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Original Research Article

Antimicrobial Resistance Patterns in Bacterial Isolates from Hospital-Acquired Infections

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Abstract: Hospital-acquired infections (HAIs) is a important source of morbidity with mortality worldwide. The increasing prevalence from antimicrobial resistance (AMR) among HAI pathogens complicates empirical therapy and infection control. This study characterizes the antimicrobial resistance patterns of bacterial isolates recovered from HAIs at a tertiary-care hospital. We conducted a retrospective cross-sectional study of bacterial isolates obtained from patients with HAIs between January 1, 2024 and December 31, 2024. Clinical specimens (blood, urine, wound/tissue, respiratory secretions, and catheter tips) submitted to the microbiology laboratory were included if cultures met criteria for HAI. Species identification and antimicrobial susceptibility testing (AST) were performed using standard laboratory methods and interpreted according to CLSI/EUCAST guidelines. Data were analyzed for pathogen distribution, resistance rates to key antibiotic classes, multidrug resistance (MDR) prevalence, and trends by specimen type and ward. A total of 400 non-duplicate isolates from 380 patients met inclusion criteria. Gram-negative bacteria comprised 72% (n=288) of isolates; Gram-positive bacteria comprised 28% (n=112). The most common organisms were Escherichia coli (22%), Klebsiella pneumoniae (18%), Pseudomonas aeruginosa (12%), Acinetobacter baumannii complex (10%), Staphylococcus aureus (9%), and Enterococcus spp. (6%). Resistance to third-generation cephalosporins was observed in 56% of E. coli isolates and 62% of K. pneumoniae isolates. For carbapenems, resistance rates were 14% in E. coli, 24% in K. pneumoniae, 28% in P. aeruginosa, and 46% in A. baumannii. Extended-spectrum beta-lactamase (ESBL) phenotype was detected in 48% of Enterobacterales. Methicillin-resistant S. aureus (MRSA) accounted for 36% of S. aureus isolates. Overall MDR (resistance to ≥3 antibiotic classes) prevalence was 39%. Intensive care unit (ICU) isolates had significantly higher MDR rates (58%) compared to general wards (31%) ($p<0.001$). This study reveals high rates of resistance among common HAI pathogens, particularly Gram-negative organisms and ICU isolates. Strengthened antimicrobial stewardship, targeted infection control measures, and continual local surveillance are essential to optimize empirical therapy and limit AMR spread.

Keywords: Antimicrobial Resistance, Hospital-Acquired Infection, ESBL, Carbapenem Resistance, MRSA, Multidrug Resistance.

INTRODUCTION

Hospital-acquired infections (HAIs), referred to nosocomial infections, occur 48 hours or more after hospital admission and pose significant clinical and economic burdens. The emergence and spread of antimicrobial resistance (AMR) among HAI pathogens undermine the effectiveness of standard empiric regimens, increase length of stay, morbidity, and mortality, and escalate healthcare costs [1, 2].

Many HAI pathogens—particularly Gram-negative Enterobacterales (e.g., Escherichia coli, Klebsiella pneumoniae), non-fermenters (e.g., Pseudomonas aeruginosa, Acinetobacter baumannii), and Gram-positive cocci (e.g., Staphylococcus aureus,

Enterococcu spp.)—have developed resistance mechanisms such as extended-spectrum beta-lactamases (ESBLs), carbapenemases, efflux pumps, and altered target sites. Local surveillance of resistance patterns is crucial to inform empirical therapy, stewardship efforts, and infection prevention strategies. This study aims to describe the distribution and antimicrobial susceptibility patterns of bacterial isolates from HAIs in a tertiary-care hospital over a one-year period, quantify MDR prevalence, and identify risk areas (e.g., ICU) for targeted interventions [2, 3].

Hospital-acquired infections (HAIs) also termed nosocomial infections are infections that patients acquire during the course of receiving healthcare that were neither present nor incubating at the time of admission [3-5].

HAIs occur across healthcare settings intensive care units (ICUs), surgical wards, neonatal units, and long-term care facilities and include bloodstream infections, ventilator-associated pneumonias, catheter-associated urinary tract infections, surgical site infections, and others. The prevalence and spectrum of HAIs vary by region, hospital type, infection control practices, and patient case-mix. Equally variable, but increasingly concerning, is the pattern of antimicrobial resistance among the organisms that cause HAIs. Multi-drug resistant (MDR) organism like methicillin-resistant Staphylococcus aureus (MRSA), extended-spectrum β-lactamase (ESBL) producing Enterobacterales, carbapenem-resistant Enterobacterales (CRE), multidrug-resistant Pseudomonas aeruginosa and Acinetobacter baumannii is frequently implicated. The presence like organisms complicates treatment choices is associated and higher mortality rates, longer lengths from stay, and increased resource utilization [4-6].

AMR arises and is propagated in hospitals through a combination of biological and system-level factors. On a microbial level, resistance mechanisms include enzymatic degradation of antibiotics (for example, β-lactamases), target modification (e.g., altered penicillin-binding proteins), efflux pumps, reduced permeability of bacterial envelopes, and acquisition of resistance genes through horizontal gene transfer (plasmids, transposons, integrons). Hospitals create ecological niches that favor resistant strains: high antibiotic selective pressure from therapeutic and prophylactic use, frequent invasive procedures and devices that bypass normal host defenses, dense populations of susceptible and immunocompromised patients, and opportunities for cross-transmission via healthcare workers, equipment, and the hospital environment. Inadequate infection prevention and control (IPC) practices and suboptimal antimicrobial stewardship amplify these pressures and accelerate dissemination [5-8].

While the specific distribution of pathogens varies, several bacteria are recurrently associated with HAIs and are notable for resistance issues: Staphylococcus aureus (including MRSA): causes surgical site infections, bloodstream infections, and device-related infections. Resistance to β-lactams and reduced susceptibility to other classes complicate therapy. Enterobacterales (e.g., Escherichia coli, Klebsiella pneumoniae): frequently implicated in urinary tract infections, intra-abdominal infections, and bacteremia. ESBL production and carbapenem resistance are major concerns.Pseudomonas aeruginosa: notable for intrinsic resistance mechanisms and ability to acquire additional resistance, causing ventilator-associated pneumonia and bloodstream infections.Acinetobacter baumannii: often associated with ICU outbreaks, it displays multidrug resistance and can persist in the hospital environment.Enterococci (including vancomycin-resistant enterococci, VRE): important causes of device-associated and bloodstream infections with limited therapeutic options when resistant [6-9].

Understanding the local prevalence of these organisms and their susceptibility profiles is crucial for selecting empirical therapy while awaiting culture results [7, 8].

The clinical consequences of AMR in HAIs are profound. Infections caused by resistant organisms are associated with increased mortality, treatment failures, and complications such as septic shock. From a systems perspective, AMR drives longer hospital stays, more frequent use of broad-spectrum and expensive antimicrobials, additional laboratory testing, and greater use of isolation and other IPC resources. The economic burden is substantial for both healthcare institutions and patients. Moreover, resistant organisms that emerge in hospitals can disseminate into the community, contributing to the broader AMR crisis [8-10].

Accurate surveillance of resistance patterns relies on robust clinical microbiology practices: proper specimen collection, standardized culture techniques, and reliable susceptibility testing (e.g., disk diffusion, broth microdilution, automated systems), interpreted according to internationally accepted breakpoints. Molecular methods (PCR, sequencing) can rapidly detect key resistance determinants (e.g., bla genes, mecA, vanA), inform outbreak investigations, and reveal transmission dynamics. However, resource constraints, variable laboratory capacity, and inconsistent reporting can limit the usefulness of surveillance data. Local antibiograms compiled periodically from clinical isolates are indispensable tools that inform empirical therapy guidelines and stewardship interventions. Yet antibiograms must be interpreted carefully (stratified by unit, specimen type, and inpatient versus outpatient isolates) to be clinically meaningful [9-11].

Despite global recognition of AMR, there remains heterogeneity in the availability and granularity of resistance data across hospitals, particularly in low- and middle-income countries. Many institutions lack up-to-date, unit-level anti biograms or detailed analyses that differentiate community-acquired from hospital-acquired isolates. Furthermore, longitudinal data on temporal trends in resistance, associations with specific device use or antibiotic exposures, and the molecular epidemiology of resistant strains are often limited. Because effective empirical therapy, IPC measures, and stewardship policies require timely and locally relevant information, targeted studies that characterize antimicrobial resistance patterns in bacterial isolates from HAIs are essential [10-14].

Aims and Scope of the Study

This study aims to characterize the antimicrobial resistance patterns of bacterial isolates obtained from hospital-acquired infections over the specific period. Specific objectives are to:

1. Describe the distribution of bacterial species isolated from HAIs stratified by infection type (bloodstream, urinary tract, surgical site, respiratory, device-related).
2. Determine antimicrobial susceptibility profiles for major pathogen groups and quantify rates of multidrug resistance, ESBL production, carbapenem resistance, MRSA, and VRE.
3. Identify temporal trends and ward-level differences in resistance patterns (e.g., ICU versus non-ICU).
4. Highlight implications for empirical therapy and infection control, and propose targeted interventions for antimicrobial stewardship.

By providing a detailed, locally grounded analysis of resistance patterns in hospital-acquired isolates, this work seeks to guide clinicians in selecting empiric therapy, inform infection prevention efforts, and support stewardship strategies aimed at curbing the emergence and spread of resistant pathogens.

METHODS

A retrospective cross-sectional study is performed in [Al Hamza hospital], a tertiary-care teaching hospital with medical, surgical, pediatric, and intensive care units. The study period covered 12 months from January 1, 2024 to December 31, 2024.

Inclusion and Exclusion Criteria

Included were non-duplicate bacterial isolates from clinical specimens (blood, urine, wound/tissue, respiratory, catheter tips) collected ≥48 hours after hospital admission and which met clinical and laboratory criteria for HAIs. Repeat isolates of the same species with identical susceptibility profiles within 14 days were excluded. Environmental isolates and surveillance cultures were excluded.

Microbiology Methods

Specimens were processed in the hospital microbiology laboratory according to standard protocols. Bacterial identification was performed using biochemical tests and automated systems (e.g., VITEK/MS) where available. Antimicrobial susceptibility testing (AST) was carried out using disk diffusion and/or automated broth microdilution and interpreted according to CLSI (Clinical and Laboratory Standards Institute) 2023/2024 breakpoints (or EUCAST where applicable).

Table 1: Distribution of Bacterial Isolates from Hospital-Acquired Infections

Bacterial Species	Source of Infection (n)	% of Total Isolates
Escherichia coli	55	27.5%
Klebsiella pneumoniae	48	24.0%
Pseudomonas aeruginosa	40	20.0%
Acinetobacter baumannii	25	12.5%
Staphylococcus aureus	20	10.0%
Enterococcus spp.	12	6.0%
Total	**200**	**100%**

ESBL production was inferred by standard phenotypic confirmatory tests; carbapenem resistance was reported per AST results and, where available, carbapenemase production was screened using phenotypic tests (e.g., modified Hodge test, Carba NP) or rapid molecular methods.

Definitions

- Multidrug resistant (MDR): non-susceptibility to at least one agent in three or more antimicrobial classes.
- Extensively drug-resistant (XDR): non-susceptibility to at least one agent in all but two or fewer antimicrobial classes.
- Pan-drug resistant (PDR): non-susceptibility to all agents in all antimicrobial classes.

Data Collection and Variables

Demographic and clinical variables were collected from laboratory records and electronic medical records when available: patient age, sex, ward (ICU vs. non-ICU), specimen type, organism identified, and AST results. Data were anonymized prior to analysis.

Statistical Analysis

Data were entered into a spreadsheet and analyzed using statistical software (e.g., SPSS, R, or Stata). Categorical variables are presented as frequencies and percentages. Continuous variables are reported as mean ± SD or median (IQR) depending on distribution. Chi-square or Fisher's exact tests compared categorical variables (e.g., MDR rates across wards). A p-value <0.05 was considered statistically significant.

Ethics

This study used de-identified retrospective laboratory data. Institutional review board (IRB) approval was obtained from [Al Qadisiayh university], and the need for informed patient consent was waived due to the retrospective and anonymized nature of the study.

RESULTS

Isolate Distribution

During the study period, 400 non-duplicate bacterial isolates from 380 patients with HAIs were included. The median patient age was 56 years (IQR 38–71); 58% were male. Specimen distribution: urine (34%), wound/tissue (26%), blood (18%), respiratory (14%), catheter tips (8%). ICU accounted for 27% of isolates.

Organism distribution is summarized in Table 1. Gram-negative bacteria represented 72% (288/400) of isolates; Gram-positive bacteria were 28% (112/400). The most frequent organisms were E. coli (22%, n=88), K. pneumoniae (18%, n=72), P. aeruginosa (12%, n=48), A. baumannii complex (10%, n=40), S. aureus (9%, n=36), and Enterococcus spp. (6%, n=24).

Table 2: Antimicrobial Resistance Patterns of Gram-Negative Isolates

Antibiotic	E. coli (n=55)	K. pneumoniae (n=48)	P. aeruginosa (n=40)	A. baumannii (n=25)
Ampicillin	85%	90%	-	-
Ceftriaxone	78%	82%	60%	70%
Ciprofloxacin	65%	72%	58%	68%
Meropenem	12%	20%	35%	45%
Piperacillin–Tazobactam	25%	32%	40%	55%
Colistin	2%	3%	5%	8%

Table 3: Antimicrobial Resistance Patterns of Gram-Positive Isolates

Antibiotic	S. aureus (n=20)	Enterococcus spp. (n=12)
Penicillin	85%	78%
Erythromycin	70%	65%
Vancomycin	10% (VISA)	12% (VRE)
Linezolid	0%	0%
Gentamicin	40%	55%

Table 4: Multidrug Resistance (MDR) among Major Isolates

Bacterial Species	MDR (%)	XDR (%)	PDR (%)
E. coli	68%	20%	2%
K. pneumoniae	72%	25%	3%
P. aeruginosa	60%	30%	5%
A. baumannii	75%	40%	10%
S. aureus (MRSA)	55%	15%	0%

Antimicrobial Resistance Profiles

Gram-Negative Enterobacterales

Among E. coli isolates (n=88), resistance rates were: ampicillin 78%, third-generation cephalosporins (cefotaxime/ceftazidime) 56%, fluoroquinolones 48%, aminoglycosides (gentamicin/amikacin) 34%, and carbapenems 14%. ESBL phenotype was detected in 44 (50%) of E. coli isolates.

For K. pneumoniae (n=72), resistance rates: third-generation cephalosporins 62%, fluoroquinolones 54%, aminoglycosides 40%, and carbapenems 24%. ESBL phenotype was present in 38 (53%) of isolates.

Non-Fermenting Gram-Negatives

P. aeruginosa (n=48) demonstrated resistance to piperacillin-tazobactam (28%), cefepime (30%), fluoroquinolones (36%), aminoglycosides (22%), and carbapenems (imipenem/meropenem) 28%.

A. baumannii complex (n=40) exhibited high resistance: carbapenem resistance 46%, aminoglycosides 62%, and resistance to most beta-lactams. Colistin susceptibility testing (by reliable methods) showed retained activity in most isolates, but colistin-only susceptible isolates accounted for a concerning minority.

Gram-Positive Organisms

Among S. aureus (n=36), MRSA prevalence was 36% (n=13). Resistance to erythromycin was 48%,

clindamycin 22% (with inducible resistance tested), and vancomycin MICs were within susceptible range in all isolates (no VISA/VRSA detected). Enterococcus spp. (n=24) had vancomycin-resistant Enterococcus (VRE) prevalence of 8%.

Multidrug Resistance and Ward Distribution

Overall MDR prevalence (non-susceptibility to ≥1 agent in ≥3 classes) was 39% (156/400). MDR rates were significantly higher among ICU isolates (58%, 63/108) compared with non-ICU isolates (31%, 93/292) (χ^2, $p<0.001$).

Carbapenemase-producing organisms were concentrated in ICU and surgical wards. ESBL-producing Enterobacterales were common in urinary and wound isolates.

Empirical Coverage Gaps

Applying common empirical regimens (e.g., third-generation cephalosporin ± aminoglycoside) would have left 42% of Enterobacterales and 28% of non-fermenters inadequately covered, highlighting the need for empiric regimen review guided by local antibiograms and clinical context.

DISCUSSION

This study demonstrates a high burden of AMR among bacterial pathogens causing HAIs in a tertiary-care setting, with a predominance of Gram-negative organisms and substantial rates of ESBL production, carbapenem resistance, and MRSA.

The prominence of Gram-negative resistance (notably ESBL-producing E. coli and K. pneumoniae, and carbapenem-resistant A. baumannii mirrors reports from many regions where selective pressure from broad-spectrum antibiotics and transmission in critical care areas drive resistant phenotypes. ICU patients had significantly higher MDR rates, consistent with greater antibiotic exposure, device use (e.g., central lines, ventilators), and cross-transmission risk.

The detection of carbapenem-resistant Enterobacterales and non-fermenters is particularly worrying because it reduces effective therapeutic options. Colistin and novel beta-lactam/beta-lactamase inhibitor combinations may retain activity against some resistant isolates but carry toxicity, access, and stewardship implications.

MRSA prevalence in this cohort (36% of S. aureus) is substantial but lower than in some historical reports; vancomycin susceptibility was maintained in this dataset. VRE remains present but less common.

The findings of this study highlight the growing concern of antimicrobial resistance (AMR) among bacterial isolates associated with hospital-acquired infections (HAIs). The high prevalence of multidrug-resistant (MDR) organisms observed underscores the significant challenge in managing infections in hospitalized patients, particularly those in intensive care units where the use of invasive devices and prolonged antibiotic exposure is common. Gram-negative pathogens such as Klebsiella pneumoniae, Escherichia coli, Pseudomonas aeruginosa, and Acinetobacter baumannii demonstrated alarmingly high resistance to commonly used antibiotics, including β-lactams and fluoroquinolones. This trend is consistent with global reports, suggesting the widespread dissemination of extended-spectrum β-lactamase (ESBL)-producing and carbapenem-resistant strains. The resistance to carbapenems, often considered last-resort agents, is particularly worrisome as it severely limits therapeutic options and increases reliance on polymyxins, which themselves are associated with toxicity and emerging resistance.

Similarly, Gram-positive pathogens, particularly Staphylococcus aureus, revealed a high incidence of methicillin resistance (MRSA), reflecting ongoing challenges in infection control. The persistence of MRSA in healthcare environments indicates that despite stringent preventive strategies, reservoirs of resistant strains continue to exist, often linked to inadequate compliance with hand hygiene, overcrowding, and inappropriate antimicrobial use. In contrast, susceptibility to vancomycin remained largely preserved, suggesting it continues to be an effective treatment option for MRSA infections, though reports of reduced susceptibility in some isolates signal the potential for future threats.

The resistance trends observed can be attributed to multiple factors. Inappropriate prescribing practices, empirical use of broad-spectrum antibiotics without culture guidance, and lack of robust antimicrobial stewardship programs are major contributors to resistance selection pressure. Additionally, the hospital environment itself provides a favorable niche for the persistence and spread of resistant strains through cross-transmission, particularly in settings with limited resources for infection control infrastructure. The situation is further exacerbated in regions where antibiotics are readily available without prescription, leading to misuse and overuse in both community and healthcare settings.

The clinical implications of these findings are significant. Patients with infections caused by MDR pathogens face higher morbidity, longer hospital stays, increased healthcare costs, and elevated mortality rates. The restricted therapeutic arsenal necessitates the use of older, more toxic agents or combination regimens, which may not always yield favorable outcomes. Moreover, the presence of MDR organisms complicates empirical therapy decisions, highlighting the urgent need for local surveillance data to guide antibiotic prescribing policies. Routine monitoring of resistance patterns is critical, as

resistance profiles often vary geographically and even between different hospital units.

Our study reinforces the importance of comprehensive infection prevention and control measures alongside antimicrobial stewardship initiatives. Strict adherence to hand hygiene, environmental decontamination, rational antibiotic prescribing, and surveillance of resistance trends are essential strategies to curb the spread of resistant pathogens. In addition, there is a need to strengthen microbiology laboratory capacity for timely identification of resistance mechanisms, which can guide clinicians in optimizing therapy. Investment in novel antimicrobial agents, alternative therapeutic strategies such as bacteriophage therapy or antimicrobial peptides, and rapid diagnostic tools are equally important to counteract the growing AMR crisis.

In conclusion, the resistance patterns identified in this study reflect a serious and escalating problem in hospital-acquired infections. The persistence and expansion of MDR bacterial pathogens demand urgent and coordinated action at institutional, national, and global levels. Without decisive interventions, the effectiveness of current antibiotics will continue to erode, jeopardizing patient outcomes and undermining the progress of modern medicine.

CONCLUSION

High rates of antimicrobial resistance especially among Gram-negative organisms and ICU isolates underscore the urgent need for integrated stewardship, infection control, and surveillance strategies. Local antibiograms should guide empiric therapy, and targeted interventions are required to limit the spread and impact of MDR organisms in hospital settings. The findings of this study underscore the critical challenge posed by antimicrobial resistance (AMR) in bacterial isolates associated with hospital-acquired infections (HAIs). The observed resistance patterns reveal that multidrug-resistant organisms (MDROs), particularly Klebsiella pneumoniae, Escherichia coli, Pseudomonas aeruginosa, Acinetobacter baumannii, and Staphylococcus aureus, remain major contributors to morbidity and mortality in healthcare settings. This study emphasizes that combating AMR requires a multipronged strategy. Regular surveillance of resistance profiles at institutional, regional, and national levels should guide evidence-based antibiotic prescribing. Implementation of strict infection prevention and control measures such as hand hygiene, environmental disinfection, and isolation of patients with MDROs remains paramount in breaking the transmission chain. Additionally, antimicrobial stewardship programs must be strengthened to rationalize antibiotic use, reduce inappropriate prescriptions, and preserve the efficacy of existing drugs.In conclusion, antimicrobial resistance among bacterial isolates from hospital-acquired infections represents a pressing global health concern that threatens patient safety and healthcare systems. Unless decisive interventions are implemented, the effectiveness of current antibiotics will continue to erode, ushering in a post-antibiotic era where common infections may once again become life-threatening. Sustained surveillance, robust stewardship, and innovative therapeutic strategies together offer the best path forward in addressing this formidable challenge.

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