Original Article

Current Trends of Antibiotic Resistance Patterns among Adult Patients in the Intensive Care Unit of a Periphery Hospital, Bangladesh.

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Abstract

Background: *Antimicrobial resistance (AMR) in intensive care units (ICUs) cause significant mortality, particularly in resource-limited settings. The traditional antibiotics become ineffective in our hospital settings.*

Objectives: *This study aimed to evaluate the current trends of antibiotic resistance patterns among adult patients in ICU settings of a peripheral hospital in Bangladesh.*

Materials and Methods: *A cross-sectional study was conducted between January 2023 to December 2023, analyzing bacterial isolates from adult ICU patients. Samples were collected from blood, urine, respiratory secretions, and wound swabs. Identification of bacteria and antimicrobial susceptibility testing were performed using automated BD Phoenix™ M50 System and manual (disc diffusion) methods. Data analysis was conducted using SPSS version 25.*

Results: *Among 100 patients studied (65% male, mean age 51.70 ±17.96 years), blood was the majority of specimens (40%). Escherichia coli was the most frequently isolated organism (31%), followed by Staphylococcus species (27%). E. coli demonstrated resistance to 15 out of 16 tested antibiotics, while Klebsiella pneumoniae and Staphylococcus aureus showed resistance to 12 antibiotics each. The highest resistance rates were observed to clindamycin (76.09%), ceftazidime (70.83%), and colistin (70.27%), while amikacin showed the lowest resistance rate (29.87%).*

Conclusions: *The study revealed alarming levels of antimicrobial resistance among ICU isolates, particularly concerning the high resistance to colistin. These findings emphasize the urgent need for robust antibiotic stewardship programs and enhanced infection control measures in ICU settings of peripheral hospitals in Bangladesh.*

Key words: *Antibiotic Resistance, Resistance Patterns, Intensive care Unit (ICU)*

Date of received: *11.12.2024*

Date of acceptance: *26.02.2025*

DOI: https://doi.org/10.3329/kyamcj.v16i01.79212

KYAMC Journal. 2025; 16(01): 09-13.

Introduction

Antimicrobial resistance (AMR) has emerged as a critical global health threat, as recognized by the World Health Organization (WHO), significantly impacting mortality and morbidity worldwide. This challenge is particularly acute at Intensive Care Unit (ICU) settings, where patient outcomes heavily depend on effective antimicrobial therapy.[1] ICUs present distinct challenges due to their unique environment, housing critically ill patients in confined spaces with high antimicrobial usage. These units have become recognized as focal points for infection, creating conditions where resistant strains readily develop and spread.[2] Multiple factors contribute to elevated AMR rates in ICU settings, including inappropriate antimicrobial use, frequent invasive procedures, extended hospital stays, and suboptimal infection control measures.[2, 3] One study found that AMR prevalence increases two to three-folds when ICU stays extend beyond seven days.[4] This pattern is especially pronounced in developing nations where control measures are often limited.[5] One meta-analysis found high antibiotic resistance rates that

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have compromised the effectiveness of many first-line antibiotics in Bangladesh.[6] A seven-year analysis of AMR trends in Bangladeshi ICUs revealed increasing antibiotic resistance, particularly among gram-negative organisms such as Pseudomonas species, associated with significant mortality rates.[7]

Multi-drug resistance (MDS) is a common problem in hospital settings. It seems that MDS causes difficulties to choose a suitable antibiotic in ICU. It also causes the increased hospital staying. This study aimed to identify the prevalent antibiotic resistance patterns among major pathogens isolated from ICU patients, providing data that can inform local antibiotic stewardship programs and optimize infection control practices.

Materials and Methods

This cross-sectional study was conducted between January 2023 to December 2023, in a major tertiary hospital Khwaja Yunus Ali Medical College and Hospital. All ICU patients who were 18 years and above with laboratory confirmed bacterial infections were selected for this study including patients suffering from sepsis, intraabdominal infection, hospital acquired pneumonia, urinary tract infection, surgical site infection. Culture samples were collected from blood, urine, respiratory secretions and wound swab. Pathogens were isolated using automated BD Phoenix™ M50 System. The equipment was operated by the instruction of the manufacturer. Statistical analysis was conducted using SPSS V 25.

Table I: Distribution of patients according to age group.

Age group years (N)			
15 – 34	35 – 54	55 – 74	>74
22	27	49	2

Among the patients, males contributed 65%.

Antibiotic sensitivity test was done by automated BD Phoenix ™ M50 System according to the manufacturer's instruction. The total number of studied specimens were 100. Among these bile 1, blood 40, central venous catheter tip 2, pus 12, sputum 11, stool 1, wound swab 1, tracheal aspirate 18, drain tube 1, urine 13 were analyzed.

Results

Figure 1 describes the distribution of the different organisms from the samples. E coli was the most prevalent of the bacteria – comprising (31%), closely followed by Staphylococcus species (27%). Among the isolated strains a significant number (18%) of environmental strains were also isolated from the samples.

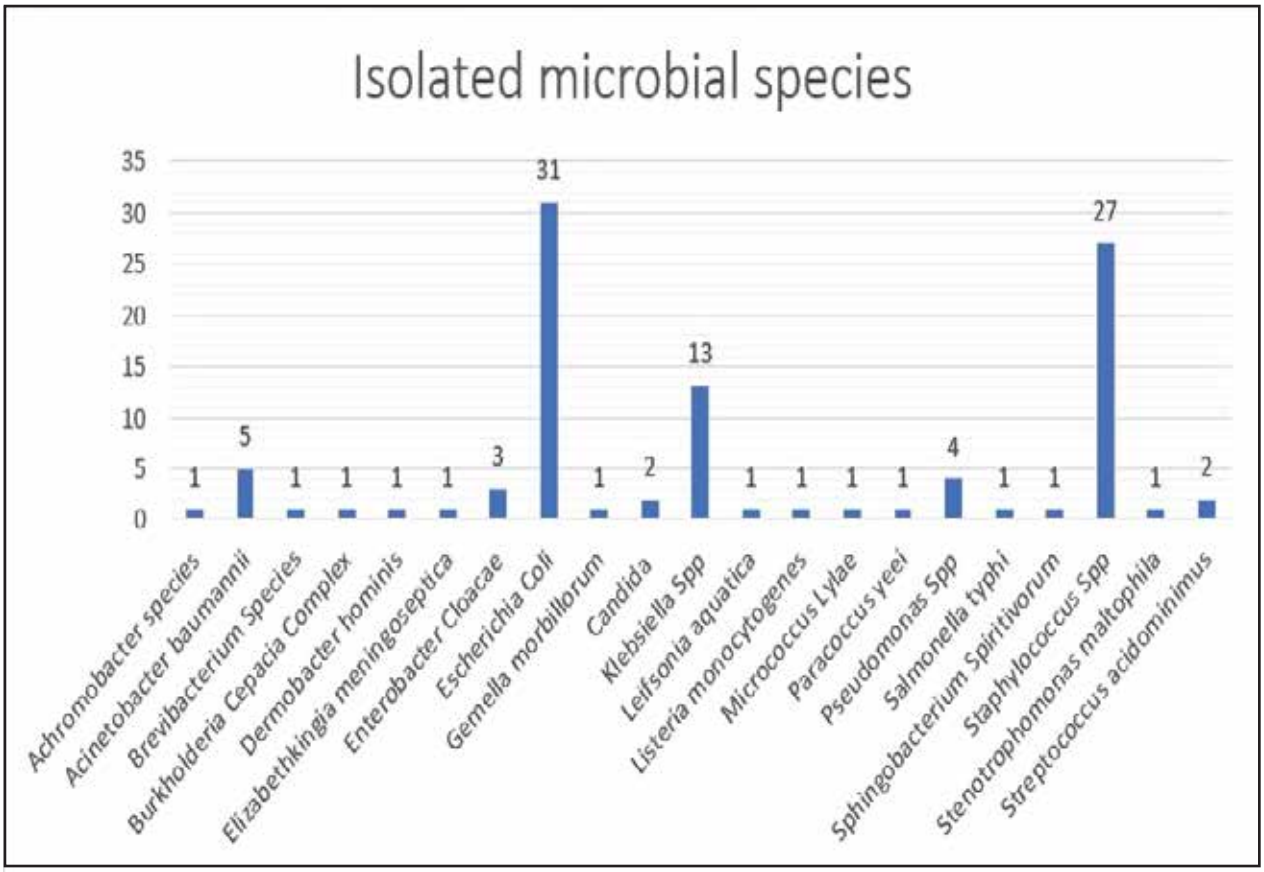

Figure 1: Isolated microbial species.

Table II: Antibiotic susceptibility patterns of the isolates

Antibiotics	Resistance pattern	*Staph. aureus* (%)	*Staph. epidermidis* (%)	*E. coli (%)*	*Kleb. Pneumoniae* (%)	*Pseudomonas* (%)	*Acinetobacter baumannii* (%)
Augmentin	R	3	4	21	7	3	5
	S	1	4	8	3	1	0
Piperacillintazobactam	R	2	1	17	6	2	4
	S	1	6	13	4	2	1
Ceftriaxone	R	4	6	17	3	3	N/A
	S	0	1	9	3	1	
Cefepime	R	1	0	12	3	0	4
	S	1	7	14	5	2	1
Meropenem	R	1	0	11	6	1	4
	S	2	8	20	4	3	0
Gentamicin	R	1	1	11	5	1	4
	S	1	0	20	5	3	1
Amikacin	R	0	2	8	0	0	3
	S	2	3	23	6	3	2
Ciprofloxacin	R	2	3	20	4	2	4
	S	1	0	9	6	1	1
Levofloxacin	R	2	5	20	8	2	4
	S	2	2	9	2	1	1
Colistin	R	4	8	15	10	2	N/A
	S	0	1	12	0	2	
Vancomycin	R	2	3	28	10	4	N/A
	S	2	2	3	0	0	
Linezolid	R	2	N/A	13	N/A	4	N/A
	S	2		14		0	
Trimethoprim-sulfamethoxazole	R	0	3	16	5	4	2
	S	2	6	14	5	0	0
Doxycycline	R	2	0	24	N/A	2	N/A
	S	1	3	7		1	
Clindamycin	R	1	6	11	N/A	4	N/A
	S	2	3	16		0	
Ceftazidime	R	3	2	19	8	2	4
	S	1	6	10	2	1	0
Total		4	9	31	10	4	5

Table II displays the sensitivity pattern of the most common organisms to different antibiotics. E. coli was the most prevalent isolated organism and displayed resistant to antibiotics. Majority of the strains are resistance to Augmentin, Piperacillin-Tazobactam and Ceftriaxone. Staphylococcus aureus also showed significant resistance to almost all antibiotics except to amikacin and trimethoprim-sulfamethoxazole.

Our study also focus on the frequency of multi-drug resistance of different microbes. Out of 16 tested antibiotics, E coli showed resistance to 15, closely followed by Klebsiella pneumoniae and Staphylococcus aureus, displaying resistance to 12.

Clindamycin had the highest instances of resistance (76.09%), closely followed by ceftazidime (70.83%) and colistin (70.27%). Amikacin had the lowest instances of resistance (29.87%)

Discussion

This study provides significant insights into the pattern of AMR in ICU setting in a peripheral hospital, which is often neglected. Our findings revealed several concerning trends that require further evaluation.

Our findings demonstrate E. coli as the predominant pathogen (31% of isolates), which aligns with a similar study in Kenya.[8] This predominance may be attributed to E. coli's remarkable adaptability in transitioning from commensal to pathogenic states, coupled with its multiple virulence factors including adhesins, toxins, and iron acquisition mechanisms. The high prevalence in ICU settings is further facilitated by patients' compromised immune status and frequent invasive procedures.[9]

Among gram-positive organisms, Staphylococcus aureus was most frequently isolated species (27%). This finding is consistent with another Bangladeshi study.[7] This prevalence can be attributed to S. aureus's exceptional capacity for surface adherence and biofilm formation, characteristics that enhance its persistence in healthcare environments.[9]

The antimicrobial susceptibility testing revealed extensive multidrug resistance, with E. coli exhibiting resistance to 15 out of 16 antibiotics tested. This alarming pattern of resistance can be attributed to multiple genetic adaptations, including the presence of blaNDM gene, ESBL genes including blaOXA, and AmpC gene.[10] The horizontal gene transfer in ICU environments further facilitates the rapid spread of resistance genes.[11] The mortality burden associated with multidrug-resistant (MDR) organisms, particularly gram-negative bacteria, represents a significant global healthcare challenge in intensive care settings. Recent epidemiological data demonstrates mortality rates reaching 50.3% among patients with MDR gram-negative bloodstream infections.[12] This alarming trend is particularly significant in low- and middle-income countries (LMICs), where resource limitations and inadequate infection control measures exacerbate the problem.[8] A comprehensive analysis from Indian healthcare facilities revealed that infections with MDR and extensively drug-resistant (XDR) strains of E. coli, K. pneumoniae, and A. baumannii were associated with two to three-fold higher mortality rates compared to susceptible strains.[13] Another concerning finding is the high colistin resistance rate (70.27%) observed in our study, which significantly exceeds global averages. This finding aligns with recent trends observed in India, where colistin sensitivity has dramatically decreased from 92% to 28% over four years.[14] The elevated resistance to other first-line antibiotics, including clindamycin (76.09%) and ceftazidime (70.83%), suggests a critical limitation in therapeutic options.

The limitations of this study include its single-center design and cross-sectional nature, which may not fully capture temporal trends in resistance patterns. Future multi-center, longitudinal studies are warranted to establish comprehensive regional resistance patterns and inform evidence-based antimicrobial stewardship programs.

Conclusion

These findings underscore the urgent need for enhanced surveillance systems and implementation of robust antibiotic stewardship programs in ICU settings, particularly in resource-limited environments where the burden of antimicrobial resistance is increasingly concerning

Acknowledgement

Our investigation team is expressing gratitude to Khwaja Yunus Ali Medical College and Hospital authority for supporting the study.

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