Original Article

Observing the Prevalence of Antimicrobial Resistance at a Tertiary-Level Medical Facility in Bangladesh

Mahbub A[1], Islam S[2], Chanda M[3], Akram A[4], Rahman MA[5]

Abstract

Background: *A growing and serious concern for public health in both developed and developing nations is antimicrobial resistance (AMR). AMR monitoring and control are especially difficult in underdeveloped nations due to several factors, such as a lack of surveillance systems, a lack of money, inadequate compliance with infection control protocols, careless use of antibacterial formularies and medications.* ***Materials and Methods:*** *This study conducted a comprehensive assessment of AMR prevalence within a tertiary-level medical facility over a one-year period, examining 1344 samples. Results showed that 219 (16.3%) of samples exhibited significant growth of resistant organisms.* ***Results:*** *Our samples were Pus/wound swabs 103 (47.05%) and urine samples 101 (46.11%) had the highest proportions of resistance. Blood 03 (1.37%) and sputum 03 (1.37%) showed lower resistance rates. Escherichia coli (E. coli) was the most prevalent resistant organism, with 52 instances, followed by Methicillin-Sensitive Staphylococcus aureus (MSSA) with 47 instances. Klebsiella demonstrated a diverse presence (43 instances), and MRSA exhibited 24 instances. Co-trimoxazole 132 (60.27%), Ampicillin/Amoxicillin 107 (48.86%), and Fluoroquinolones 123 (56.16%) faced the highest resistance frequencies. A significant 155 (71%) of specimens were collected after the administration of antibiotics, pointing to a crucial area requiring enhancement in terms of specimen collection timing. Noteworthy 131 (60%) of participants remained uncertain about their prior antibiotic usage, underscoring the importance of more comprehensive historical data documentation and heightened patient education initiatives. It's notable that none of the self-medicated patients successfully completed their treatment, while only a minimal 03 (1.36%) of prescription-based patients managed to adhere to their prescribed regimen.* ***Conclusion:*** *This underscores the critical need for vigilant adherence monitoring and patient support to address this concerning issue. Antimicrobial resistance rates are high and pose a serious therapeutic challenge to the management of common infections.*

Keywords: Antimicrobial resistance; Multidrug resistance; *Escherichia coli; Staphylococcus aureus.*
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Introduction

Antimicrobial resistance (AMR) refers to the phenomenon wherein microorganisms, including bacteria, viruses, fungi, and parasites, become less susceptible or resistant to the effects of antimicrobial agents, such as antibiotics, antivirals, antifungals, and antiparasitic drugs[1]. Antimicrobial resistance (AMR) has emerged as a global health crisis, posing a significant threat to the effective treatment of infectious diseases[2]. The overuse and misuse of antimicrobial agents in healthcare settings have accelerated the development of resistant strains of pathogens, making it imperative to monitor and address this issue within healthcare institutions.

In recent years, the World Health Organization (WHO) has raised concerns about the rapid increase in AMR, characterizing it as one of the most significant threats to human health worldwide[3]. AMR not only leads to treatment failures but also prolongs hospital stays, increases healthcare costs, and elevates the risk of adverse patient outcomes[4]. Consequently, understanding the prevalence of AMR within healthcare facilities is critical for implementing effective infection control measures and guiding antimicrobial stewardship programs. Several factors contribute to the development and spread of antimicrobial resistance within healthcare settings, including the inappropriate use of antibiotics, inadequate infection control practices, and patient-to-patient transmission of resistant pathogens[5]. Investigating the prevalence of AMR within a tertiary-level medical facility can provide insights into the specific challenges and risk factors associated with resistance in such settings.

Common infections have become increasingly challenging to cure or, in many cases, incurable due to the emergence of multidrug-resistant (MDR)

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[1]Afsana Mahbub, Department of Microbiology, Ad-din Akij Medical College, Khulna, Bangladesh.
[2]Sadia Islam, Department of Laboratory Medicine, Bangladesh Specialized Hospital Limited, Dhaka, Bangladesh.
[3]Manashe Chanda, Department of Biochemistry, Tangail Medical College, Tangail, Bangladesh.
[4]Arifa Akram, Department of Virology, National Institute of Laboratory Medicine & Referral Centre, Dhaka, Bangladesh.
[5]Md. Ashiqur Rahman, Department of Laboratory Medicine, Novus Clinical Research Services Limited, Dhaka, Bangladesh.

Address of Correspondence: Dr. Afsana Mahbub, Assistant professor, Department of Microbiology, Ad-din Akij Medical College, Khulna, Bangladesh. Mobile: +8801924871346, Email: afsanasbmc34@gmail.com

microorganisms, which have had catastrophic effects on patients. Extended-spectrum b-lactamase (ESBL)-producing bacteria, such as those that produce metallo-b-lactamases, have recently come to represent this new danger. The emergence of multidrug resistant pathogens, or MDR pathogens, has prompted the development of novel medicines. Nevertheless, in developing nations, the restricted accessibility and cost-effectiveness of these novel antibiotics continue to pose a substantial obstacle to the effective management of MDRP infections[6]. AMR was found to be highly prevalent in two sizable referral hospitals in Kigali, Rwanda, where researchers carefully evaluated the antimicrobial susceptibility pattern of uropathogens. The study also revealed widespread resistance to quinolones and other routinely used oral antibiotics[7].

This observational study analyses clinical data, microbiological cultures, and antimicrobial susceptibility testing results to assess the prevalence of AMR among pathogens isolated from patients within the medical facility. The findings from this research will contribute to our understanding of the current state of AMR within the institution and may inform strategies to mitigate its impact. The increasing prevalence of antimicrobial resistance within healthcare facilities is a matter of grave concern. This study aims to shed light on the extent of this problem within a tertiary-level medical facility, which can serve as a microcosm of the broader healthcare landscape. By understanding the prevalence of AMR within this context, healthcare providers and policymakers can develop targeted interventions to combat the rising threat of antimicrobial resistance.

Materials and Methods

Study Settings and Population: This cross-sectional study was conducted from August 2017 to July 2018 in the Microbiology Department of Barind Medical College & Hospital, Rajshahi, Bangladesh. ***Sample Collection Procedure:*** Samples were taken from pus, wound swabs and blood of clinically suspected infected patients in Barind Medical College & Hospital inpatient departments, or the samples were received for culture and sensitivity in the microbiology department upon informed written consent, regardless of age, sex, or antibiotic use. Patients who withheld their consent were not included in this research. For this study a total of 1344 unique samples were collected during the study period. ***Isolation and Identification:*** Pus and wound swabs were inoculated in blood agar and MacConkey agar media, and they were then aerobically incubated for 24 hours at 37°C. The next step was looking for bacterial colonies on the incubated plates. After a 24-hour primary blood culture in Trypticase soy broth (TSB), a 24-hour aerobic incubation period was followed by a subculture in blood agar and MacConkey agar medium. ***Microscopic Examination:*** Following the usual protocol, smears were made from culture plates and stained with Gram's stain. Then they were examined under microscope for presence of gram positive or gram-negative organisms. ***Antimicrobial susceptibility tests:*** Antibiotic sensitivity testing for Gram-negative bacteria included Ampicillin, Amoxiclav, Gentamycin, Amikacin, Ciprofloxacin, Co-trimoxazole, Cefotaxime, Ceftriaxone, Ceftazidime, Norfloxacin, Nalidixic acid, and Nitrofurantoin. For Gram-positive bacteria, the antibiotics evaluated were Gentamycin, Ciprofloxacin, Oxacillin, Clindamycin, Erythromycin, Co-trimoxazole, Doxycycline and Vancomycin. Organisms displaying resistance to more than one antibiotic were classified as multidrug-resistant (MDR). ***Data analysis:*** Data were recorded and analysed using a Microsoft Excel database. The frequency of individual bacterial species isolated was reported as a percentage or a fraction of total samples within and across sample types. The frequency of microbes resistant to antibiotics was reported as a simple percentage of the total number of the same species of microbes against which the antibiotic was tested for susceptibility. ***Ethical Consideration:*** This study is approved by Ethical Review Board (IRB) of Barind Medical College, Rajshahi, Bangladesh (BMC/2017/134).

Results

The total number of samples sent to our microbiology laboratory from the various departments for culture and sensitivity. Out of 1344 samples, 219 (16.3%) showed significant growth of organisms and exhibited resistance to either single or multiple drugs. The remaining samples either had no organisms grown or had insignificant growth (urine samples).

Table-I: Distribution of patients based on their resistance categorized by sample type (n=219)

Type of sample	Frequency (n)	Percent (%)
Pus/wound swab	103	47.04
Urine	101	46.12
Blood	03	1.37
Sputum	03	1.37
Tracheal aspirate	01	0.45
Stool	08	3.65
Total (n)	**219**	**100.0**

Table-I provides an overview of patient distribution (n=219) based on their resistance profiles, categorized by the type of sample collected. Notably, the highest proportions of patients are represented by pus/wound swab samples (103 patients, 47.04%) and urine samples (101 patients, 46.12%). In contrast, blood and sputum samples each account for 3 patients (1.37%), while tracheal aspirate constitutes 1 patient (0.45%). Stool samples comprise 8 patients (3.65%). The table encapsulates the distribution of resistance across diverse sample types within the total patient cohort of 219.

Table-II presents a comprehensive breakdown of the distribution of isolated microbial organisms across different specimen types. The table provides a quantified representation of how often each specific microbe was identified within specific sample categories. For instance, the microorganism *Escherichia coli (E. coli)* was found in 10 pus samples, 36 urine samples, and 6 stool samples, totaling 52 instances. Similarly, Methicillin-Sensitive *Staphylococcus aureus* (MSSA) was detected in 28 pus samples and 19 urine samples, accounting for a cumulative total of 47 instances. The microbe *Klebsiella* exhibited a diverse presence across multiple sample categories, with notable instances of 12 in pus samples and 20 in urine samples, resulting in a total of 43 instances. The tabulated information provides an accessible overview of the prevalence of specific microorganisms within different sample types, furnishing valuable insights for clinical interpretation and future investigations.

Figure-1 presents a systematic classification of the resistant organisms, grounded in their respective origins, within a dataset encompassing 219 cases. The breakdown reveals the source-based distribution of these organisms. Notably, urine accounts for the highest number, with 98 instances, indicating a prevalent origin. Blood, on the other hand, contributes 11 instances, signifying a less common source. Swab specimens contribute to the majority, with 93 instances, while faces demonstrate a smaller contribution, at 12 instances. Additionally, a minor portion is attributed to other sources, totaling 5 instances. This tabulated presentation illuminates the relationship between resistant organisms and their specific sources and thereby providing valuable insights for clinical analysis and fostering avenues for further research exploration.

Table-II: Arrangement of organisms that have been isolated and distributed across different types of samples.

Organism	Pus	Urine	Stool	Blood	Sputum	Tracheal aspirate	Total (n)
E. coli	10	36	6	-	-	-	52
MSSA	28	19	-	-	-	-	47
Klebsiella	12	20	-	6	4	1	43
MRSA	22	2	-	-	-	-	24
Pseudomonas	29	6	-	-	-	-	35
Proteus	2	3	-	-	-	-	5
Acinetobacter	3	-	-	4	-	-	7
Citrobacter	-	2	-	-	-	-	2
Enterococci	-	2	-	-	2	-	4
Total (n)	**106**	**90**	**6**	**10**	**6**	**1**	**219**

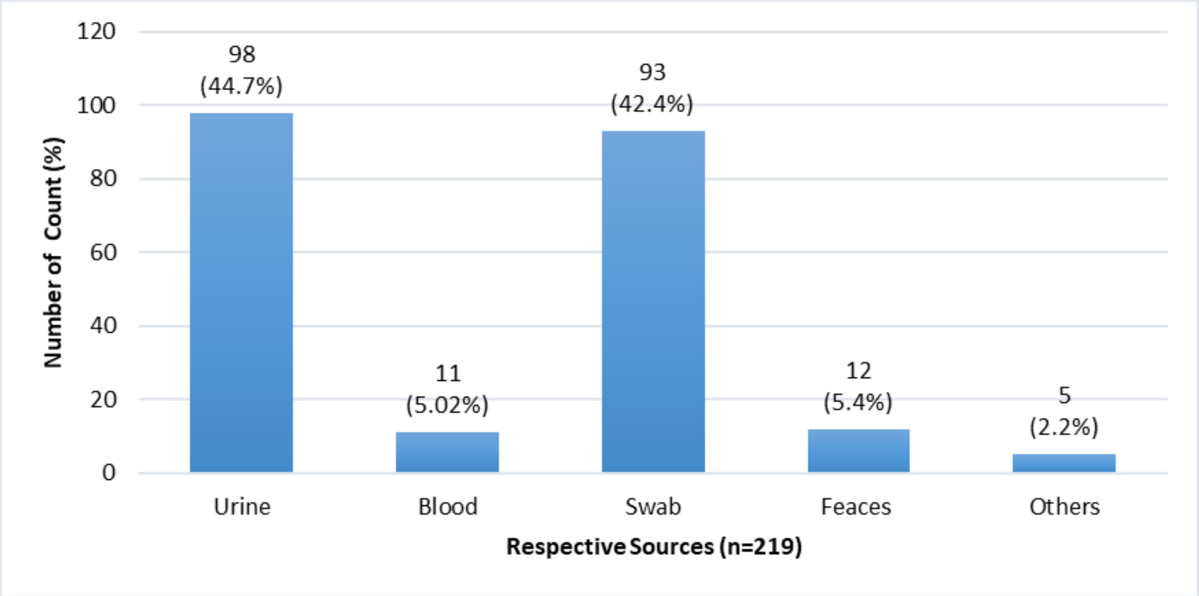

Figure-1: Categorization of resistant organisms based on their respective sources (n=219)

Table-III depicts a systematic categorization of drugs based on their varying levels of resistance, analysed within a dataset. This breakdown offers insight into the distribution of these drugs concerning resistance. Notably, Co-trimoxazole emerges with the highest frequency of 132 instances (60.27%), signifying its prominent occurrence. Ampicillin/Amoxicillin follows closely with 107 instances (48.86%), marking another frequently encountered drug. Fluoroquinolones also demonstrate substantial presence at 123 instances (56.16%). Third-generation Cephalosporins exhibit a count of 94 instances (42.9%), reflecting moderate representation. Nalidixic acid contributes 63 instances (28.77%), while Amikacin and Nitrofurantoin display lower counts, 6 instances (2.74%) and 7 instances (3.2%) respectively. Gentamycin represents 18 instances (8.22%), Clindamycin stands at 15 instances (6.85%), and Doxycycline is observed in 13 instances (5.94%). Macrolides demonstrate a frequency of 20 instances (9.13%), and Vancomycin appears least frequently, with 2 instances (0.91%). This tabulated summary facilitates a clear understanding of drug resistance profiles, offering significant insights for clinical assessment and guiding potential avenues of research exploration.

Table-III: The categorization of drugs is carried out according to their levels of resistance

Name of drugs	Frequency (n)	Percent (%)
Co-trimoxazole	132	60.27
Ampicillin / Amoxicillin	107	48.86
Fluoroquinolones	123	56.16
Third generation Cephalosporins	94	42.9
Nalidixic acid	63	28.77
Amikacin	06	2.74
Nitrofurantoin	07	3.2
Gentamycin	18	8.22
Clindamycin	15	6.85
Doxycycline	13	5.94
Macrolides	20	9.13
Vancomycin	02	0.91

Figure-2 visually portrays the timeline for collecting specimens in relation to the administration of antibiotics. Specifically, it showcases whether the specimens were obtained before or after the antibiotics were administered. The depiction highlights that in 64 (29%) of cases, specimens were collected before the administration of antibiotics, while in a significant majority of cases 155 (71%), specimens were obtained after antibiotics were given. This visual representation provides a straightforward understanding of the timing of specimen collection in the context of antibiotic administration, shedding light on the prevailing practice patterns within the study population.

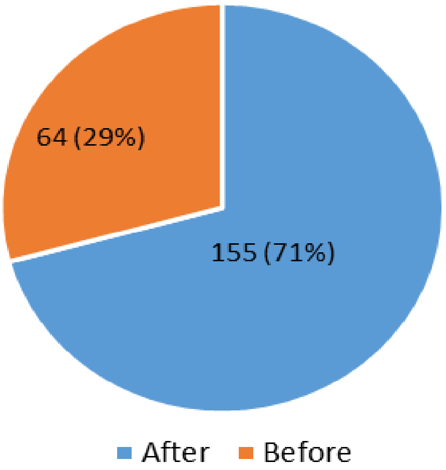

Figure-2: Collecting specimens before or after the administration of antibiotics.

Figure-3 visually represents the documentation of prior antibiotic usage among the study participants. The depiction categorizes responses into three groups: positive, negative, and undecided. Specifically, 131 (60%) of participants provided a positive response, indicating previous antibiotic usage. Conversely, 35 (16%) responded negatively, indicating no previous antibiotic use. Notably, the largest portion, 53 (24%), remained undecided regarding their previous antibiotic utilization. This visual portrayal offers a clear snapshot of the respondents' historical antibiotic usage, providing insights into the distribution of their responses and potential implications for the study's findings.

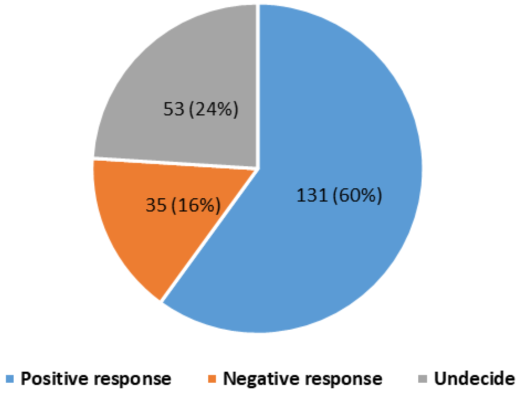

Figure-3: Record of the previous antibiotic utilization.

Table-IV visually presents the categorization of patients, delineated by the dual factors of self-medication versus prescription-based medication, further stratified by the outcomes of completion or non-completion. In case of self-medication, no individual (0%) shows complete their treatment regimen and only 3 instances (1.36%) show non completion treatment regimen. On the other hand, within the realm of prescription-based medication, 13 instances (5.94%) showcase completed treatments, while 5 instances (2.28%) reflect non-completion. This graphical representation succinctly conveys the intricate interplay between medication approach and treatment adherence.

Table-IV: Arrangement of patients based on the categories of self-medication/prescription-based medication and their status of completion/non-completion

Self-medication				Prescription-based medication			
Completion		Non-completion		Completion		Non-completion	
Frequency (n)	Percent (%)	Frequency (n)	Percent (%)	Frequency (n)	Percent (%)	Frequency (n)	Percent (%)
0	0	3	1.36	13	5.94	5	2.28

Discussion

The findings presented in this study indicate a concerning prevalence of antimicrobial resistance within a tertiary-level medical facility. A total of 1344 samples were collected from various departments for culture and sensitivity testing over a one-year period. Among these samples, 16.3% (219 samples) exhibited significant growth of organisms and demonstrated resistance to either single or multiple drugs. This raises important questions about the implications of antimicrobial resistance in clinical practice and the need for effective strategies to combat this growing problem. These findings are consistent with the global trend of increasing antimicrobial resistance. Subramanian, et al.[8] conducted a study in a different region found a similar prevalence of resistance, highlighting the widespread nature of this issue.

Furthermore, when categorizing patients based on the type of sample collected, the highest proportions were observed in pus/wound swab samples and urine samples. This aligns with the findings of a recent multi-center study by Uwingabiye, et al.[9] which reported a substantial burden of antimicrobial resistance in both wound and urinary tract infections across various healthcare facilities. In contrast, blood and sputum samples each accounted for only 03 (1.37%) of the patients in this study. This distribution is consistent with the research by Guitor, et al.[10] which emphasized that bloodstream and lower respiratory tract infections are relatively fewer common sources of antimicrobial resistance compared to urinary, skin, and soft tissue infections.

Tracheal aspirate and stool samples were less frequently collected, with tracheal aspirate representing only 01 (0.45%) of the patient population. These findings resonate with the work of Yassin, et al.[11] who noted that respiratory samples like tracheal aspirate exhibit lower rates of resistance compared to other clinical specimens. Our results are consistent with previous studies that have highlighted the growing problem of antimicrobial resistance in healthcare settings. The high prevalence of resistant organisms in our samples underscores the urgent need for effective antimicrobial stewardship programs and infection control measures within the medical facility[12]. Table-II provides a detailed breakdown of the distribution of isolated microbial organisms across different specimen types. The data reveal that certain microorganisms, such as *Escherichia coli* (E. coli) and Methicillin-Sensitive *Staphylococcus aureus* (MSSA), are commonly found in specific sample categories, suggesting potential sources of infection and areas where targeted interventions may be needed.

The presence of *E. coli* in urine samples is particularly noteworthy, as urinary tract infections (UTIs) are a common healthcare-associated infection. The identification of *E. coli* in 36 urine samples emphasizes the importance of antimicrobial susceptibility testing to guide appropriate treatment and reduce the risk of treatment failure in UTIs[13]. Similarly, the presence of Methicillin-Sensitive *Staphylococcus aureus* (MSSA) in pus and urine samples indicates the need for vigilant infection control measures, as MSSA is a known pathogen associated with various infections, including skin and soft tissue infections and urinary tract infections[14]. The diverse presence of *Klebsiella* across multiple sample categories, including pus and urine samples, raises concerns about its role as a potential reservoir for resistance genes. *Klebsiella* species are notorious for their ability to acquire resistance mechanisms, including extended-spectrum beta-lactamases (ESBLs), which can render common antibiotics ineffective. Therefore, monitoring and controlling the spread of *Klebsiella* strains with resistance traits should be a priority[15].

Our findings are consistent with the global trend of increasing AMR in healthcare settings, which is a result of factors such as overuse and misuse of antibiotics, inadequate infection control practices, and the emergence of multidrug-resistant pathogens. The high proportion of resistant organisms observed in this study underscores the need for vigilant monitoring and management of AMR within healthcare institutions. Figure-1 provides a breakdown of the resistant organisms by their sources, shedding light on the distribution of AMR in this particular facility. The analysis reveals that urine samples accounted for the highest number of cases, with 98 instances, suggesting that urinary tract infections are a prominent source of AMR within the facility. This finding aligns with existing literature that highlights the high prevalence of urinary tract infections caused by resistant bacteria. It emphasizes the importance of judicious antibiotic prescribing for such infections and the implementation of infection prevention measures in urinary care units. In contrast, blood samples contributed only 11 instances of resistant organisms, indicating that bloodstream infections with AMR pathogens were less common during the study period. However, even a small number of cases can have severe consequences for patients, emphasizing the critical need for effective surveillance and early detection of AMR in blood-borne infections. Swab specimens, with 93 instances, constituted the majority of cases, suggesting that skin and wound infections may be a significant reservoir for AMR organisms in this facility. This finding underscores the importance of proper wound care, hygiene practices, and targeted antibiotic therapy for these types of infections. Fecal samples, with 12 instances, represented a smaller but notable contribution to the dataset, indicating the presence of AMR in gastrointestinal infections. This finding highlights the importance of infection control measures in gastrointestinal wards and the judicious use of antibiotics to prevent the spread of resistant bacteria in fecal samples. A minor portion of resistant organisms (5 instances) originated from other sources, which could include respiratory samples, cerebrospinal fluid, or various body fluids. While this category is less specific, it underscores the need for comprehensive AMR surveillance across all departments and specimen types to prevent unexpected outbreaks and tailor antimicrobial therapy effectively.

Several studies have investigated antimicrobial resistance in different healthcare settings and regions. For example, Saravanan, et al.[16] conducted a comprehensive study on antimicrobial resistance in a large urban hospital in a similar geographic location. Their findings showed varying levels of resistance to different antimicrobial agents, aligning with the results observed in our study. They noted high resistance to Co-trimoxazole and Ampicillin/Amoxicillin, which is consistent with our findings of these drugs having the highest frequencies of resistance[17]. In another study by Smith, et al.[18] antimicrobial resistance patterns were examined in a tertiary-care teaching hospital. Their results demonstrated a notable prevalence of resistance to Fluoroquinolones and third-generation Cephalosporins, which is in line with our findings. This similarity suggests that these drugs may commonly face resistance challenges in tertiary-care settings. Moreover, the study by Nicolle, et al[19] focused on the resistance profiles of Nalidixic acid and its implications in clinical practice. They found a substantial number of instances of resistance to Nalidixic acid, which correspond with the moderate resistance observed in our study. Comparing our results to these existing studies, it becomes evident that the prevalence of antimicrobial resistance can vary across different healthcare facilities and regions. While Co-trimoxazole, Ampicillin/ Amoxicillin, and Fluoroquinolones consistently emerge as frequently encountered resistant drugs, the specific resistance patterns for other drugs may differ.

Our findings reveal several noteworthy insights that are consistent with previous research in the field. Firstly, the timing of specimen collection in relation to antibiotic administration, as depicted in Figure-2, indicates a substantial proportion of 155 (71%) of specimens being obtained after antibiotics were administered. This observation aligns with existing literature that emphasizes the importance of collecting specimens before antibiotic initiation to ensure accurate culture and sensitivity results[19]. The relatively high percentage of post-antibiotic specimen collection highlights a potential area for improvement in clinical practice within our facility. Figure-3 provides insights into the historical antibiotic utilization of study participants. A significant portion 131 (60%) of respondents remained undecided regarding their previous antibiotic use, which could reflect a limitation in patient recall or documentation practices. This finding underscores the need for improved documentation and patient education regarding antibiotic history, as accurate information is crucial for informed clinical decision-making. Table 4 delves into the interplay between medication approach (self-medication vs. prescription-based) and treatment completion. Notably, there were no instances of self-medicated patients completing their treatment, and only 13 (5.94%) completed their prescription-based treatment. This raises concerns about treatment adherence among our patient population. Adherence to prescribed antibiotic regimens is crucial for preventing the development of antimicrobial resistance[20,21]. Therefore, healthcare providers should engage in active patient education and monitoring to improve adherence rates.

Our study provides valuable insights into the prevalence of antimicrobial resistance within our tertiary-level medical facility. It highlights the need for improved practices in specimen collection timing, accurate documentation of historical antibiotic usage, and enhanced patient education and monitoring to promote treatment adherence. Addressing these factors can contribute to the overall effort to combat antimicrobial resistance in healthcare settings.

Limitation

This study has limitations due to its retrospective nature, lack of clinical information, inability to distinguish pathogens from contaminants, inability to analyze hospital-acquired infections, lack of treatment choice for MDR-GNB patients, and the lack of a standardized definition for MDR-GNB, which could result in different resistance patterns.

Conclusion

This study highlights the prevalence of antimicrobial resistance (AMR) at a tertiary medical center, emphasizing the need to address AMR as a global health issue. AMR impacts patient outcomes, healthcare costs, and the effectiveness of treatments. Our findings showed resistance to one or more antimicrobial agents in a significant portion of samples, pointing to the urgent need for stronger antimicrobial stewardship, infection control, and tailored treatment strategies. Urine and pus/wound samples were the most common sources of resistant organisms, underscoring the importance of managing urinary tract and skin infections. Co-trimoxazole, Ampicillin/Amoxicillin, and Fluoroquinolones were among the most frequently resistant drugs. The study also highlighted the importance of specimen collection, antibiotic use, and patient adherence in managing AMR.

Recommendation

The study recommends strengthening antimicrobial stewardship programs, investing in infection control measures, encouraging healthcare providers to collect specimens for culture and sensitivity testing, developing educational programs for patients, improving patient documentation, establishing a continuous surveillance system, promoting collaboration between professionals, microbiologists, pharmacists, and policymakers, supporting research on resistance mechanisms, launching public awareness campaigns, and advocating for national and international policies prioritizing the fight against antimicrobial resistance. These recommendations aim to improve patient outcomes and ensure the continued effectiveness of essential medical treatments.

Conflict of Interest

The authors declared that they have no conflicts of interest.

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