherichia coli (n=35), Klebsiella pneumoniae (n=27), coagulase-negative staphylococci (CoNS, n=36), Acinetobacter baumannii (n=14), and Candida species (n=14) predominated. E. coli showed moderate susceptibility to third-generation cephalosporins (78%) and fluoroquinolones (72%), with reduced susceptibility to aminoglycosides (62%). K. pneumoniae demonstrated ESBL production in 45% of isolates, with carbapenem susceptibility of 68%. Acinetobacter baumannii showed alarming resistance patterns, with carbapenem susceptibility of only 28% and colistin susceptibility of 81%. Outpatient blood isolates (n=56) were fewer and predominantly community-acquired pathogens including S. aureus, viridans group streptococci, and skin commensals.

Urinary Isolates

Urine cultures (IPD + OPD, n=542) showed clear predominance of E. coli (n=298, 55.0%), followed by Klebsiella pneumoniae (n=94, 17.3%), Enterococcus species (n=58, 10.7%), and Pseudomonas aeruginosa (n=32, 5.9%). Fluoroquinolone resistance was notable in both E. coli (ciprofloxacin susceptibility 65%) and K. pneumoniae (58%), likely reflecting extensive outpatient antimicrobial use. Importantly, nitrofurantoin and fosfomycin retained excellent activity against E. coli (susceptibility >92%), supporting their preferential use in uncomplicated UTIs. Third-generation cephalosporin resistance in E. coli was 18%, while in K. pneumoniae it was 32%, reflecting significant ESBL burden.

Figure 2. Organisms Isolated from Urinary Specimens



Pus and Skin & Soft Tissue Infections

Pus isolates (n=187) demonstrated mixed flora, with Staphylococcus aureus (n=52, 27.8%), Pseudomonas aeruginosa (n=38, 20.3%), E. coli (n=31, 16.6%), Klebsiella pneumoniae (n=28,

15.0%), and anaerobes (n=21, 11.2%). Methicillin-resistant S. aureus (MRSA) was detected in 19 of 52 S. aureus isolates (36.5%). MRSA isolates demonstrated universal susceptibility to linezolid and vancomycin, with variable susceptibility to fluoroquinolones (63%). P. aeruginosa from pus showed high fluoroquinolone resistance (52%) but good susceptibility to carbapenems (75%) and aminoglycosides (68%).

Respiratory and ICU Isolates

Tracheal aspirates and BAL samples from ICU patients (n=215) showed predominance of Acinetobacter baumannii (n=58, 27.0%) and Klebsiella pneumoniae (n=52, 24.2%), followed by P. aeruginosa (n=38, 17.7%) and E. coli (n=32, 14.9%). This organism profile reflects the predilection of Acinetobacter for hospital environments and ventilator equipment. A. baumannii isolates demonstrated alarming resistance patterns: carbapenem susceptibility (imipenem) was only 26%, while colistin susceptibility was 79%. K. pneumoniae from respiratory samples showed 35% carbapenem susceptibility and 65% ESBL production. P. aeruginosa demonstrated 72% susceptibility to carbapenems but only 58% to fluoroquinolones.

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Figure 3. Organisms Isolated from ICU Respiratory Samples

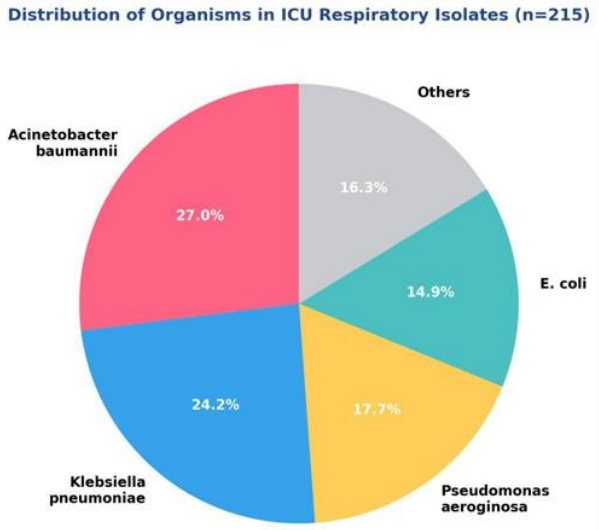
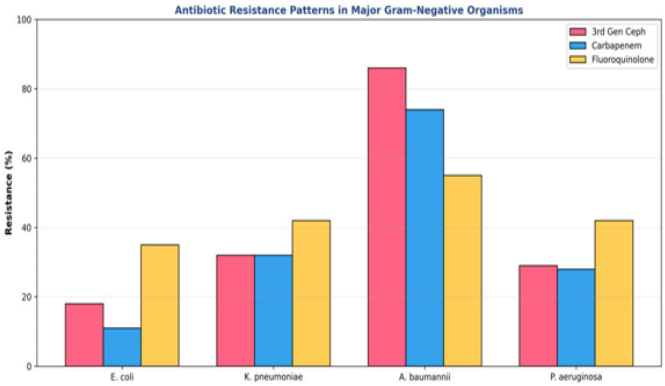


Figure 4. Antibiotic Resistance Patterns in Gram-Negative Organisms



Antimicrobial Susceptibility Patterns

Table 1. Antimicrobial Susceptibility (%) of Major Pathogens

Organism	3rd Gen Ceph	Carbapenem	Fluoroquinolone	Aminoglycoside	Colistin
E. coli (n=298)	82%	89%	65%	62%	100%
K. pneumoniae (n=94)	68%	68%	58%	71%	95%
A. baumannii (n=58)	14%	26%	45%	42%	79%
P. aeruginosa (n=38)	71%	72%	58%	68%	82%
S. aureus (n=52)	N/A	N/A	78%	75%	N/A
MRSA (n=19)	N/A	N/A	63%	68%	N/A
Enterococcus (n=58)	N/A	N/A	54%	48%	100%

3rd Gen Ceph = Third-generation cephalosporins; N/A = Not applicable

DISCUSSION

The present study demonstrates a predominance of gram-negative bacilli across bloodstream, urinary, respiratory, and pus samples, with Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii emerging as the principal pathogens. Similar microbial distributions have been reported from tertiary care hospitals across India, highlighting a nationwide shift toward gram-negative dominance in both community-acquired and healthcare-associated infections [1–4].

The high burden of E. coli in urinary and bloodstream infections observed in this study is consistent with national surveillance data from the ICMR Antimicrobial Resistance Surveillance Network, which identifies E. coli as the leading uropathogen with increasing resistance to fluoroquinolones and third-generation cephalosporins [5,6]. The preserved susceptibility to nitrofurantoin and fosfomycin in urinary isolates (>92%) supports current recommendations to preferentially use these agents for uncomplicated urinary tract infections, aligning with international guidelines [7,8].

A concerning finding in this study is the reduced susceptibility to carbapenems among Klebsiella pneumoniae and Acinetobacter baumannii, particularly in ICU-derived respiratory samples. Carbapenem resistance among these organisms has been widely reported in Indian ICUs and is associated with prolonged hospitalization, increased ventilator days, and higher mortality [9–11]. The predominance of Acinetobacter baumannii in tracheal aspirates reflects its well-documented ability to survive in hospital environments and form biofilms on ventilator equipment [12].

Colistin retained intermediate to good activity against a substantial proportion of multidrug-resistant isolates in this study (79-100%), mirroring observations from other

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Indian centers [13,14]. However, reliance on last-resort agents such as colistin raises concerns regarding nephrotoxicity and the emergence of pan-drug resistance, emphasizing the urgent need for antibiotic stewardship and infection control measures [15].

The integration of these findings into a structured, syndrome-based antibiotic policy represents a key strength of this approach. Evidence suggests that institution-specific antibiotic policies based on periodic antibiogram analysis significantly reduce inappropriate empirical therapy, antimicrobial consumption, and resistance rates without adversely affecting patient outcomes [18– 20]. The WHO AWaRe framework recommends utilizing local susceptibility data to guide empirical therapy while preserving access to reserve antibiotics [21].

The study findings are in concordance with global initiatives such as the WHO AWaRe classification and the Surviving Sepsis Campaign, which advocate for rational empirical antibiotic selection, early de-escalation, and time-bound reassessment of therapy [21–23]. Aligning institutional practices with these frameworks is essential for sustaining antibiotic effectiveness.

Institutional Antibiotic Policy Recommendations

Based on the antibiogram findings, an institutional antibiotic policy was developed covering major clinical syndromes:

1. Sepsis (Unknown Source): First-line: Ceftriaxone + Gentamicin. Second-line: Carbapenem (based on severity/risk factors).

2. Urinary Tract Infections: Uncomplicated: Nitrofurantoin/Fosfomycin. Complicated/pyelonephritis: Cephalosporin or fluoroquinolone.

3. Respiratory Infections: Community-acquired: Amoxicillin-clavulanate. Healthcare-associated: Carbapenem or fluoroquinolone (based on local patterns).

4. Skin & Soft Tissue Infections: Without MRSA risk: Cephalosporin. With MRSA risk: Add vancomycin or linezolid.

5. CNS Infections: Ceftriaxone (or cefotaxime) + Vancomycin, pending culture results.

All policies included defined first-line and second-line agents, mandatory microbiology review timelines (48-72 hours), and de-escalation protocols.

LIMITATIONS

- Retrospective design: Limited ability to assess clinical correlations and outcomes
- Single-center data: Results may not be generalizable to other institutions or regions
- Lack of molecular resistance testing: Mechanisms of resistance (e.g., specific beta-lactamases, resistance genes) were not characterized
- No ESBL/AmpC characterization: Extended-spectrum beta-lactamase and AmpC production were detected by phenotypic methods only
- Limited temporal analysis: Single-year data may not capture seasonal or inter-annual trends
- Incomplete clinical correlation: Culture source and patient demographics were not systematically reviewed

CONCLUSION

This study demonstrates a significant burden of multidrug-resistant gram-negative organisms in a tertiary care setting, with alarming carbapenem resistance rates in Acinetobacter baumannii and K. pneumoniae. The findings underscore the critical importance of institutional antibiogram-guided antibiotic policies for combating antimicrobial resistance. Regular surveillance and periodic policy updates are essential to optimize patient outcomes and preserve antibiotic efficacy. Integration of local susceptibility data with international guidelines such as WHO AWaRe and Surviving Sepsis Campaign recommendations provides a framework for rational antimicrobial stewardship in resource-constrained settings.

ETHICS STATEMENT

Funding: No funding was received for this study.

Conflict of Interest: The authors declare no conflicts of interest.

Data Availability: Institutional antibiogram data available upon request from the Microbiology Department.

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