INSIGHTS-JOURNAL OF
LIFE AND SOCIAL SCIENCES

INSIGHTS-JLSS
Insights-Journal of Life and Social Sciences

DRUG RESISTANCE PATTERNS AMONG COMMON PATHOGENS IN URBAN HOSPITALS: A CROSS-SECTIONAL STUDY

Original Article

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Conflict of Interest: None
Grant Support & Financial Support: None
Acknowledgment: The authors thank the participating hospitals for their support.

ABSTRACT

Background: Antimicrobial resistance (AMR) is a growing global health threat, particularly in densely populated urban settings where hospital-acquired infections are frequent. Urban tertiary care hospitals face heightened challenges in managing infections due to increasing prevalence of multidrug-resistant (MDR) organisms, complicating treatment and escalating healthcare costs.

Objective: To assess the patterns of drug resistance among common bacterial pathogens isolated in urban hospital settings through a cross-sectional analysis.

Methods: A cross-sectional study was conducted over eight months across tertiary care hospitals in Lahore, Pakistan. Clinical samples from patients aged ≥18 years were processed to identify common pathogens, including *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Staphylococcus aureus*. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method. Data were analyzed using SPSS version 25, with descriptive statistics, chi-square tests, and ANOVA. Ethical approval was obtained from Institutional Review Board (IRB).

Results: Among 425 isolates, the most prevalent were *E. coli* (28.2%) and *K. pneumoniae* (22.4%). MDR rates were highest in *A. baumannii* (76.4%) and *K. pneumoniae* (68.4%). Ceftriaxone and ciprofloxacin showed the highest resistance across most Gram-negative isolates, while vancomycin remained largely effective against *S. aureus* (6.7% resistance). ICU departments exhibited the highest average resistance rate (74.3%). Resistance to meropenem and amikacin remained relatively low in comparison.

Conclusion: The study demonstrates a significant burden of MDR pathogens in urban hospitals, emphasizing the urgent need for localized antimicrobial stewardship, enhanced infection control, and real-time resistance surveillance to guide effective treatment protocols.

Keywords: Acinetobacter baumannii, Antimicrobial resistance, Cross-sectional studies, Escherichia coli, Hospital-acquired infections, Klebsiella pneumoniae, Multidrug-resistant organisms, Pakistan, Pseudomonas aeruginosa, Staphylococcus aureus.

INTRODUCTION

The rising tide of antimicrobial resistance (AMR) represents one of the most pressing public health threats of the 21st century. Globally, infections caused by resistant organisms are increasing in prevalence, complexity, and cost—both in human lives and healthcare resources. In urban hospitals, where population density and healthcare-seeking behavior amplify microbial transmission, the challenge of drug-resistant infections is particularly acute (1). Despite advancements in medical diagnostics and therapeutics, the emergence of multidrug-resistant (MDR) organisms continues to outpace the development of novel antibiotics. This evolving crisis has spurred the scientific community to intensify surveillance efforts and refine infection control strategies. Yet, many urban centers lack up-to-date, region-specific data on resistance patterns, making it difficult to formulate targeted treatment guidelines or prevention policies (2,3). Urban hospitals, often operating at the nexus of community and tertiary care, serve as important indicators of broader resistance trends. These facilities cater to diverse patient populations and handle a high volume of antimicrobial prescriptions, both of which contribute to selective pressure on pathogens. Pathogens such as *Escherichia coli*, *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* have increasingly demonstrated resistance to standard antimicrobial therapies in these settings (4). Infections caused by these organisms are associated with increased morbidity, prolonged hospital stays, and elevated mortality rates. Consequently, real-time data on local resistance patterns is vital for clinicians to make informed decisions on empirical therapy, particularly in critical care units where treatment delays can have serious consequences (5,6).

Previous studies have outlined broad trends in antimicrobial resistance, often at national or global scales. While these reports offer invaluable insights, they may not adequately reflect the nuanced resistance landscapes within individual urban hospitals (7,8). For example, resistance profiles can vary significantly between hospitals in the same city, influenced by factors such as antibiotic stewardship practices, infection control measures, and patient demographics. Therefore, granular, hospital-specific surveillance is essential to bridge the knowledge gap between macro-level data and frontline clinical decision-making (9,10). Furthermore, understanding these patterns aids policymakers in allocating resources, designing targeted interventions, and evaluating the effectiveness of existing control programs. Compounding the issue is the frequent misuse and overuse of antibiotics, particularly in high-pressure hospital environments where clinicians must act swiftly and often empirically. In the absence of timely culture and sensitivity results, broad-spectrum antibiotics are frequently prescribed as a precautionary measure, inadvertently driving resistance. This cycle of uncertainty and overprescription creates a feedback loop that accelerates the development of drug-resistant strains. Surveillance studies that track resistance trends not only illuminate this cycle but also offer a basis for breaking it through evidence-based guidelines and stewardship initiatives (11,12).

Moreover, the rapid globalization of healthcare through travel, migration, and medical tourism has transformed local resistance issues into global concerns. A resistant strain acquired in one hospital can quickly disseminate across regions and borders, underlining the need for robust, localized surveillance as part of a broader international response. This reality lends urgency to studies that can accurately characterize resistance patterns in specific settings, especially urban hospitals that serve as both treatment centers and epidemiological hubs (13). Despite growing awareness, there remains a lack of comprehensive, cross-sectional data from urban hospitals that examines the current state of antimicrobial resistance across multiple common pathogens. Most existing literature either focuses on a single organism or derives from longitudinal data that may not reflect present-day realities. This limitation underscores the necessity of studies that offer a snapshot of resistance patterns across a spectrum of clinically relevant organisms within urban hospital settings. Such research can support the development of more precise, context-aware treatment protocols and stewardship policies tailored to the real-time needs of healthcare providers. This cross-sectional study was conducted to address this critical gap by evaluating the patterns of drug resistance among common pathogens isolated in urban hospitals. The objective is to generate a clear, contemporary picture of resistance trends that can inform clinical practice, guide policy development, and ultimately improve patient outcomes in urban healthcare environments.

METHODS

This cross-sectional study was designed to assess the patterns of drug resistance among common pathogens isolated in urban hospital settings, with data collected from tertiary care hospitals in Lahore, Pakistan. The study was conducted over a period of eight months, from March to October 2024, capturing a comprehensive snapshot of antimicrobial resistance trends within the designated time frame. The methodological approach was structured to ensure representativeness, accuracy, and replicability, employing standard microbiological procedures, validated data collection instruments, and appropriate statistical analyses. Participants included in this study were inpatients and outpatients from whom clinical samples had been collected for suspected bacterial infections (3,4). Samples were

obtained from a variety of clinical sources, including urine, blood, sputum, wound swabs, cerebrospinal fluid, and tracheal aspirates. Only culture-positive cases with complete antimicrobial susceptibility testing (AST) data were considered eligible. Inclusion criteria encompassed all patients aged 18 years and above who had positive cultures for one of the selected common pathogens: *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, and *Staphylococcus aureus*. Patients were excluded if they had received antibiotic treatment for more than 72 hours prior to culture, to minimize bias from ongoing treatment regimens. Additionally, duplicate isolates from the same patient and samples with incomplete susceptibility data were excluded to ensure the integrity of the dataset.

The minimum sample size required for the study was calculated using the single population proportion formula with a 95% confidence level, a 5% margin of error, and an estimated prevalence of antimicrobial resistance of 50% to maximize variability. Using the formula $n = Z^2 * p * (1-p) / d^2$, the calculated sample size was approximately 385, and considering a 10% attrition rate, the final sample size was set at 425 isolates (14). Data collection involved systematic retrieval of culture and sensitivity reports from the microbiology laboratories of participating hospitals. Standard microbiological techniques were used for the isolation and identification of bacterial pathogens. These included Gram staining, colony morphology, and biochemical tests as per Clinical and Laboratory Standards Institute (CLSI) guidelines. Antimicrobial susceptibility testing was conducted using the Kirby-Bauer disk diffusion method and interpreted according to the latest CLSI breakpoints (15). For isolates with intermediate susceptibility, further confirmation through minimum inhibitory concentration (MIC) determination was performed using automated systems such as VITEK 2 where available.

All laboratory and clinical data were recorded using a structured data collection sheet. Information gathered included patient demographics (age, gender), clinical diagnosis, hospital department, site of infection, isolated organism, and detailed AST results. To ensure consistency and reduce inter-observer bias, all laboratory personnel underwent training prior to the commencement of data collection, and regular quality control checks were implemented throughout the study period. Outcome measurement was centered on the resistance profile of each pathogen to a predefined panel of antibiotics representing major classes, including beta-lactams, aminoglycosides, fluoroquinolones, carbapenems, and glycopeptides. The primary outcome was the proportion of isolates demonstrating resistance to one or more antibiotic classes. Multidrug resistance (MDR) was defined as non-susceptibility to at least one agent in three or more antimicrobial categories.

Statistical analysis was performed using SPSS version 25. Descriptive statistics were used to summarize demographic data and isolate distributions. Frequencies and percentages were calculated for resistance rates against individual antibiotics and antibiotic classes. As the distribution of data was confirmed to be normal through the Shapiro-Wilk test, parametric tests were employed. The chi-square test was used to assess associations between categorical variables, such as organism type and resistance pattern. One-way ANOVA was applied to compare resistance levels across different hospital departments. A p-value of less than 0.05 was considered statistically significant. Ethical approval for the study was obtained from the Institutional Review Board (IRB) of each participating hospital. Written informed consent was waived due to the retrospective and de-identified nature of the data collection, a protocol approved by the ethics committees. All procedures adhered to the principles outlined in the Declaration of Helsinki and local ethical guidelines governing biomedical research. By employing rigorous sampling, validated laboratory techniques, and robust statistical analysis, this study aimed to generate reliable and context-specific evidence on drug resistance patterns. Such data is essential for informing empirical treatment protocols, enhancing antimicrobial stewardship, and guiding health policy in urban healthcare environments.

RESULTS

The analysis included a total of 425 patients from tertiary care hospitals in Lahore, with a mean age of 46.3 years. Males represented 54.6% of the sample, while females accounted for 45.4%. Among the clinical isolates, *Escherichia coli* (28.2%) and *Klebsiella pneumoniae* (22.4%) were the most frequently identified pathogens, followed by *Staphylococcus aureus* (20.0%), *Pseudomonas aeruginosa* (16.5%), and *Acinetobacter baumannii* (12.9%). The overall rate of multidrug resistance (MDR) was highest in *Acinetobacter baumannii* at 76.4%, followed by *Klebsiella pneumoniae* (68.4%), *E. coli* (63.3%), *P. aeruginosa* (55.7%), and *S. aureus* (41.2%). These results indicate a significant presence of MDR organisms in the hospital environment, particularly among Gram-negative bacteria. Antibiotic resistance profiling showed that *E. coli* had high resistance to ceftriaxone (72.5%) and ciprofloxacin (66.7%), while maintaining lower resistance to meropenem (15.8%) and amikacin (24.2%). Similarly, *K. pneumoniae* exhibited resistance rates of 75.1% to ceftriaxone and 68.4% to ciprofloxacin, with meropenem and amikacin resistance reported at 22.1% and 33.6% respectively. *A. baumannii* demonstrated alarming resistance to ceftriaxone (82.9%) and ciprofloxacin (75.0%), with notable resistance to meropenem

(47.3%) and amikacin (39.2%). *P. aeruginosa* presented moderately high resistance across all agents, especially to meropenem (34.1%) and ciprofloxacin (52.6%). In contrast, *S. aureus* showed relatively low resistance to vancomycin (6.7%) and amikacin (18.6%), though ciprofloxacin resistance remained high at 34.1%.

Department-wise distribution revealed that the Intensive Care Unit (ICU) recorded the highest average resistance rate at 74.3%, followed by Emergency (66.2%), Surgery (62.1%), and Medicine (58.4%). This pattern suggests that critical care environments bear a greater burden of drug-resistant infections. Two visual charts complement the tabular data. The first bar chart illustrates MDR rates among the five key pathogens, with *A. baumannii* and *K. pneumoniae* showing the most significant resistance levels. The second chart compares resistance to selected antibiotics between *E. coli* and *K. pneumoniae*, demonstrating their shared vulnerability profiles, especially against third-generation cephalosporins and fluoroquinolones.

Table 1: Demographic Characteristics of Study Participants

Variable	Value
Total Patients	425
Mean Age (years)	46.3
Male (%)	232 (54.6%)
Female (%)	193 (45.4%)

Table 2: Multidrug Resistance (MDR) by Pathogen

Pathogen	Total Isolates	MDR (%)
E. coli	120	63.3
K. pneumoniae	95	68.4
P. aeruginosa	70	55.7
A. baumannii	55	76.4
S. aureus	85	41.2

Table 3: Antibiotic Resistance Profile of Pathogens

Antibiotic	*E. coli* (%)	*K. pneumoniae* (%)	*P. aeruginosa* (%)	*A. baumannii* (%)	*S. aureus* (%)
Ceftriaxone	72.5	75.1	58.2	82.9	NA
Meropenem	15.8	22.1	34.1	47.3	NA
Amikacin	24.2	33.6	28.4	39.2	18.6
Ciprofloxacin	66.7	68.4	52.6	75.0	34.1
Vancomycin	NA	NA	NA	NA	6.7

Table 4: Average Resistance Rate by Hospital Department

Department	Average Resistance Rate (%)
ICU	74.3
Surgery	62.1
Medicine	58.4
Emergency	66.2

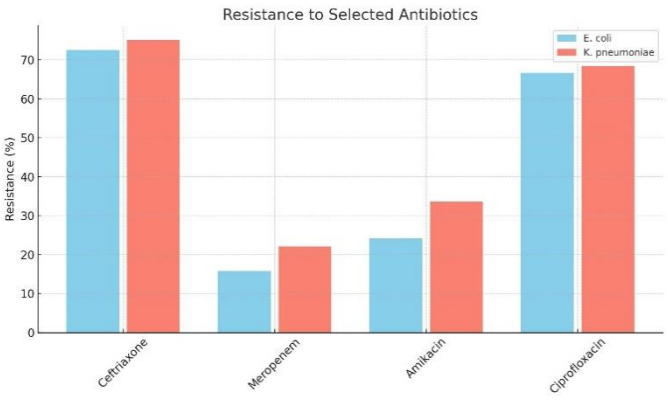

Figure 1 Resistance to Selected Antibiotics

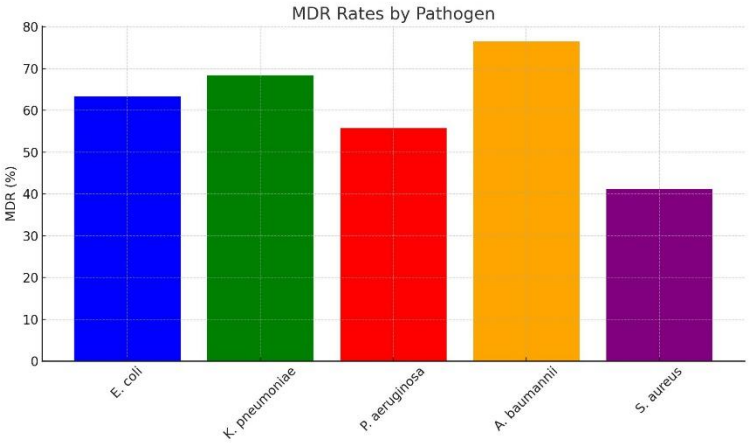

Figure 2 MDR Rates by Pathogen

DISCUSSION

The results of this study underscore a disturbing pattern of high multidrug resistance (MDR) among key bacterial pathogens in tertiary care hospitals in Lahore, a trend that mirrors findings from similar urban healthcare settings worldwide. The particularly elevated resistance rates observed in *Acinetobacter baumannii* (76.4%) and *Klebsiella pneumoniae* (68.4%) align with growing global concerns regarding the limited therapeutic options remaining for these organisms (15,16). This pattern is consistent with data from Southeast Asia, the Middle East, and African regions, where *A. baumannii* has shown resistance rates exceeding 70% in ICUs and surgical wards (17). Ceftriaxone resistance was notably high across all Gram-negative isolates, reaching 75.1% in *K. pneumoniae* and 72.5% in *E. coli*, echoing similar patterns identified in Ethiopian and Bangladeshi studies, where third-generation cephalosporins were broadly ineffective against Enterobacteriaceae (17,18). Resistance to carbapenems, although lower, remains clinically significant in *A. baumannii* (47.3%) and *P. aeruginosa* (34.1%), which continues to reduce the efficacy of last-line treatments (19).

One of the most alarming findings was the predominance of MDR pathogens in critical care settings, particularly in ICUs, which recorded a 74.3% average resistance rate. These results resonate with a recent multicenter surveillance from China, where ICUs consistently showed the highest resistance rates, especially for carbapenem-resistant *A. baumannii* and ESBL-producing Enterobacteriaceae (20). The observed trends may be attributed to high antibiotic consumption, severity of illness, prolonged hospital stays, and extensive use of invasive procedures in these units. The study also highlights the relatively preserved activity of amikacin and vancomycin against Gram-negative and Gram-positive pathogens respectively, indicating that some conventional therapies retain utility. However, the increase in fluoroquinolone resistance across all organisms, particularly *E. coli* (66.7%) and *K. pneumoniae* (68.4%), is consistent with data showing the decline of ciprofloxacin efficacy in both clinical and wastewater isolates across multiple countries (20,21).

A key strength of this study is its comprehensive cross-sectional design, encompassing a wide array of common bacterial isolates and incorporating data from multiple departments and sample types. This allowed for a nuanced understanding of resistance patterns across both Gram-negative and Gram-positive organisms, and across various clinical contexts. Furthermore, the study's reliance on CLSI-standardized methods for antimicrobial susceptibility testing enhances the comparability and reproducibility of findings. Nevertheless, the study has notable limitations. The exclusion of pediatric patients limits generalizability to younger populations, who may have different resistance patterns. The study's retrospective reliance on laboratory records may also introduce selection bias, as only culture-positive cases were included. Additionally, molecular testing for resistance genes was not conducted, which would have enriched understanding of the underlying resistance mechanisms. Future research should aim to incorporate molecular diagnostics to detect resistance genes such as bla_KPC, bla_NDM, and bla_CTX-M, which are increasingly identified in both clinical and environmental isolates (22). Longitudinal surveillance is also warranted to capture evolving trends over time and assess the impact of stewardship interventions. Expanding the study to include multiple cities could provide a national-level overview of resistance dynamics, enabling more effective public health responses. In conclusion, the findings from this study reinforce the growing burden of antimicrobial

resistance in urban hospital settings and the urgent need for robust surveillance, stringent stewardship policies, and continued investment in research to develop new therapeutic strategies.

CONCLUSION

This study highlights a critical burden of multidrug-resistant pathogens, particularly *Acinetobacter baumannii* and *Klebsiella pneumoniae*, in urban tertiary care hospitals. The high resistance rates to commonly used antibiotics underscore the urgent need for enhanced antimicrobial stewardship, targeted infection control strategies, and regular local surveillance to guide empirical therapy and policy decisions.

AUTHOR CONTRIBUTION

Author	Contribution
Azka Ilyas	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Syeda Ranna Fatima*	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published
Taj Muhammad Khan	Substantial Contribution to acquisition and interpretation of Data Has given Final Approval of the version to be published
Marriam Ali	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Atika Masood	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Syed Ahmad Raza	Substantial Contribution to study design and Data Analysis Has given Final Approval of the version to be published
Asma Aslam	Contributed to study concept and Data collection Has given Final Approval of the version to be published

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