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Article

Understanding Pattern of Antibiotic Resistance in Bangladeshi Patients in Intensive Care Units

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Abstract: The fate of critically sick patients with infections in intensive care units (ICUs) is significantly influenced by antimicrobial resistance, which has become a serious concern in developing nations. This observational study was conducted at the IBN Sina Specialised Hospital in Dhaka, Bangladesh, over a 12-month period from January 2021 to December 2021, in order to track the pattern of antibiotic resistance among the patients admitted to the intensive care unit (ICU). Aspiration pneumonia (29%) and diabetes mellitus (24%), among 200 patients, were the most common main diagnoses. 65 samples (or 26%) of the 250 samples had 85 bacteria identified from them. Urine (14.12%) and tracheal aspirate (64.71%) were the most frequently found sites of infection. In the sample from the tracheal aspirate, Pseudomonas spp. (30.59%), Escherichia coli (24.71%), Acinetobacter spp. (20%), and Klebsiella spp. (14.12) were the most frequently isolated microorganisms. The following antibiotics were shown to have the highest overall patterns of resistance: levofloxacin (68.24), amikacin (64.71), meropenem (49.41), ceftazidime (75.29), ciprofloxacin (78.82), and gentamicin (82.35). The most effective antibiotic against Klebsiella species was meropenem (64.61%), while Acinetobacter species were mostly susceptible to cotrimoxazole (64.67%) and piperacillin + tazobactam (60.50%). Most susceptible to netilmicin (70.48%) and meropenem (49.32%) were Escherichia coli, while Pseudomonas spp. were mostly responsive to colistin (55.14%) and netilmicin (52.25%). Antibiotic resistance is common among intensive care unit (ICU) patients, and most isolated microbes have resistance to traditional medicines.

Keywords: resistance to antibiotics; ICU; pneumonia.; diabetes; infection; Bangladesh

Introduction

Resistance-strain infections are a major source of morbidity and mortality among hospitalised patients, particularly among critically sick patients in the intensive care unit (ICU) (Hanberger et al., 1999; Vincent et al., 1995; Singh et al., 2002; Alam et al., 2023). According to Vandijck et al. (2008), Blot (2008), Blot (2007), Rice (2003), Bari et al. (2023), greater morbidity, less mobility, and increased usage of invasive equipment enhance the susceptibility of patients admitted to intensive care units to infection. Moreover, a number of medications that increase the risk of infection are routinely taken. For instance, muscle relaxants, sedatives, and stress ulcer prophylaxis can cause pneumonia by impairing cough and swallow reflexes, or they might alter the natural nonpathogenic bacterial flora, which increases the risk of infection (Marwick and Davey, 2009; Vincent et al, 2009, Faruk et al: 2023).

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Many of the medical advancements of the last century are in risk of being undermined by the growing global health concern of antibiotic resistance. Globally, since the 1940s, when antibiotics were first used in medicine, people's health and well-being have improved dramatically (Ferdous et al., 2023, Mithun et al., 2023; Tufael et al., 2023). The globe is now confronted with a severe threat of bacterial infections and antibiotic resistance, which is prevalent in every nation on the planet and adds to the worldwide concern of a "post-antimicrobial era," despite many decades of success with antibiotics. Developing nations also have significant prevalences of resistance in E. Coli and other *Klebsiella* spp., in addition to resistance to malaria. The ICU patients are at a 5-to7-fold increased risk of nosocomial infection in comparison to other patients because of underlying medical conditions, weakened immune systems, frequent invasive device use, exposure to wide spectrum antibiotics, and the colonisation of resistant microbes. According to Picard et al. (2006), Chakma et al. (2022), Hasan et al. (2023), Hossain et al. (2023), pneumonia, meningitis, intra-abdominal infections, and urinary tract infections, among others, may be suspected diseases. The continuous rise of resistance in the community and hospital is regarded as a serious threat to public health, in addition to the issue of nosocomial infections. Because of the unique risk profile of its patients, the intensive care unit (ICU) is considered the centre of resistance development. It has even been likened to a factory for the production, dissemination, and intensification of antimicrobial resistance (Carlet et al., 2007; Islam et al., 2018; Islam et al., 2023). Clinical and financial burdens are significant due to both infection and multidrug resistance (MDR). Thus, the detrimental effects of nosocomial infection are increased when MDR is present (Salgado et al, 2005; Cosgrove, 2006; Kuddus et al., 2020; Kuddus et al., 2021). However, the greater incidence of improper empirical antibiotic therapy linked to illnesses caused by multidrug-resistant bacteria is likely more responsible for this burden of resistance than the virulence of specific multidrug-resistant strains (Figueiredo Costa, 2008). Pseudomonas aeruginosa, *Klebsiella* spp., *Escherichia coli*, *Acinetobacte*r spp., *Staphylococcus aureus*, and *Streptococcus pyogenes* were the most frequently found pathogens in an Indian ICU investigation (Patwardhan et al, 2008; Kuddus et al., 2022). However in an ICU in Europe, *Staphylococcus aureus* was discovered to be the most often isolated bacterium (30.1%), with *Pseudomonas aeruginosa* (28.7%), Coagulase-negative *Staphylococcus* (19.1%), and yeast (17.1%) following closely after (Spencer, 1996). In almost all cases, there is a need to initiate empirical antimicrobial treatment before obtaining the microbial culture results, but the situation is further complicated during the past decades, a shift in the MDR dilemma has been noted from gram-positive to gram-negative bacteria, especially due to the scarceness of new antimicrobial agent's active against resistant gramme negative microorganisms (Boucher et al, 2009; Sazzad et al., 2023;). Gram-negative bacteria *Klebsiella pneumonia*, *Escherichia coli*, *Proteus mirabilis*, *Enterobacter* spp, *Citrobacter* spp, *Pseudomonas aeruginosa*, *Acinetobacter* spp., and *Stenotrophomonas maltophilia* are of great concern (Jones, 2001; Kaul et al, 2007; Sunny et al., 2022). Gram-positive organisms such as *Staphylococcus aureus* and vancomycin-resistant enterococci are of great concern (Boucher et al, 2009; Jones, 2001; Sunny et al., 2020). These important studies all point to the necessity of gathering information on antibiotic resistance in the intensive care unit (ICU) as well as the susceptibility pattern in order to inform future revisions to antibiotic policies and to assist physicians treat patients more effectively. This also eliminates unnecessary usage of broad spectrum antibiotics and prevents emergence of drug resistant bacterial strains. The current study was therefore conducted to ascertain the pattern of antimicrobial resistance of bacterial isolates among ICU patients, which would assist doctors in organizing antibiotic recommendations and antibiotic cycling in ICU environments.

Materials and Procedures

Location and time of study

This investigation was carried out in Bangladesh at the IBN Sina Specialised Hospital's Microbiology Laboratory in Dhanmondi, Dhaka-1209. This investigation collected samples from patients hospitalised to this ICU between January and December of 2021 who had a clinical suspicion of infection.

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Data collection

Patients who met the inclusion criteria were asked a series of questions about their demographics and clinical history. Age, gender, major cause for admission, medical history, vital signs, and Glasgow coma score were ascertained in addition to specifics about the ICU hospitalisation. Standard biochemistry tests included blood urea nitrogen, blood glucose, serum creatinine, complete blood count (CBC), and blood electrolytes. Further testing, including an ECG, chest X-ray, arterial blood gases, and specialised diagnostics, were performed in the event that a symptom was detected. For patients undergoing mechanical ventilation, the initial configurations included of closed suctioning, assist control mode, 100% inspired oxygen fraction (FIO2), 10% tidal volume per kg, 14 repetitions per minute, and 1.2 seconds of inhalation time. After being on mechanical ventilation for 48 hours, they were assessed again for temperature, sputum category, oxygen demand, and antibiotic use.

Examine the sample and the microbial isolates.

A clinical suspicion regarding the source of infection led to the collection of patient samples, including blood, urine, sputum/tracheal aspirate (respiratory secretions), pus, and wound swabs. These were forwarded to the department of Microbiology, IBN Sina for routine procedures such as microbial culture, isolation, identification, and antibiotic susceptibility testing (Murray et al, 1999). To sum up, each specimen was put on a plate that contained either MacConkey agar (MCA), chocolate agar (CA), or blood agar (BA), and it was then incubated at 37°C for 18 to 24 hours. Blood cultures that show favourable growth were processed in an automated blood culture system (Bact Alert 3D, bioMeriux, France) and then subcultured onto the previously described bacterial culture substrate. Standard microbiological procedures, such as colony morphology, Gramme stain, biochemical reaction, serologic testing, and antibiotic susceptibility testing, were applied to further define and identify the positively growing suspected pathogenic bacteria (Murray et al, 1999). All Intensive Care Unit patients who gave informed consent to participate in the study were involved. We requested the patient's next of kin for substituted consent if the patient was unable to grant informed consent. Patients who were pregnant or younger than eighteen years of age were excluded from the study.

Antimicrobial resistance assessment

The Antimicrobial Susceptibility Test was performed using a panel of antibiotic discs for both gramme positive and gramme negative microorganisms using the Kirby-Bauer method. In summary, Muller-Hinton broth was used to prepare test organism suspensions, turbidity was adjusted to meet McFarland 0.5 standards, and the mixture was then incubated for two hours. The Mueller Hinton Agar (MHA) plates were then covered with antibiotic discs after a bacterial lawn had been established on them. After the plates were incubated for 24 hours at 370C, the results were assessed for susceptible, intermediate, or resistant status using criteria supplied by the Clinical Laboratory Standard Institute (CLSI). The diameter of the zone of inhibition was also measured.

Table 1. List of antimicrobials utilized in the research.

Antimicrobials' names	
1. Amikacin	7. Ceftazidime
2. Gentamicin	8. Ceftriaxone
3. Netilmicin	9. Piperacillin + tazobactam
4. Ciprofloxacin	10. Cotrimoxazole
5. Levofloxacin	11. Colistin
6. Meropenem	

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Data analysis

All patient's information was electronically saved in a relational database system created especially for the research. After that, a spreadsheet containing the data was exported for statistical analysis. The percentage of positive results throughout the whole study sample was used to determine the prevalence of antibiotic resistance. SPSS 17 has performed statistical analysis on Windows. Z-test of proportion has been used to compare quantitative data that has been reported as a percentage. P values are considered significant if they are less than 0.05.

Results

In the ICU, 200 patients were diagnosed between January and December of 2021. Of these patients, 250 blood samples were examined; of these, 65 samples from 55 patients produced the growth of 85 microorganisms (Figure 1). Table 2 lists the initial parameters for the patients whose blood cultures revealed the proliferation of microorganisms. Ninety-three percent of the patients had an age beyond thirty. Nonetheless, 58.2% of patients in this age category were over 60, followed by 41.8% of those between 46 and 60. 56.3% of all isolates recovered from patients, regardless of age group, were from male patients, and 43.7% came from female patients with male patients.

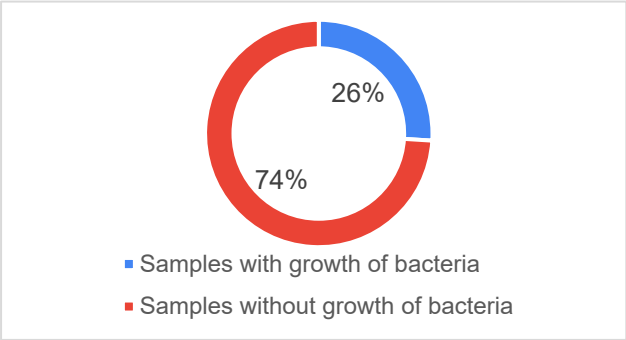

Figure 1. Pie chart indicating proportion of blood sample yielded growth of microbes.

Aspiration pneumonia (29%) and diabetes mellitus (24%), in that order, were the most prevalent primary diagnoses (Table 2). Urinary tract infections (12%), chronic kidney disease (12%), cerebral-vascular disease (10%), and COPD with respiratory failure (8%). The most common sites for infection were tracheal aspirate (64.71%) and urine (14.12%) (Table 3). *Acinetobacter* spp. (20%), *Klebsiella* spp. (14.12%), *Escherichia coli* (24.71%), and *pseudomonas* spp. (30.59%) were the most frequently isolated bacteria and were primarily detected in the tracheal aspirate sample (Table 4).

Table 2. the patients' primary diagnosis in the intensive care unit. (N total: 200).

Initial diagnosis	Frequency	Percentage
Aspiration pneumonia	58	28.5
Diabetes Mellitus (DM)	48	24.0
Urinary Tract Infections (UTI)	24	12.0
Chronic Kidney Disease (CKD)	24	12.0
Cerebral-Vascular Disease (CVD)	20	10.1
COPD with respiratory failure	16	7.9
Surgical wound infection	10	5.5
Total	200	100.0

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Table 3. The characteristics of the samples and the percentage of positive cultures from each sample (N total: 250).

Sample	Total number of samples	Growth of organism	
		Number	Percentage
Blood	80	8	9.41
Urine	75	12	14.12
Tracheal secretion	55	55	64.71
Wound swab Pus	40	10	11.76
Total	250	85	100

Table 4. The distribution of microbes isolated from ICU patients (N total: 85).

Microorganism	Number	Percentage (%)
Pseudomonas spp.	26	30.59
Escherichia coli	21	24.71
Acinetobacter	17	20
Klebsiella spp.	12	14.12
Staphylococcus aureus	3	3.53
Streptococcus pneumoniae	2	2.35
Proteus mirabilis	2	2.35
Citrobacter	1	1.18
Enterococcus	1	1.18
Total	85	100

Table 5 shows the sensitivity and resistance of various microorganisms to familiar antibiotics. In Table 6, out of 85 samples, 71.76% showed resistance to ceftriaxone and 75.29% found resistance to ceftazidime which were mostly for *Pseudomonas spp., Escherichia coli, Acinetobacter spp.* and *Klebsiella spp. Klebsiella spp.* showed high resistance to ceftriaxone (82.21%) followed by ciprofloxacin (81.33%), levofloxacin (81.21%), gentamicin (71.22%), amikacin (70.18%), ceftazidime (42.39%), netilmicin (37.89%), cotrimoxazole (36.89%), Piperacillin+tazobactam (36.89%), Meropenem (32.63%) and colistin (0.00%) (Table 5). *Acinetobacter spp.* showed high resistant to ciprofloxacin (89.67%) followed by ceftazidime (78.17%), levofloxacin (77.17%), Meropenem (74.44%), gentamicin (72.33%), amikacin (64.67%), ceftriaxone (57.44%), colistin (41.67%), netilmicin (49.21%), cotrimoxazole (32.33%) and Piperacillin+tazobactam (31.50%) (Table 5). *Pseudomonas spp.* showed high resistant to ceftazidime (92.29%) followed by levofloxacin (77.17%), ceftriaxone (76.24%), ciprofloxacin (75.15%), Meropenem (73.29%), gentamicin (72.29%), cotrimoxazole (72.29%), amikacin (67.57%), netilmicin (43.75%) colistin (41.86%), and Piperacillin+tazobactam (24.72%) (Table 5). *E. coli* showed high resistant to ceftriaxone (84.71%) followed by gentamicin (83.71%), ceftazidime (81.1%), ciprofloxacin (80.14%), levofloxacin (76.57%), amikacin (69.43%), cotrimoxazole (55.14%), Meropenem (48.98%), netilmicin (26.57%), Piperacillin+tazobactam (20.43%) and colistin (0.00%) (Table 5). Meropenem was the most sensitive antibiotic against *Klebsiella spp.* (64.61%) and *Acinetobacter spp.* was found highly sensitive to cotrimoxazole (64.67%) and Piperacillin + tazobactam (60.50%) (Table 5). *Escherichia coli* was found greatly sensitive to netilmicin (70.48%) and meropenem (49.32%) where Pseudomonas spp. was mostly sensitive to colistin (55.14%) and netilmicin (52.25%).

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Table 5. Distribution of bacteria based on antimicrobial susceptibility (N total: 85).

Antibiotic drugs		*Pseudomonas spp.*	*E. coli*	*Acinetobacter*	*Klebsiella spp.*
Amikacin (N/%)	Sensitivity	9(28.41)	7(26.57)	7(29.33)	4(25.78)
	Resistance	22(67.57)	19(69.43)	15(64.67)	12(70.18)
Gentamicin (N/%)	Sensitivity	8(23.71)	3(15.29)	5(23.11)	4(26.78)
	Resistance	23(72.29)	21(83.71)	17(72.33)	12(71.22)
Netilmicin (N/%)	Sensitivity	17(52.25)	18(70.48)	11(48.99)	10(60.11)
	Resistance	15(43.75)	7(26.57)	11(49.21)	6(37.89)
Ciprofloxacin (N/%)	Sensitivity	7(20.85)	4(15.86)	2(7.33)	3(14.67)
	Resistance	25(75.15)	21(80.14)	20(89.67)	14(81.33)
Levofloxacin (N/%)	Sensitivity	12(39.32)	5(20.43)	4(19.83)	4(15.78)
	Resistance	20(59.22)	21(76.57)	18(77.17)	12(81.21)
Colistin (N/%)	Sensitivity	19(55.14)	0(00)	13(58.33)	0(00)
	Resistance	14(41.86)	0(00)	7(41.67)	0(00)
Cotrimoxazole (N/%)	Sensitivity	8(24.71)	10(41.86)	14(64.67)	10(60.11)
	Resistance	24(72.29)	14(55.14)	7(32.33)	6(36.89)
Piperacillin + tazobactam (N/%)	Sensitivity	24(73.28)	20(75.57)	14(60.50)	10(59.11)
	Resistance	8(24.72)	5(20.43)	8(31.50)	6(36.89)
Ceftriaxone (N/%)	Sensitivity	7(21.86)	3(13.29)	9(40.66)	2(15.67)
	Resistance	25(76.24)	23(84.71)	12(57.44)	13(82.21)
Ceftazidime (N/%)	Sensitivity	1(4.11)	4(16.85)	4(19.83)	9(53.55)
	Resistance	31(92.29)	21(81.15)	18(78.17)	6(42.39)
Meropenem (N/%)	Sensitivity	8(24.71)	12(49.32)	5(23.43)	10(64.61)
	Resistance	24(73.29)	12(48.98)	16(74.44)	5(32.63)

Table 6. The main microbes recovered from various samples and their antibiotic resistance patterns.

Antibiotics	Number	Percentage (%)
Gentamicin	70	82.35
Ciprofloxacin	67	78.82
Ceftazidime	64	75.29
Ceftriaxone	61	71.76
Levofloxacin	58	68.24
Amikacin	55	64.71
Meropenem	42	49.41
Netilmicin	35	41.18

Discussion

Since drug resistance, notably antimicrobial resistance, affects people worldwide, especially in impoverished nations, it is a global concern. The microbiology and epidemiology of infections in the ICU patients at IBN Sina Specialized Hospital are analyzed in this study. Aspiration pneumonia and diabetes mellitus are the two most prevalent disorders in this study; these findings are consistent with those of Kumari et al. (2007). Infections with gram-negative organisms and patterns of resistance have increased noticeably in recent years (Carlet et al, 2007). According to Bayram and Balci (2006), *Acinetobacter spp., Klebsiella spp., Pseudomonas spp.,* and *Escherichia coli* are the organisms that have shown to be the most harmful for patients in the intensive care unit. Gram-negative organisms including *Pseudomonas spp*. (30.59%), *Escherichia coli* (24.71%), *Acinetobacter spp.* (20%), and *Klebsiella spp.* (14.2%) were the most often isolated microorganisms from samples in our investigation; these results are consistent with a study conducted in a private hospital in Dhaka (Islam et al, 2014). *Acinetobacter spp.* have become significant ICU pathogens in recent years; the majority of these bacteria are resistant to gentamicin, ampicillin, carbenicillin, cefotaxime, and chloramphenicol

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(Kumari et al., 2007; Islam et al., 2014). Based on samples obtained from the tracheal aspirate, *Acinetobacter spp.* was found to be the primary cause of pneumonia in our study. It also demonstrates resistance to high concentrations of ciprofloxacin (89.67%). Other resistance markers that were found to be associated with this pathogen include ceftazidime (78.17%), levofloxacin (77.17%), Meropenem (74.44%), gentamicin (72.33%), amikacin (64.67%), ceftriaxone (57.44%), colistin (41.67%), netilmicin (49.21%), cotrimoxazole (32.33%), Piperacillin+tazobactam (31.50%). These results align with those of related research carried out in Bangladesh and India (Kumari et al, 2007; Islam et al, 2014; Jamshdi et al, 2009). *Acinetobacter spp.* in our study were sensitive to cotrimoxazole (64.67%) but resistant to meropenem (74.44%); Similar results were found in another Bangladeshi investigation (60 % sensitivity to cotrimoxazole and 79.3% resistance to meropenem). (Islam et al, 2014).

Nosocomial infections in intensive care units are frequently associated with gram-negative bacteria. Intensive Care Unit (ICU) samples are frequently used to identify Pseudomonas species, and data from a multicenter ISS in the United States revealed that these organisms are especially resistant to fluoroquinolones. (Friedland et al, 2004). In this investigation, 30.59% of the isolates of *Pseudomonas spp.* were from tracheal aspirate. *Pseudomonas spp.* exhibited high resistance to ceftazidime (92.29%) in this study, which is in close agreement with other studies conducted by Bayram and Balci (2006) and Islam et al. (2014). Following *Pseudomonas spp.*, there was high resistance to levofloxacin (77.17%), ceftriaxone (76.24%), ciprofloxacin (75.15%), Meropenem (73.29%), gentamicin (72.29%), cotrimoxazole (72.29%), amikacin (67.57%), netilmicin (43.75%), colistin (41.86%), and Piperacillin+tazobactam (24.72%).

Extended spectrum beta lactamase-producing *Klebsiella* spp. are another commonly observed resistant infection in intensive care unit (ICU) patients. (Jamshdi et al, 2009). A significant increase in ESBLs has resulted in multidrug-resistant *Escherichia coli* and *Klebsiella pneumonia*, making the choice of the best course of treatment challenging. Ceftriaxone (82.21%) was the most resistant antibiotic to which our isolates of *Klebsiella spp.* showed high resistance, followed by ciprofloxacin (81.33%), levofloxacin (81.21%), gentamicin (71.22%), amikacin (70.18%), ceftazidime (42.39%), netilmicin (37.89%), cotrimoxazole (36.89%), Piperacillin+tazobactam (36.89%), Meropenem (32.63%), and colistin (0.00%), but meropenem (64.61%) showed higher sensitivity. Once more, our results are strikingly comparable to those of a recent Dhaka study (Islam et al, 2014).

According to our observations, the most common pathogen found in UTI patients' samples was *Escherichia coli.* The results of earlier research (Islam et al., 2014; Islam, 2012) are comparable to this. *Escherichia coli* in the study by Islam et al. was resistant to ceftriaxone but completely sensitive to meropenem. *Escherichia* coli in our study exhibited strong resistance to ceftriaxone (84.71%), followed by gentamicin (83.71%), ceftazidime (81.1%), ciprofloxacin (80.14%), and levofloxacin (76.57%). However, Escherichia coli was largely responsive to piperacillin + tazobactam (75.57%) and netilmicin (70.48%). *Acinetobacter, E. coli, Klebsiella spp*, and *Pseudomonas spp* that are resistant to many drugs have added additional facets to the issue of infections linked to hospitals. It is hoped that the combination of piperacillin and tazobactam shown less than 40% resistance against these four species. The concerning problem is the *Acinetobacter spp.* infection, for which there was no effective antibiotic sensitivity.

Our findings have important therapeutic implications for the management of patients in intensive care units, particularly those with ventilator-associated pneumonia. First and foremost, doctors should be aware that patients with ventilator-associated pneumonia are likely to be infected with one of the three common bacteria, and that treatment resistance to numerous medications is a real risk. Second, the high rate of multidrug resistance shown in this study raises serious concerns about the management of patients in intensive care units. It recommends lowering antibiotic resistance rates more systematically and minimizing the use of broad-spectrum antibiotics. Third, when multidrug resistance is present, developing rapid diagnostic tools is essential for prompt targeted therapy. To optimize drug distribution and enable a more customized treatment plan, a drug monitoring system also needs to be implemented. Nonetheless, the study's benefits and drawbacks should be considered when interpreting the findings. The experiment included a well-characterized group of patients under close observation. Our capacity to look into a broad range of diseases and

antibiotic treatments has allowed us to fairly fully document the prevalence of antimicrobial resistance in ICU patients.

However, our study is subject to certain important limitations. The study is a one-center investigation with a small sample size. As such, the results may not be generalizable. Anaerobic cultures or cultures suitable for isolating the finicky microorganisms were not worked on. It is conceivable that certain antibiotics that are used less frequently yet are becoming important for treating patients concurrently were not included in the sensitivity testing. Moreover, the disc diffusion method was utilized to determine the antibiotic sensitivity instead of the broth dilution approach, which leaves out information on the lowest inhibitory concentration of antibiotics. Because the study was carried out at a tertiary hospital and the data only covered ICU patients, the findings might not correctly reflect community-acquired illnesses in Bangladesh. The study's tiny sample size prevented it from having the power to detect rare events or smaller effect sizes. It was unknown what specifically caused the infections and comorbidities. Furthermore, we did not thoroughly look into every aspect of our patients' care that might have resulted in the prescription of needless antibiotics.

Conclusion

The rapid emergence and spread of antibiotic-resistant bacteria is a global concern for intensive care units. These days, the number of organisms and their resistance to the medications that are currently available is gradually increasing. Gramme negative bacteria make up the bulk of antibiotic-resistant organisms. Commercially available antibiotics might not always be effective against frequently identified microorganisms. The results of culture and sensitivity testing must, if possible, be used to guide antibiotic selection. When using empirically, third-generation cephalosporins or carbapenems (such as meropenem) may be the best choice to begin with. Piperacillin + tazobactam and colomycin (colistin) should be stored for later use. Antibiotic stewardship programs and infection control policies are crucial parts of the overall strategy to reduce antibiotic resistance and improve the care of critically ill patients, since inappropriate antibiotic usage is known to be a major driver of resistance and there aren't many new drugs in the works. If not, we would quickly return to the pre-antibiotic era, when people would die from very minor ailments and simple infections would not be treated.

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