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RESEARCH ARTICLE

Isolation identification & antibiotic sensitivity of pus & tracheal aspirate isolates among tertiary hospital patients

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ABSTRACT

Background: The study aims to identify bacterial isolates and drug susceptibility patterns from patients with pus and wound discharge, addressing the issue of antibiotic resistance and the need for rational use in controlling infections. **Methods and Materials**: The cross sectional study at Bangladesh University of Health Sciences involved purposive sampling and Pus & tracheal aspirates from patients. It followed standard laboratory procedures for bacterial species identification and antimicrobial susceptibility testing using disk diffusion method following CLSI guidelines 2017. **Results:** This study examined 400 samples over a year, with most being pus (84%) and tracheal aspirate (16%). Males were predominant (56%), and gram-negative bacteria were predominant (74%). Staphylococcus aureus was the most sensitive to tigecycline (83%), followed by Meropenem & Doxycycline (67%), Gentamicin (58%), Cotrimoxaxole, Chloramphenicol & Colistin (42% each). Klebsiella pneumoniae were 100% sensitive to Meropenem, Ciprofloxacin & Tigecycline, and were 100% resistant to Cefotaxime, Cefixime & Cotrimoxazole. Escherichia coli were highly sensitive

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to Meropenem & Tigecycline, followed by Ceftazidime (69%), Gentamicin (63%), Ciprofloxacin & Colistin (62%), Doxycycline, Cefotoxime, Cefoxitin, Cotrimoxazole & Chloramphenicol (50%), Cefixime (31%), Amoxycillin (25%), and Ampicillin (24%). Staphylococcus aureus were most resistant to Vancomycin & Linezolid (75%). Multidrug resistance was found in 320 (80%) organisms in pus & tracheal aspirate**. Conclusion**: Multiple organisms were isolated from tracheal aspirate and pus, with most being multidrug resistant. The appropriate antibiotic for treatment should be chosen based on culture sensitivity.

Keywords: Extensively drug resistant (XDR); Multidrug resistant (MDR); Antibiotic; Gram Positive Bacteria; Gram Negative bacteria

1. Introduction

Infectious diseases are still a significant cause of morbidity and mortality among people, particularly in underdeveloped nations[1]. Various bacteria species exist on human skin, the gastrointestinal system, the nasopharynx, and other areas of the body, with reduced possibility for disease transmission due to the body's first line of defense[2]. Skin abrasion caused by surgical procedures, trauma, burns, illnesses, diet, and other factors affects this first line defense and leads to microbial contamination, resulting in infections[3]. Wound infections are predominantly hospital acquired, and the infecting bacteria vary not only from nation to country, but even from one hospital to another within the same country[4].

The problem of hospital acquired infection remains a serious health hazard worldwide. As described by World Health Organization (WHO), it is one of the major sources of infectious diseases which results for the huge economic impact with significant rate of morbidity and mortality[5]. Despite advances in control of infections, wound infections have not completely been prevented due to the problem of drug resistance[6]. Antibiotics' extensive use, combined with the length of time they have been available, has resulted in serious problems of resistant organisms contributing to illness and mortality[7]. Knowledge of the causative agents of wound infection has proven to be helpful in the selection of appropriate antimicrobial therapy and on infection control measures taken in health institutions[8]. The human skin and soft tissue infections (SSTIs) caused by microbial pathogens during or after trauma, burn injuries, and surgical procedures result in the production of pus, a white to yellow fluid comprised of dead WBCs, cellular debris, and necrotic tissues[9].

The intensive care unit (ICU) is sometimes referred to as the infection epicenter because to its particularly vulnerable population of weakened host defenses, deregulated immunological responses, and higher risk of infection from many procedures. The use of invasive technologies, such as intubation, mechanical breathing, and vascular access, disrupts the anatomical integrity and protective barriers of patients. Administration of several drugs (sedatives, muscle relaxants) also predispose for infections by reducing the cough and swallow reflexes or by distorting the normal non-pathogenic bacterial flora[10]. Both aerobic and anaerobic bacteria have been implicated in wound infections which commonly occur under hospital environment and result in significant morbidity, prolonged hospitalization, and huge economic burden[11]. The emergence of antibiotic resistance and its rapid spread among pathogenic bacterial isolates are considered as grave threats to the public health worldwide[13]. During the last few decades, multidrug-resistant Gram-negative bacterial strains such as *Acinetobacter baumannii, E. coli, Klebsiella pneumoniae, Pseudomonas aeruginosa*, and Gram-positive methicillin-resistant *Staphylococcus aureus* (MRSA) were increasingly associated with pus infections under hospital settings due to extensive mis prescription and inadequate dose regimen of antibiotics[14]. The rapid growth of multidrug-resistant bacteria poses a severe danger to global public health due to restricted treatment choices and the slow identification of new antibiotic classes[15]. The majority of nosocomial infections occur in intensive care units (ICUs) and are associated with increased death and morbidity rates[16,17]. Despite significant advancements in infection

control, wound and respiratory infections, particularly those associated with pus and tracheal aspirates, continue to pose major challenges in healthcare settings. The increasing prevalence of antibiotic-resistant bacteria, fueled by the widespread and often inappropriate use of antibiotics, has become a critical issue, leading to increased morbidity, prolonged hospital stays, and higher mortality rates. The rise of multidrug-resistant (MDR) bacteria exacerbates the difficulty of managing infections, especially in tertiary care hospitals where patients are often critically ill.

It is vital to understand the bacterial profile and antibiotic sensitivity patterns of pathogens isolated from these infections to guide appropriate antibiotic use and curb the growing problem of antimicrobial resistance. This study aims to fill this gap by identifying the bacterial isolates from pus and tracheal aspirates and analyzing their drug susceptibility, providing valuable insights for effective infection management and antibiotic stewardship. Aim of the study to investigate the bacterial isolates from pus and tracheal aspirate samples and assess their antibiotic sensitivity patterns in patients at a tertiary hospital, aiming to improve infection management and contribute to the control of antibiotic resistance.

2. Materials and methods

Study setting and study population:

This study was conducted in the Department of Microbiology at Bangladesh University of Health Sciences (BUHS) Mirpur-1, Dhaka. Patients attending outdoor & indoor at BIHS General Hospital, Mirpur-1, Dhaka. Sample was collected by purposive sampling techniques. Pus & tracheal aspirates were collected from patients attending inpatients and outpatients.

Study design and period:

This study was designed as Hospital based descriptive cross-sectional study. This study was carried out from June 2022 to May 2023 for a period of 12 months.

Inclusion criteria:

1. Clinical Presentation: Patients presenting with clinical signs of infection who had pus or tracheal aspirate samples collected for microbiological analysis.
2. Age and Gender: Patients aged 18 years and above, regardless of gender, admitted to or attending outpatient services at the BIHS General Hospital.
3. Consent: Patients willing to provide informed written consent and participate in the study.
4. Bacterial Growth: Patients whose samples (pus or tracheal aspirates) yielded bacterial growth on culture.

Exclusion criteria:

1. Negative Cultures: Patients whose pus or tracheal aspirate samples showed no bacterial growth on culture.
2. Recent Antibiotic Use: Patients with a history of antibiotic use within the 48 hours prior to sample collection, which could interfere with the culture results.
3. Chronic Non-Infectious Diseases: Patients with chronic, non-infectious diseases that do not involve bacterial infections, such as autoimmune disorders or cancer, unless there is an active bacterial infection.

4. Severely Ill Patients: Severely ill patients in critical care units who were unable to give consent or participate in the study.
5. Non-Compliance: Patients unwilling to provide written consent or unable to comply with study procedures.

Sample processing

Upon collection, all pus and tracheal aspirate samples were subjected to standard laboratory processing protocols. Each sample underwent a thorough microscopic inspection to assess cellular morphology and the presence of any bacteria. Subsequently, relevant biochemical testing was performed to aid in the identification of bacterial isolates. Colony morphology, including size, shape, and pigmentation, was observed on various culture media, particularly MacConkey agar, which is utilized to differentiate lactose fermenters from non-lactose fermenters.

Identification tests

The identification of bacterial isolates was conducted through a series of biochemical tests. Observations of colony color on MacConkey agar helped identify non-lactose fermenting pale colonies. Additional tests included assessments of motility and the oxidase reaction, with positive results indicating certain types of bacteria. Various fermentation tests, such as the Indole test, Methyl red test, Citrate test, and Urease test, were performed to ascertain the biochemical characteristics of the isolates. Additionally, triple sugar iron agar tests, arginine dihydrolase activity tests, nitrate reduction tests, and the ability to produce bluish-green pigmentation were also employed to confirm the identity of the isolates accurately[18].

Antimicrobial susceptibility testing

Antimicrobial susceptibility of the identified bacterial isolates was evaluated using the disk diffusion method in accordance with CLSI guidelines. This involved applying antibiotic discs to agar plates inoculated with the bacterial isolates. The following antibiotics were tested along with their respective concentrations: Ampicillin (10 µg), Gentamicin (10 µg), Meropenem (10 µg), Doxycycline (10 µg), Ceftazidime (30 µg), Ciprofloxacin (5 µg), Chloramphenicol (30 µg), Cefotaxime (30 µg), Azithromycin (15 µg), Vancomycin (30 µg), Clindamycin (10 µg), Linezolid (30 µg), Amoxicillin (30 µg), Cefoxitin (30 µg), Tigecycline (15 µg), and Colistin (10 µg)[19]. The zones of inhibition around each disc were measured to determine the susceptibility or resistance of the isolates to these antibiotics, providing critical insights into the antimicrobial resistance patterns present in the samples.

Statistical analysis

Data were collected, compiled and tabulated according to key variables and functional assessment scoring. The analysis of different variables was done according to standard statistical analysis. Quantitative data were expressed as frequency & percentage and quantitative data were expressed as mean & standard deviation. Quantitative data were analyzed by student t-test and qualitative data by chi-square test. Data were processed and analyzed using software Statistical Package for Social Science (SPSS) version 20. For all analyses level of significance was set at 0.05 and p-value <0.05 was considered significant.

3. Results

A total of 400 samples were examined in this study during this one year. **Table 1** showed the proportion of samples. Most of the specimens were pus 336 (84%) followed by tracheal aspirate 64 (16%). Male were predominant in study 224 (56%) followed by female 176 (44%).

Table 1. Demographic information of study subjects (n=400).

Variable	Frequency	Percentage (%)
Gender		
Male	224	56
Female	176	44
Proportion of Pus and tracheal aspirate in the study		
Pus	336	84
Tracheal Aspirate	64	16

Table 2. Morphological Identification of Bacterial Isolates from Pus and Tracheal Aspirate Samples.

Bacterial Species	Gram Stain	Morphological Characteristics	Colony Appearance on Culture Media
Staphylococcus aureus	Gram-positive	Cocci in clusters	Golden-yellow colonies on nutrient agar
Staphylococcus saprophyticus	Gram-positive	Cocci in clusters	Smaller, white colonies on nutrient agar
Pseudomonas aeruginosa	Gram-negative	Rods	Pale, translucent colonies with greenish pigmentation (pyocyanin) on MacConkey agar
Klebsiella pneumoniae	Gram-negative	Rods	Large, mucoid, lactose-fermenting, pink colonies on MacConkey agar
Escherichia coli	Gram-negative	Rods	Pink lactose-fermenting colonies (dry) on MacConkey agar
Acinetobacter species	Gram-negative	Rods	Small, pale, non-lactose fermenting colonies on MacConkey agar
Proteus species	Gram-negative	Rods; characteristic swarming motility	Non-lactose fermenting colonies on MacConkey agar

Table 2 summarizes the morphological identification of bacterial isolates obtained from pus and tracheal aspirate samples, based on Gram staining and colony characteristics on selective culture media. *Staphylococcus aureus* and *Staphylococcus saprophyticus* are both Gram-positive cocci, distinguished by colony colors on nutrient agar—*S. aureus* forms golden-yellow colonies, while *S. saprophyticus* produces smaller, white colonies. In contrast, *Pseudomonas aeruginosa* is identified as a Gram-negative rod, characterized by pale, translucent colonies with distinctive greenish pigmentation due to pyocyanin production on MacConkey agar. Similarly, *Klebsiella pneumoniae* and *Escherichia coli* are Gram-negative rods, with *K. pneumoniae* forming large, mucoid, pink colonies from lactose fermentation, whereas *E. coli* produces pink, typically dry colonies. Acinetobacter species appear as small, pale, non-lactose fermenting colonies on MacConkey agar, also categorized as Gram-negative rods. Lastly**,** Proteus species are noted for their characteristic swarming motility and form non-lactose fermenting colonies on MacConkey agar, further classified as Gram-negative rods.

Tables 3 showed the distribution of bacteria in study population according to gram stain. Out of 400, gram negative bacteria were predominant 296 (74%) followed by gram positive bacteria 104 (26%). Out of 104 (26%) gram positive bacteria, *Staphylococcus aureus* was 96 (92.3%) followed by *Staphylococcus saprophyticus* was 8 (7.7%). Out of 296 (74%) gram negative bacteria, *Pseudomonas aeruginosa* was 96 (32.4%), followed by *Klebsiella pneumoniae* 80 (27.1%), *Escherichia coli* 64 (21.6%), Acinetobacter species 32 (10.8%), *Proteus vulgaris* 16 (5.4%) and *Proteus mirabilis* 08 (2.7%).

Table 3. Distribution of bacteria according to gram stain in study population (n=400).

Type	Name of organism	Frequency	Percentage (%)
Gram positive n=104 (26%)	• *Staphylococcus aureus*	96	92.3
	• *Staphylococcus saprophyticus*	08	7.7
Gram negative n=296 (74%)	• *Pseudomonas sp.*	96	32.4
	• *Klebsiella pneumoniae*	80	27.1
	• *Escherichia coli*	64	21.6
	• *Acinetobacter sp.*	32	10.8
	• *Proteus vulgaris*	16	5.4
	• *Proteus mirabilis*	08	2.7

Pseudomonas aeruginosa, *Klebsiella pneumoniae*, *Escherichia coli*, *Staphylococcus aureus*, *Acinetobacter sp*, and *Proteus mirabilis* were all found to be sensitive to various antibiotics in their tracheal aspirate. *Pseudomonas aeruginosa* was most sensitive to tigecycline (83%), followed by Meropenem & Doxycycline (67%), Gentamicin (58%), Cotrimoxaxole, Chloramphenicol & Colistin (42% each). *Klebsiella pneumoniae* were 100% sensitive to Meropenem, Ciprofloxacin & Tigecycline, and were 100% resistant to Cefotaxime, Cefixime & Cotrimoxazole. Escherichia coli was also highly sensitive to Meropenem & Tigecycline, followed by Ceftazidime (69%), Gentamicin (63%), Ciprofloxacin & Colistin (62%), Doxycycline, Cefotoxime, Cefoxitin, Cotrimoxazole & Chloramphenicol (50%), Cefixime (31%), Amoxycillin (25%), and Ampicillin (24%) (**Table 4a**). Staphylococcus aureus was most resistant to Vancomycin & Linezolid (75%), followed by Chloramphenicol (67%), Meropenem & Doxycycline (64%), Gentamicin, Azithromycine & Clindamycin (58%), Cefotaxime & Cefoxitin (50%), Ceftazidime & Ciprofloxacin (42%), Amoxycillin (34%), and Ampicillin (25%) (**Table 4b**).

Table 4(a). Antibiotic sensitivity pattern of Gram-negative bacteria (n=296).

SI	Antibiotics	*Pseudomonas aeruginosa*		*klebsiella pneumoniae*		*Escherichia coli*		*Acinetobacter sp*	*Proteus mirabilis*	*Proteus Vulgaris*
		Pus (n=88)	Tracheal aspirate (n=8)	Pus (n=64)	Tracheal aspirate (n=16)	Pus (n=48)	Tracheal aspirate (n=16)	Pus (32)	Pus (08)	Pus (16)
1	Ampicillin	17%	0%	30%	50%	24%	0%	25%	0%	0%
2	Gentamicin	58%	0%	70%	50%	63%	0%	75%	100%	50%
3	Meropenem	67%	0%	90%	100%	75%	50%	75%	100%	100%
4	Doxycycline	67%	0%	60%	50%	50%	0%	50%	0%	50%
5	Amoxycillin	17%	0%	50%	50%	25%	0%	25%	0%	0%
6	Cefotaxime	17%	0%	70%	100%	50%	0%	25%	100%	50%
7	Ceftazidime	17%	0%	60%	50%	69%	0%	25%	100%	50%
8	Cefoxitin	17%	0%	50%	0%	50%	0%	75%	100%	50%
9	Cefixime	8%	100%	40%	0%	31%	0%	25%	100%	0%
10	Cotrimoxazole	42%	0%	40%	0%	50%	100%	25%	0%	50%
11	Chloramphenicol	42%	0%	50%	50%	50%	0%	50%	0%	50%
12	Ciprofloxacin	17%	0%	50%	50%	62%	0%	50%	100%	50%
13	Tigecycline	83%	0%	70%	100%	75%	50%	75%	100%	100%
14	Colistin	42%	100%	60%	50%	62%	100%	25%	0%	50%

Table 4(b). Antibiotic sensitivity pattern of Gram-positive bacteria (n=104).

SI	Antibiotics	*Staphylococcus aureus*		*Staphylococcus Saprophyticus*
		Pus (n=80)	Tracheal aspirate (n=16)	Tracheal aspirate (08)
1	Ampicillin	25%	0%	0%
2	Gentamicin	58%	50%	0%
3	Meropenem	64%	50%	0%
4	Doxycycline	64%	0%	0%
5	Amoxycillin	42%	0%	0%
6	Cefotaxime	42%	0%	0%
7	Ceftazidime	67%	0%	0%
8	Cefoxitin	50%	0%	0%
9	Cefixime	58%	50%	0%
10	Cotrimoxazole	75%	50%	0%
11	Chloramphenicol	58%	0%	0%
12	Ciprofloxacin	75%	0%	0%
13	Tigecycline	34%	0%	0%
14	Colistin	50%	0%	0%

Table 5 showed the proportion of microorganisms isolated from pus & tracheal aspirate. Seven organism were isolated from pus sample of which *Pseudomonas aeruginosa* (88) were predominant followed by *Staphylococcus aureus (80), Klebsiella pneumonia (64), Escherichia coli (48), Acinetobacter sp (32), Proteus vulgaris (16), Proteus mirabilis (8).* And 5 organisms were isolated in tracheal aspirate sample such as *Pseudomonas aeruginosa* (8), *Staphylococcus aureus (16), Klebsiella pneumonia (16), Escherichia coli (16), Staphylococcus saprophyticus (8).*

Table 5. Proportion of microorganisms isolated from pus and Tracheal aspirate.

S. No	Organisms	Pus	Tracheal aspirate
1	*Pseudomonas aeruginosa*	88	8
2	*Staphylococcus aureus*	80	16
3	*Klebsiella pneumoniae*	64	16
4	*Escherichia coli*	48	16
5	*Acinetobacter sp*	32	-
6	*Proteus vulgaris*	16	-
7	*Proteus mirabilis*	8	-
8	*Staphylococcus saprophyticus*	_	8

Table 6 showed proportion of enzymes responsible for multidrug resistance. ESBl was singly positive in 64 (16%) cases, AmpC BL singly in 88 (22%), Carpenemase singly in 96 (24%) cases. ESBL & AmpC BL jointly in 40 (10%)cases. ESBL and Carbapenemase jointly in 48 (12%) cases. Amp C BL and Carbapenemase jointly in 64 (16%) cases.

Table 6. Proportion of Enzymes Responsible for Multidrug Resistance (n=400).

Type of Resistance	Frequency	Percentage (%)
Extended-Spectrum Beta-Lactamase (ESBL) only	64	16%
AmpC Beta-Lactamase only	88	22%
Carbapenemase only	96	24%
ESBL + AmpC Beta-Lactamase	40	10%
ESBL + Carbapenemase	48	12%
AmpC Beta-Lactamase + Carbapenemase	64	16%

Table 7 presents the distribution of bacterial isolates exhibiting different levels of antibiotic resistance among pus and tracheal aspirate samples. Multidrug Resistant (MDR) organisms, which are resistant to multiple antibiotics but not all, accounted for 320 cases (80%). Extensively Drug Resistant (XDR) organisms, resistant to all but a limited number of antibiotics, comprised 40 cases (10%). Finally, Pandrug Resistant (PDR) organisms, which are resistant to all available antibiotics, also represented 40 cases (10%). This highlights the significant prevalence of antibiotic resistance among the isolates in the study.

Table 7. Proportion of Multidrug Resistant (MDR), Extensively Drug Resistant (XDR), and Pandrug Resistant (PDR) Organisms.

Type of Resistance	Frequency	Percentage (%)
Multidrug Resistant (MDR)	320	80
Extensively Drug Resistant (XDR)	40	10
Pandrug Resistant (PDR)	40	10

5. Discussion

Infections remain a leading cause of morbidity and mortality in intensive care units (ICUs), particularly among patients with endotracheal tubes. The use of invasive devices such as intubation and mechanical ventilation compromises the anatomical integrity of patients, increasing the risk of infections. An international study conducted in 2007 revealed that patients with prolonged ICU stays exhibited higher rates of infections caused by resistant organisms, including *Staphylococci*, *Acinetobacter*, *Pseudomonas species*, and *Candida species*[20,21].

A recent analysis in India focused on aerobic bacteria isolated from endotracheal secretions of mechanically ventilated patients, highlighting the antibiotic sensitivity and prevalence of multidrug resistance. Pyogenic infections, characterized by pus production, can involve both aerobic and anaerobic bacterial species[23]. The likelihood of wound infections is influenced by local wound conditions, microbial burden, and host defenses. A comprehensive understanding of the causative pathogens, the pathophysiology of the infectious process, and the pharmacological properties of therapeutic agents is essential for effective treatment[24].

Multidrug-resistant organisms continue to pose significant challenges in hospital settings, contributing to the rise of hospital-acquired infections. The antibiotic pipeline is dwindling, emphasizing the need to reserve potent antibiotics such as carbapenems for treating these resistant organisms[25]. The present study provides valuable insights into the bacterial profile of wound infections and their antibiotic sensitivity patterns, which are crucial for guiding empirical treatment while awaiting culture results.

Some studies concluded that collected a total of 400 samples, predominantly pus (336 samples) and tracheal aspirate (64 samples)[26,27,28]. Male patients were more frequently affected, as noted in the studies by

Batra et al[3]. and Rakshit[29], with Othman[30] reporting a male predominance of 66.7%. All collected samples were culture-positive, with gram-positive bacteria accounting for 26% and gram-negative bacteria for 74%. In contrast, Othman[30] observed a higher prevalence of gram-negative bacteria (90.5%). Strausbaugh[31] found that out of 101 positive cultures, 52.5% were gram-negative, while Rai [13] reported gram-positive bacteria as 61%.

Among the 104 gram-positive cocci isolated, Staphylococcus aureus was the predominant species, followed by *Staphylococcus saprophyticus*. Other studies reported similar findings, with S. aureus constituting 62.5% of the isolates[32]. In Othman [30] study, *A. baumannii* (36.5%), *K. pneumoniae* (21.5%), and *P. aeruginosa* (16.2%) were identified as the most prevalent gram-negative bacteria.

In terms of antibiotic sensitivity, *Pseudomonas aeruginosa* demonstrated high sensitivity to tigecycline (83%) and meropenem (67%), while exhibiting the least sensitivity to ampicillin, amoxicillin, cefotaxime, and ciprofloxacin (17% each). *Klebsiella pneumoniae* showed a sensitivity of 90% to meropenem, whereas E. coli was sensitive to meropenem and tigecycline at 75%. *S. aureus* was notably sensitive to vancomycin and linezolid (75%), while Acinetobacter species showed substantial sensitivity to meropenem, gentamicin, and tigecycline (75% each).

The present study identified 320 organisms as multidrug resistant (MDR), with 40 exhibiting extensively drug resistance (XDR) and 40 being pan drug resistant (PDR). Previous studies have reported similar trends, with Sinleton[33] finding that 76% of isolated bacteria were MDR, while Tenaillon (2010)[34] reported MDR in 68.5% of isolates.

Furthermore, the study identified various β-lactamase producers, with extended-spectrum β-lactamase (ESBL) detected in 64 cases (16%), AmpC β-lactamase in 88 cases (22%), and carbapenemase in 96 cases (24%). Joint production of these enzymes was observed in some isolates, underlining the complexity of antibiotic resistance mechanisms in clinical settings.

6. Conclusion

This research highlights the significant prevalence of multidrug-resistant organisms in pus and tracheal aspirate samples from patients in a tertiary care setting, underscoring the urgent need for effective antimicrobial stewardship and robust infection control measures in healthcare facilities. The predominant isolation of gram-negative bacteria, particularly *Pseudomonas aeruginosa, Klebsiella pneumoniae*, and *Acinetobacter* species, emphasizes their critical role in hospital-acquired infections and the necessity for tailored empirical therapies while awaiting microbiological results, especially in the context of invasive procedures in intensive care units. Additionally, the identification of various β-lactamase producers complicates treatment approaches, highlighting the importance of understanding the mechanisms of antibiotic resistance. Overall, this study contributes valuable insights into the rising challenge of antibiotic resistance, emphasizing the need for continuous surveillance and collaborative efforts to mitigate its impact on patient care and healthcare delivery systems.

Conflict of interest

The authors declare no conflict of interest.

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