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Original Research Article

Antimicrobial Susceptibility Patterns Across Clinical Isolates in A Tertiary Center

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Abstract:

Background: Antimicrobial resistance (AMR) has become a major global public health concern, particularly in tertiary care hospitals where extensive antibiotic use and invasive procedures promote the emergence of multidrug-resistant organisms. Continuous surveillance of antimicrobial susceptibility patterns is essential for guiding empirical therapy, improving antimicrobial stewardship, and preventing the spread of resistant pathogens.

Methods: A prospective observational study was conducted in the Department of Microbiology at Government Medical College, Quthbullapur, Medchal–Malkajgiri, from November 2025 to February 2026. Clinically significant bacterial isolates obtained from various clinical specimens including blood, pus, respiratory samples, urine, and genital specimens were included. Bacterial identification was performed using standard microbiological techniques. Antimicrobial susceptibility testing was carried out by the Kirby–Bauer disc diffusion method according to CLSI guidelines. Resistance mechanisms such as ESBL, carbapenemase production, methicillin resistance, and vancomycin resistance were identified using phenotypic methods.

Results: Gram-negative organisms including *Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa* predominated among isolates. High resistance rates were observed for beta-lactams (72%), aminoglycosides (68%), and carbapenems (65%). *Acinetobacter* species showed the highest resistance prevalence (75%). Among Gram-positive bacteria, methicillin-resistant *Staphylococcus aureus* and vancomycin-resistant *Enterococcus* were notable. Colistin and linezolid retained comparatively better activity against multidrug-resistant isolates.

Conclusion: The study highlights a high prevalence of multidrug-resistant pathogens in a tertiary care setting. Regular surveillance of antimicrobial susceptibility patterns and implementation of effective antimicrobial stewardship programs are crucial to optimize treatment and control the spread of resistant organisms.

Keywords: Antimicrobial Resistance, Antibiogram, Multidrug-Resistant Organisms, Carbapenem Resistance, Tertiary Care Hospital.

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Introduction

Antimicrobial resistance (AMR) is eroding the effectiveness of empiric therapy and is now a routine challenge for tertiary-care hospitals where antibiotic exposure, invasive devices, and complex case-mix drive selection of multidrug-resistant pathogens [1]. Facility-level cumulative antimicrobial susceptibility data (antibiograms) transform individual isolate results into actionable guidance for initial prescribing, stewardship interventions, and monitoring of emerging resistance threats [2]. The CLSI M39 framework emphasizes standardized annual reporting, de-duplication, and adequate isolate numbers to improve reliability and comparability, yet real-world antibiograms still show substantial variability in content and presentation, which can limit interpretation at the bedside [3]. Recent tertiary-center reports continue to demonstrate high burdens of ESBL-producing Enterobacterales, MRSA, and other resistant phenotypes, underlining the need for locally generated, specimen- and unit-relevant susceptibility profiles [4]. This study aimed to describe the antimicrobial susceptibility patterns of major bacterial clinical isolates recovered in our tertiary care center and to develop a local

antibiogram that supports empirical therapy and strengthens antimicrobial stewardship policies.

Methods

This prospective observational study was conducted in the Department of Microbiology at Government Medical College, Quthbullapur, Medchal–Malkajgiri, from November 2025 to February 2026. The study included all clinically significant bacterial isolates obtained from patients attending outpatient departments, admitted to medical and surgical wards, and intensive care units during the study period. Duplicate isolates from the same patient with identical antibiograms were excluded to avoid overrepresentation. Demographic details, clinical diagnosis, hospital location (OPD/ward/ICU), and specimen type were recorded in a structured data collection form. Specimens such as blood, urine, pus, sputum, body fluids, and other relevant clinical samples were processed as per standard microbiological protocols. Ethical approval was obtained from the Institutional Ethics Committee prior to commencement of the study.

All specimens were cultured on appropriate media including blood agar, MacConkey agar, and chocolate agar where indicated, and incubated under recommended conditions. Bacterial identification was performed using standard biochemical tests and automated identification systems where available. Antimicrobial susceptibility testing (AST) was carried out using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines 2025. For fastidious organisms, recommended modifications were followed. Zone diameters were measured and interpreted as susceptible, intermediate, or resistant according to CLSI breakpoints. Quality control was ensured using standard ATCC control strains such as Escherichia coli ATCC 25922, Staphylococcus aureus ATCC 25923, and Pseudomonas aeruginosa ATCC 27853. Detection of special resistance mechanisms including extended-spectrum beta-lactamase (ESBL), methicillin resistance in Staphylococcus aureus (MRSA), carbapenem resistance, and inducible clindamycin resistance (D-test) was performed using phenotypic confirmatory methods as per standard guidelines.

Data were entered into Microsoft Excel and analyzed using SPSS version 22. Descriptive statistics were used to summarize the frequency of isolates, distribution across clinical areas, specimen-wise prevalence, and antimicrobial susceptibility patterns. Resistance percentages were calculated for each organism–antibiotic combination. Categorical variables were expressed as proportions and percentages, while continuous variables were summarized using mean and standard deviation where applicable. Comparative analysis of susceptibility patterns between ICU and non-ICU isolates and between Gram-positive and Gram-negative organisms was performed using the chi-square test or Fisher's exact test as appropriate. A p value of <0.05 was considered statistically significant. A cumulative antibiogram was prepared at the end of the study period including only the first isolate per patient, and antibiotics were reported when at least 30 isolates of a species were available to ensure statistical reliability. The findings were interpreted to identify prevalent resistance trends and to support institutional antimicrobial stewardship planning.

Results

A total of clinically significant bacterial isolates recovered during the study period demonstrated a high burden of multidrug resistance across both Gram-negative and Gram-positive organisms (Table 1). Among Gram-negative bacilli, Klebsiella pneumoniae, Escherichia coli, Acinetobacter baumannii, and Pseudomonas aeruginosa were predominant and were most frequently isolated from blood and pus specimens (Table 3). Carbapenemase production was commonly observed in Enterobacterales and non-fermenters, while ESBL and AmpC mechanisms were widely detected in K. pneumoniae and E. coli (Table 4; Figure 1). A. baumannii exhibited the highest resistance burden, particularly to aminoglycosides and quinolones (Table 5). Among Gram-positive isolates, MRSA mediated by the mecA gene and vancomycin-resistant Enterococcus (VRE) mediated by VanA/VanB were notable contributors to resistance (Table 4; Figure 1). Overall resistance rates were highest for beta-lactams (72%), aminoglycosides (68%), and carbapenems (65%), whereas glycopeptide resistance was comparatively lower (40%) (Table 2). Susceptibility to colistin remained relatively preserved among Gram-negative isolates (65–85%), while linezolid retained good activity against MRSA (95% susceptible) and moderate activity against VRE (60% susceptible) (Table 5). Specimen-wise distribution revealed bloodstream infections as the largest category (35%), followed by wound and pus isolates (28%) (Table 3). Resistance mechanisms were most prevalent among Acinetobacter spp. (75%) and Enterobacterales (60%) (Table 4; Figure 1). These findings highlight substantial therapeutic challenges and reinforce the need for strengthened antimicrobial stewardship and infection control practices.

Table 1: Distribution of major clinical isolates and resistance mechanisms			
Organism	**Major Specimens**	**Key Resistance Mechanisms**	**Notable Resistance**
K. pneumoniae	Blood, pus	ESBL, Carbapenemase	Carbapenems, aminoglycosides
E. coli	Blood, urine, pus	AmpC, Carbapenemase	Carbapenems, trimethoprim
A. baumannii	Blood, respiratory	Carbapenemase	Aminoglycosides, quinolones
P. aeruginosa	Pus, respiratory	Carbapenemase, impermeability	Cephalosporins, aminoglycosides
MRSA	Blood, pus	mecA	Beta-lactams
Enterococcus spp.	Blood, urine	HLAR, VanA/B	Vancomycin, gentamicin

Table 2: Resistance rates as per the antibiotic family	
Antibiotic Family	**Resistance Rate (%)**
Beta-lactams	72
Aminoglycosides	68
Carbapenems	65
Sulfonamides	60
Quinolones	55
Tetracyclines	48
Glycopeptides	40

Table 3: Specimen wise distribution of the pathogens		
Specimen	**Major Organisms**	**%**
Blood	K. pneumoniae, E. coli, A. baumannii, MRSA	35
Pus/Wound	P. aeruginosa, MRSA, Enterococcus	28
Respiratory	A. baumannii, P. aeruginosa	20
Urine	E. coli, K. pneumoniae	10
Genital/Semen	E. coli, MRSA	7

Table 4: Resistance mechanisms by organism group		
Organism Group	**Key Mechanisms**	**Prevalence (%)**
Enterobacterales	ESBL, AmpC, Carbapenemase	60
Acinetobacter spp.	Carbapenemase, Aminoglycoside resistance	75
Pseudomonas spp.	Carbapenemase, Impermeability	55
Staphylococcus spp.	mecA, MLSB	40
Enterococcus spp.	HLAR, VanA/B	30

Table 5: Susceptibility profile of key pathogens (% susceptible)					
Pathogen	**Car**	**Cep**	**Flu**	**Colistin**	**Lin / Van**
K. pneumoniae	20	15	30	80	NA
E. coli	40	25	35	85	NA
A. baumannii	10	5	15	70	NA
P. aeruginosa	25	20	30	65	NA
MRSA	NA	NA	40	NA	95
VRE	NA	NA	NA	NA	60
Car= Carbapenems; Cep = Cephalosporins; Flu = Fluoroquinolones; Lin / Van = Linezolid/Vancomycin					

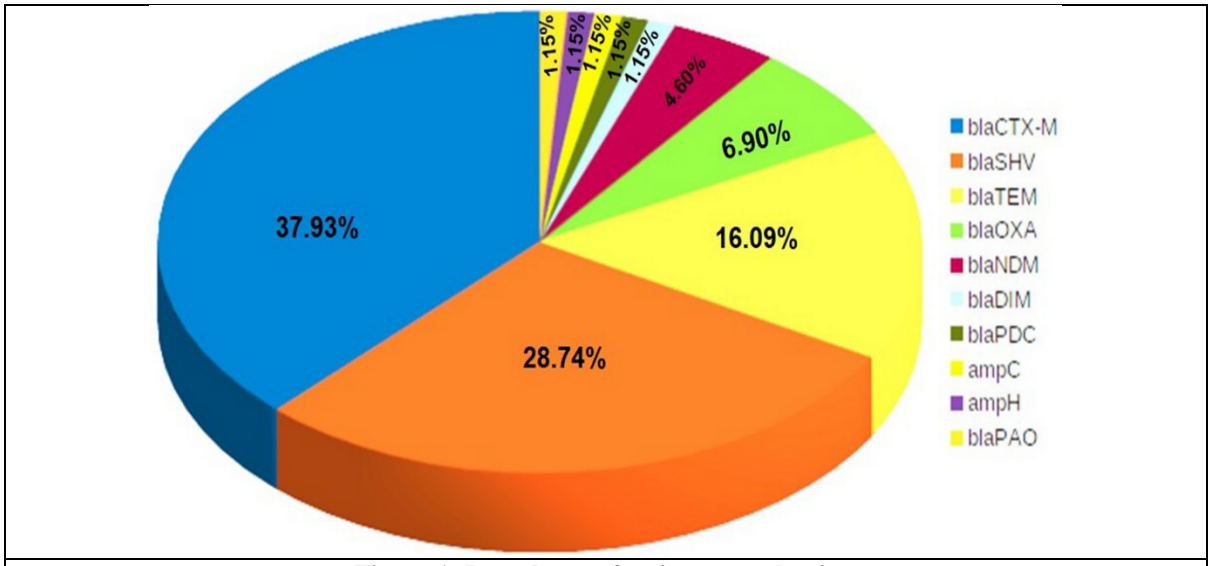

Figure 1: Prevalence of resistant mechanism

Discussion

AMR continues to emerge as one of the most pressing health challenges in modern medicine, particularly within tertiary care settings where high patient acuity, broad antibiotic use, and invasive procedures converge to select for multidrug-resistant organisms. Hospital antibiograms, which collate cumulative antimicrobial susceptibility data from clinical isolates, serve as fundamental tools to guide empiric therapy, inform stewardship policies, and monitor evolving resistance trends. Regular surveillance of pathogen distributions and resistance patterns enables clinicians to adjust empirical treatment algorithms dynamically, reducing treatment failures and adverse outcomes [5]. Reviews of AMR patterns consistently show a predominance of Gram-negative bacilli in clinical cultures, with Enterobacterales and non-fermenters exhibiting especially high levels of resistance due to accelerated acquisition of ESBL, AmpC β-lactamase, and carbapenemase genes [6]. The World Health Organization's recent surveillance data highlight that globally, more than 40 % of monitored pathogen-drug combinations showed rising resistance, and one in six documented infections in hospitals were resistant to treatment in 2023 [7].

In the present study, high proportions of multidrug-resistant Klebsiella pneumoniae, Escherichia coli, Acinetobacter baumannii, and Pseudomonas aeruginosa were observed among Gram-negative isolates. These pathogens are recognized as key causes of nosocomial sepsis, urinary tract, wound, and respiratory infections and are frequently reported in tertiary care AMR studies due to their propensity to acquire multiple resistance determinants. Carbapenem-resistant Enterobacterales (CRE), particularly carbapenemase-producing K. pneumoniae, represent a serious clinical threat when first-line β-lactams and even carbapenems become ineffective, forcing greater reliance on last-resort agents such as polymyxins and tigecycline. Gram-positive organisms such as MRSA and VRE further complicate inpatient care, as they limit the efficacy of beta-lactams and glycopeptides that traditionally formed the backbone of therapy. The coexistence of these resistant phenotypes in a single institutional ecology underscores the ever-present challenge tertiary institutions face in balancing effective therapy with stewardship.

Resistance rates in this study were notably high for broad antibiotic families including beta-lactams, aminoglycosides, and carbapenems (Table 2), consistent with findings from other tertiary care settings where resistance rates often exceed 50 % across commonly used antimicrobials [8]. Such high resistance percentages complicate therapeutic choices and may promote greater use of last-resort drugs like colistin, which itself carries significant toxicity and requires careful susceptibility confirmation [9]. The predominance of ESBL-producing Enterobacterales and carbapenemase activity in non-fermenters is consistent with global resistance trends that threaten to outpace antibiotic development pipelines, as drug discovery has lagged significantly behind the rapid evolution of resistance mechanisms [10]. Indeed, multidrug-resistant organisms are frequently defined as those resistant to at least three major antibiotic classes, and surveillance studies highlight rising proportions of MDR, extensively drug-resistant (XDR), and even pan-drug-resistant (PDR) strains in both community and hospital environments [10].

The clinical impact of these resistance patterns extends beyond therapy selection to influence patient outcomes, healthcare costs, and infection control practices. Patients infected with MDR pathogens typically have longer hospital stays,

greater likelihood of ICU admission, increased antimicrobial expenditures, and higher mortality rates compared with infections caused by susceptible strains [5]. These adverse outcomes are compounded when empirical therapy fails due to unrecognized resistance, leading to delayed effective treatment. Local surveillance data, such as generated in this and similar studies, allow hospitals to tailor empirical therapy guidelines to reflect prevalent pathogens and their susceptibility profiles rather than relying on outdated or external data that may not align with current institutional resistance ecology [6]. In regions with resource constraints, including many parts of India and LMIC settings, the lack of regular, high-quality susceptibility data further exacerbates misuse of broad-spectrum antibiotics, fueling resistance cycles that hinder long-term control [6, 11].

Instead, integrating antibiogram data with antimicrobial stewardship interventions can significantly diminish inappropriate antibiotic prescribing. Stewardship efforts that incorporate audit-and-feedback, guideline development, restriction policies, and clinician education have been shown to reduce unnecessary broad-spectrum antibiotic use, lower resistance rates over time, and improve patient outcomes across diverse geographic settings [10]. In particular, steady surveillance enables stratification of resistance patterns by location, specimen type, and patient cohort, enabling focused strategies that reduce selection pressure on critical antibiotics. For example, persistent high resistance to quinolones and aminoglycosides as seen here warrants protocols that minimize empirical use of these classes unless pathogen-specific data support their effectiveness [8, 12]. Meanwhile, enhanced infection control measures such as hand hygiene, environmental cleaning, and isolation precautions remain foundational to limiting transmission of resistant organisms within the hospital.

Looking ahead, the global burden of AMR is expected to continue rising unless multifaceted efforts are intensified across surveillance, stewardship, research, and policy domains. WHO estimates project that without substantial intervention, deaths attributable to AMR could eclipse 10 million per year by 2050, disproportionately affecting low- and middle-income regions with limited diagnostic capacity and antibiotic regulation [13]. Expansion of rapid diagnostics, broader access to susceptibility testing, newer antimicrobial agents, and enhanced AMR surveillance networks are crucial to counter this trend. At the institutional level, tertiary centers must embed routine antibiogram preparation within laboratory workflows and leverage this data to drive stewardship and clinician education. In addition, molecular diagnostics that pinpoint resistance genes and mechanisms could guide more precise therapy and limit empirical antibiotic exposure that accelerates resistance evolution. Comprehensive databases like the Comprehensive Antibiotic Resistance Database offer valuable resources for tracking resistance genes and informing both clinical and research agendas.

In conclusion, antimicrobial susceptibility patterns at tertiary institutions reflect a challenging landscape dominated by multidrug-resistant Gram-negative and Gram-positive pathogens. These patterns, shaped by local antimicrobial use, patient population, and infection control practices, demand dynamic surveillance coupled with robust stewardship interventions to optimize clinical outcomes. The high resistance burden observed across major antibiotic classes emphasizes the imperative for tailored empirical therapies grounded in up-to-date antibiogram data. Continual surveillance and stewardship are central to curbing the AMR threat, and their integration into routine clinical practice offers the greatest potential to sustain antibiotic utility for future generations.

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