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Incidence of Multi-Drug Resistant Organisms in Trauma and Surgical Intensive Care Units at Beni-Suef University Hospital: A Comparative Analysis

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Hospital acquired infections caused by multi-drug resistant organisms are a significant health risk in Trauma and Surgical Intensive Care Units (TICU and SICU), leading to increased morbidity, mortality, and healthcare costs. The rise of multidrug-resistant (MDR) organisms exacerbates these challenges, making effective infection control and antimicrobial stewardship critical for improving patient outcomes. This study aimed to investigate the microbial epidemiology and prevalence of multidrug-resistant (MDR) organisms in the Trauma and Surgical Intensive Care Units (TICU and SICU) at Beni-Suef University Hospital, with the goal of guiding targeted infection control strategies and enhancing antimicrobial stewardship efforts. A cross-sectional study was conducted over a seven-month period from September 2023 to February 2024, involving 140 patients admitted to the TICU and SICU. Clinical specimens, including blood, sputum, and urine samples, were collected and analyzed using standard microbiological methods. Microbial identification was performed through traditional culturing techniques, microscopic examination, and biochemical tests, with further verification using automated identification systems. Antimicrobial susceptibility testing was conducted following the guidelines of the Clinical and Laboratory Standards Institute (CLSI). A total of 117 isolates were obtained from 140 patients, with 88.89% identified as multidrug-resistant organisms (MDROs). A significant statistical difference was observed in the occurrence frequencies of these organisms between TICU and SICU ($p < 0.05$). The predominant bacterial pathogens included Klebsiella pneumoniae (54 isolates; 46.15% of all isolates), Pseudomonas aeruginosa (14 isolates; 11.97%), and Escherichia coli (8 isolates; 6.84%). Fungal pathogens, including Candida albicans and Aspergillus spp., were also identified. Notably, MDR strains were prevalent in Acinetobacter baumannii (5.13% of all isolates), Pseudomonas aeruginosa (11.97%), and Klebsiella pneumoniae (30.77%), highlighting the escalating threat of antibiotic resistance. The study underscores a consistent microbial burden across TICU and SICU, with variations in the frequency of specific organisms. These findings highlight the urgent need for targeted infection control measures and robust antimicrobial stewardship programs to combat the rising threat of MDR organisms. Future research should focus on developing strategies to mitigate the impact of these pathogens on patient outcomes.

Keywords: Antibiotic resistance; Hospital acquired; Multidrug-resistant Organisms (MDROs); Surgical; Trauma.

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Healthcare-associated infections (HCAIs) remain a significant and persistent challenge in hospital environments, particularly in trauma and surgical units. These units are especially vulnerable due to the invasive nature of procedures and the compromised health status of many patients. Traumatic and surgical patients are at a higher risk of developing infections due to factors such as the disruption of natural barriers, prolonged hospitalization, and exposure to multidrug-resistant organisms (MDROs)[1].

MDROs are a group of bacteria that have developed resistance to multiple classes of antibiotics, making them extremely difficult to treat and posing a serious threat to patient safety [2]. Their rise and dissemination are largely attributed to the overuse and misuse of antibiotics, insufficient infection prevention and control measures, and extended hospital stays. While fungi are not typically classified as MDROs, they can develop resistance to antifungal medications, referred to as multidrug-resistant fungi. Examples include *Candida* species, *Aspergillus* species, and *Penicillium* species. Multidrug-resistant fungi also present challenges, particularly in immunocompromised patients, requiring alternative treatment strategies.

In surgical units, the risk of MDRO transmission is exacerbated by the frequent use of invasive devices, surgical interventions, and prolonged antibiotic prophylaxis[3]. Moreover, surgical patients often have underlying health conditions and multiple comorbidities, making them more susceptible to infections and complications. The implications of MDRO infections in surgical patients are serious, leading to increased morbidity, mortality, and healthcare costs. This underscores the urgent need for comprehensive surveillance, research, and targeted interventions.

Trauma continues to be a major global health issue, contributing significantly to mortality and morbidity[4]. It accounts for approximately 9% of global deaths, with nearly 100 million people suffering temporary or permanent disabilities annually[5]. In Egypt, injury-related morbidity and mortality are on the rise, with road traffic accidents being a predominant cause[6]. Research has shown that trauma care delivered in high-volume, specialized level-one trauma centers leads to improved patient outcomes. Managing critically injured trauma patients in specialized TICUs has been associated with enhanced outcomes, especially for patients with multiple injuries and traumatic brain injury (TBI)[7].

The Surgical Intensive Care Unit (SICU) is a vital component of modern healthcare, providing specialized care for patients requiring close monitoring and advanced medical interventions due to critical illness or injury[8]. Staffed by a multidisciplinary team, the SICU aims to stabilize and treat patients with complex medical conditions that threaten vital organ systems. This unit is essential in managing diverse medical emergencies and post-operative care needs, striving to optimize patient outcomes and improve survival rates[9].

Therefore, this study aims to investigate the frequency and characteristics of MDROs in the trauma and surgical units at Beni-Suef University Hospital. By identifying patterns of MDRO prevalence, associated risk factors, and antimicrobial resistance profiles, this research seeks to inform and guide evidence-based interventions that can mitigate the spread of antibiotic resistance and enhance the quality of care for trauma and surgical patients.

MATERIALS AND METHODS

The current study is a cross-sectional investigation involving 140 patients admitted to SICU (70) and SICU (70 patients) of Beni-Suef University Hospital for 7 months, from September 2023 to February 2024. Inclusion criteria encompassed trauma patients admitted to the TICU and SICU at the time of the study, aged between 18 and 80 years, and suspected of having infections. Detailed medical histories were obtained, focusing on risk factors for MDROs, along with comprehensive clinical examinations. Patients were continuously monitored throughout their entire ICU stay. The enrolled cases were classified into two sets built on their site of admission: SICU patients with no growth, cases with MDR organisms, and non-MDR organisms, as determined by the susceptibility patterns of the isolated organisms.

Specimen collection

Blood samples were obtained for C-reactive protein (CRP), complete blood count (CBC), and blood cultures (Figure 1). Sputum (or deep tracheal aspirate) and urine samples were collected from suspected cases under strictly aseptic conditions.

Specimen processing

All samples received at the clinical microbiology laboratory underwent culture and identification. The identification of isolates was verified at the Medical Microbiology Laboratory, Faculty of Medicine, Beni-Suef University, utilizing a range of traditional methods, such as culturing on selective media, analyzing colony morphology, conducting microscopic examinations, and performing biochemical tests. Further molecular identification was performed using automated identification systems (Macrogen, Korea) as showed in Figure 1.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing of all bacterial, and fungal isolates was conducted using the Kirby-Bauer disc diffusion method on Mueller-Hinton agar and Sabouraud Dextrose Agar (Oxoid, Basingstoke, UK), following the guidelines of the Clinical and Laboratory Standards Institute (CLSI)[10]. A range of commonly used antibiotic classes, including penicillins, tetracyclines, cephalosporins, quinolones, lincomycins, macrolides, sulfonamides, glycopeptide antibiotics, aminoglycosides, carbapenems, and oxazolidinones, were tested. For instance: ampicillin (10µg), oxacillin (1µg), amoxicillin-clavulanic acid (30µg), cefoxitin (30µg), cefotaxime (30µg), ceftriaxone (30µg), ceftazidime (30µg), imipenem (10µg), vancomycin (30µg), gentamicin (10µg), amikacin (30µg), erythromycin (15µg), azithromycin (15µg), ciprofloxacin (5µg), and norfloxacin (10µg). For *Staphylococcus aureus* (*S. aureus*), methicillin resistance was identified using the cefoxitin disk test (30 µg; Bio-Rad, Marnes-La-Coquette, France), as per CLSI recommendations[11]. Methicillin resistance in Coagulase-negative Staphylococci (CONS) was determined by the growth of isolates on trypticase soy agar plates containing 6 µg of oxacillin per mL plus 4% NaCl[12]. All Gram-negative isolates were screened for extended-spectrum â-lactamase (ESBL) activity using the double-disk approximation test[13]. For yeast and fungal isolates, CLSI M44A guidelines were followed for fluconazole, voriconazole, ketoconazole, amphotericin-B, and itraconazole[14]. Isolates were classified as Multidrug Resistant (MDR) when they exhibited resistance to three or more antimicrobial classes[15].

Ethical consideration

Informed written consent was obtained from the patients before enrollment. The study design was reviewed and approved by the Scientific Research Committee of the Community Department, Faculty of Medicine, Beni Suef University.

Statistical analysis

Data was analyzed using IBM SPSS (version 23.0; Chicago, Illinois, USA). Quantitative parametric measures were presented as Mean ± SD, quantitative non-parametric measures as Minimum and Maximum, and data as both number and percentage. The statistical tests employed across the tables included the Student t-test for comparing two independent mean groups for parametric data, the Mann-Whitney test for comparing two independent groups for non-parametric data, and the Chi-square test to examine associations between variables or comparing two independent groups for categorized data. A probability of error at 0.05 was considered significant, while values at 0.01 and 0.001 were deemed highly significant.

RESULTS

Demographic Characteristics and Susceptibility to Nosocomial Infections among Patients admitted to TICU and SICU

The study comprised 140 patients, with 70 patients admitted to TICU and 70 to SICU. Table 1 provides a comprehensive overview of the demographic characteristics of patients who acquired nosocomial infections during their stay at the Trauma and Surgical Intensive Care Units. Out of the 140 patients analyzed, the 18-29 age group was the most prominently affected, comprising 36.42% (51 patients) of the total. Within this age bracket, males accounted for a significant 64.28% (90 patients), while females represented 35.71% (50 patients). The subsequent age categories showed smaller representation, with 30-39 years constituting 7.86% (11 patients), 40-49 years at 6.43% (9 patients), 50-59 years at 21.43% (30 patients), 60-69 years at 15.71% (22 patients), 70-79 years at 8.57% (12 patients), and those aged 80 and above at 3.57% (5 patients). The data underscores that younger patients, particularly males in the 18-29 age range, were more susceptible to acquiring nosocomial infections during their trauma and surgical intensive care units admission.

Distribution of microorganisms in clinical specimens

Culture results from various specimens revealed 117 isolates from 140 patients, representing 83.58% of the cases. The majority of the isolated organisms were from sputum samples (50/117, 42.73%). Table 2 and Figure 2 represents a comprehensive examination of clinical specimens that revealed a diverse distribution of microorganisms. The most prevalent organism isolated from the specimens was *K. pneumoniae*, with a total count of 54 isolates. This bacterium was predominantly found in sputum samples, accounting for 57.41% of its total presence. In blood and urine specimens, *K. pneumoniae* represented 16.66% and 25.92%, respectively. *C. albicans*, a common fungal pathogen, was identified in 6 isolates across the specimens. Sputum samples had the highest count of this organism, making up 50% of its total occurrence, followed by urine (33.33%) and blood (16.66%). *P. aeruginosa* was another notable bacterium, with 14 isolates in total. It was predominantly found in sputum samples, contributing to 50% of its total presence, while in blood and urine, it constituted 14.28% and 35.71%, respectively. *E. coli*, a

Table 1. Demographic information on patients who have acquired nosocomial infections

Age (in years)	Number	%	Male (n, %)	Female (n, %)
18-29	51	36.42	90 (64.28)	50 (35.71)
30-39	11	7.86		
40-49	9	6.43		
50-59	30	21.43		
60-69	22	15.71		
70-79	12	8.57		
80+	5	3.57		
Total	140	100		

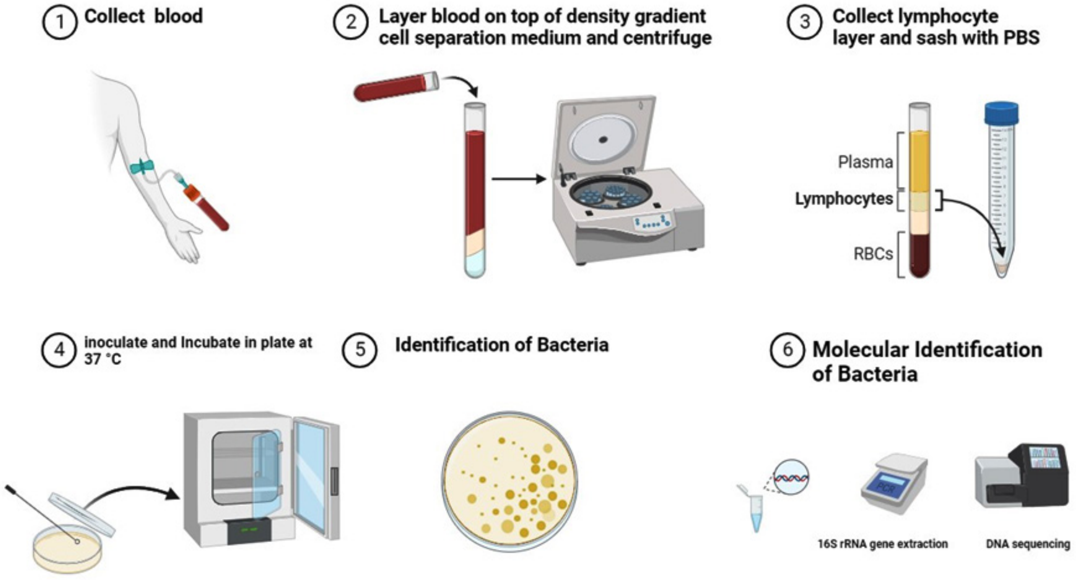

Fig. 1. Blood samples collection and identification

common gastrointestinal bacterium, was detected in 8 specimens. Interestingly, it was predominantly found in urine samples, accounting for a significant 62.50% of its total presence. In blood, it represented 37.50% of its occurrence. *S. aureus (MRSA)* and *Enterobacter sp.* both had 4 isolates each. *S. aureus* (MRSA) was evenly distributed across blood, sputum, and urine, whereas *Enterobacter sp.* was more prevalent in urine, accounting for 50% of its total presence. *A. baumanni* was identified in 6 specimens, all of which were from sputum samples, making up 66.66% of its total presence. *S. pneumoniae* accounted for 13 isolates and was predominantly found in blood samples (61.53%), followed by urine (30.76%) and sputum (7.69%). Lastly, *Aspergillus* and *Fusarium* fungi were identified in 4 and 2 specimens, respectively. *Aspergillus* was evenly distributed across blood, sputum, and urine, while *Fusarium* was found in both blood and sputum samples.

Differential antibiotic resistance patterns among microbial species

The comparative analysis of the frequency of Multi-Drug Resistant (MDR) and non-MDR organisms revealed notable differences across the examined microbial species (Table 3). The comparative analysis of multidrug-resistant (MDR) versus non-MDR organisms across the examined microbial species revealed significant differences in their prevalence and distribution. *K. pneumoniae* exhibited the highest MDR frequency, with 50 out of 54 isolates being MDR, accounting for 92.59% of the total *K. pneumoniae* isolates ($P < 0.001$). This was followed by *E. coli*, where all 8 isolates were MDR ($P < 0.001$). Similarly, *S. aureus* (MRSA) and *Enterobacter* sp. also displayed a complete resistance profile, with 4 out of 4 and 6 out of 6 isolates being MDR, respectively (both $P < 0.001$). *P. aeruginosa* showed a significant MDR prevalence, with 11 out of 14 isolates being resistant (P = 0.02-0.05). *C. albicans* and *A. baumanni* had a lower but notable MDR occurrence, with 6 out of 6 and all 6 isolates being MDR, respectively (P = 0.05-0.10 and $P < 0.001$, respectively). In contrast, *Streptococci pneumoniae*, *Aspergillus*, and *Fusarium* did not exhibit any MDR strains among the examined isolates. Overall, the data underscores the critical issue of increasing MDR prevalence among clinically significant organisms, emphasizing the urgent need for effective antimicrobial stewardship and infection control strategies.

Comparative analysis of microbial organism frequencies between TICU and SICU

The comparative analysis between TICU and SICU the revealed variable frequencies of microbial organisms (Table 4). *Klebsiella pneumoniae*, a known opportunistic pathogen, showed a slightly higher prevalence in TICU with 30 cases compared to 24 in SICU. However, this dissimilarity was not statistically significant, with a P-value exceeding 0.05, suggesting that the distribution of *Klebsiella pneumoniae* between the two units was comparable. *Candida albicans*, a common fungal pathogen, was found in 4 cases in TICU and 2 cases in SICU. Similarly to *Klebsiella pneumoniae*, the difference in frequency was not statistically significant with a P-value greater than 0.05. *Pseudomonas aeruginosa*, an environmental bacterium with clinical significance, had 8 cases in TICU and 6 in SICU. The observed difference in frequency was not statistically significant, with a P-value greater than 0.05. For *E. coli*, *S. aureus* (MRSA), and *Enterobacter sp.*, the frequencies were identical between TICU and SICU, indicating no variation in prevalence between the two units. The P-values for these organisms were equal to 1, reinforcing the absence of significant differences. *Acinetobacter baumanni*, another opportunistic pathogen, showed a slight predominance in SICU with 4 cases compared to 2 in TICU. However, this difference was not statistically significant with a P-value greater than 0.05. *Streptococci pneumoniae*, commonly associated with respiratory infections, exhibited 7 cases in TICU and 6 in SICU, indicating a comparable distribution between the two units. The detected alteration lacked statistical significance, with a P-value above 0.05.

Lastly, *Aspergillus* and *Fusarium*, fungal pathogens, were equally prevalent in both units with 2 and 1 cases, respectively. The observed frequencies for these organisms were identical, resulting in P-values of 1. Overall, the results suggest that the distribution of these microbial organisms was largely comparable between the TICU and SICU, with no statistically significant differences in their frequencies. This information is crucial for understanding the epidemiology of these organisms within intensive care settings and can

Table 2. Distribution of different organisms among specimens examined

Isolates		Specimens			
		Blood	Sputum	Urine	Total
Klebsiella pneumoniae	Count	9	31	14	54
	% within Organism	16.66	57.41	25.92	100.00%
Candida albicans	Count	1	3	2	6
	% within Organism	16.66	50.00	33.33	100.00%
Pseudomonas aeruginosa	Count	2	7	5	14
	% within Organism	14.28	50.00	35.71	100.00%
E. coli	Count	3	0	5	8
	% within Organism	37.50	0	62.50	100.00%
S. aureus (MRSA)	Count	2	1	1	4
	% within Organism	50.00	25.00	25.00	100.00%
Enterobacter sp.	Count	2	1	3	6
	% within Organism	33.33	16.66	50.00	100.00%
Acinetobacter baumanni	Count	0	4	2	6
	% within Organism	0	66.66	33.33	100.00%
Streptococci pneumoniae	Count	8	1	4	13
	% within Organism	6.15	7.69	30.76	100.00%
Aspergillus	Count	2	1	1	4
	% within Organism	50.00	25.00	25.00	100.00%
Fusarium	Count	1	1	0	2
	% within Organism	50.00	50.00	0	100.00%
Total	Count	30	50	37	117
	% within Organism	25.64	42.73	31.62	100.00%

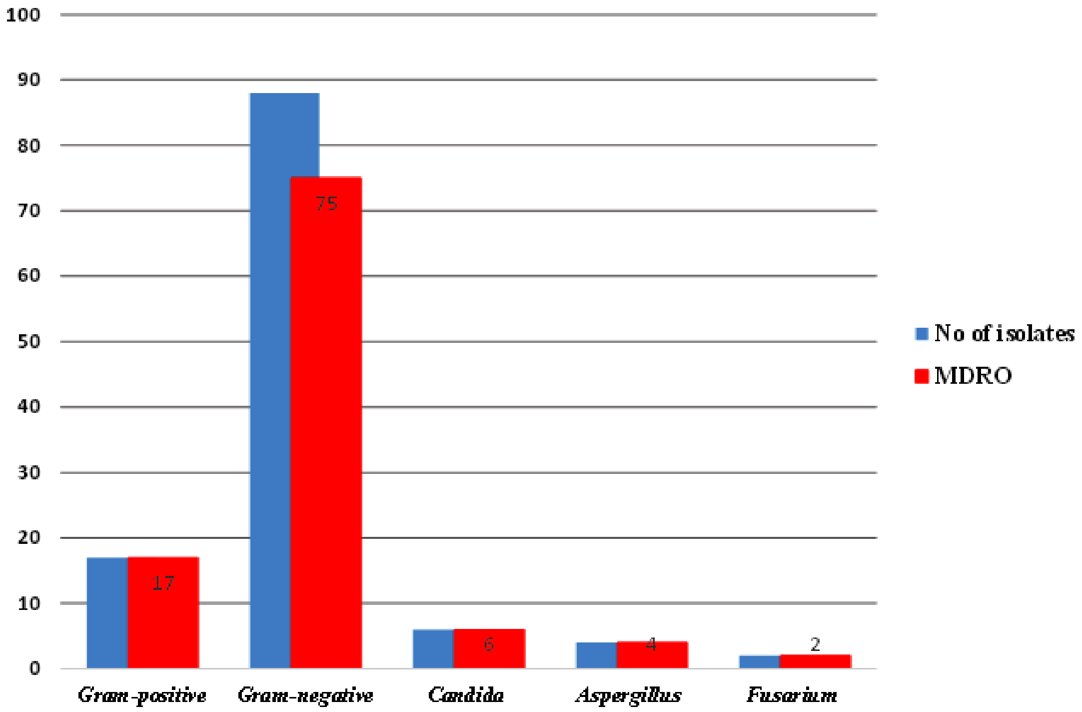

Fig. 2. Distribution of various multi-drug resistant organisms (MDROs) in the isolated cultures

Table 3. Comparisons between frequency of MDR and non-MDR organisms

organisms		Groups		Total	P-value
		MDR	Non-MDR		
Klebsiella pneumoniae	Count	50	4	54	< 0.001
Candida albicans	Count	6	0	6	0.05-0.10
Pseudomonas aeruginosa	Count	11	3	14	0.02-0.05
E. coli	Count	8	0	8	< 0.001
S. aureus (MRSA)	Count	4	0	4	< 0.001
Enterobacter sp.	Count	6	0	6	< 0.001
Acinetobacter baumanni	Count	0	6	6	< 0.001
Streptococci pneumoniae	Count	13	0	13	1
Aspergillus	Count	4	0	4	1
Fusarium	Count	2	0	2	1
Total	Count	104	13	117	-
	% within total	88.89	11.11	100.00	

*P-value significant at ≤0.05.

Table 4. Comparison between TICU and SICU regarding organisms' frequency

Organisms		Groups		Total	P-value
		TICU	SICU		
Organisms	Groups	TICU	SICU	Total	P-value
Klebsiella pneumoniae	No.	30	24	54	> 0.05
Candida albicans	No.	4	2	6	> 0.05
Pseudomonas aeruginosa	No.	8	6	14	> 0.05
E. coli	No.	4	4	8	1
S. aureus (MRSA)	No.	2	2	4	1
Enterobacter sp.	No.	3	3	6	1
Acinetobacter baumanni	No.	2	4	6	> 0.05
Streptococci pneumoniae	No.	7	6	13	> 0.05
Aspergillus	No.	2	2	4	1
Fusarium	No.	1	1	2	1

Table 5. Distribution of Healthcare-Associated Infections (HAI) across different durations of stay in the Trauma intensive care unit (Based on 70 Cases)

Departments	No. of patients	Patients staying less than 5 days	No infections less than 5 days stay	Patients staying 5-10 days	No infections 5-10 days stay	Patients staying more than 10 days	No infections more than 10 days stay
Trauma Surgery	3	2	3	2	1	2	0
Orthopedic Surgery	2	5	0	0	0	3	2
Neurosurgery	2	3	1	1	2	3	2
Emergency Medicine	2	3	2	1	1	1	0
Anesthesiology	4	1	0	0	0	2	0
Radiology	2	0	0	0	0	1	1
Cardiology (for trauma-related cardiac issues)	1	1	0	1	3	0	0
Respiratory Therapy	2	0	0	0	0	1	1

Table 6. Distribution of Healthcare-Associated Infections (HAI) across different durations of stay in the Surgical Intensive Care Unit (Based on 70 Cases)

Departments	No. of patients	Patients staying less than 5 days	No infections less than 5 days stay	Patients staying 5-10 days	No infections 5-10 days stay	Patients staying more than 10 days	No infections more than 10 days stay
General Surgery	2	4	2	4	2	3	3
Cardiothoracic Surgery	4	7	0	0	0	2	1
Vascular Surgery	4	2	1	1	2	2	1
Urology	1	2	1	1	1	1	0
Gynecologic Surgery	3	1	0	0	0	0	0
Plastic and Reconstructive Surgery	1	0	0	0	0	1	1
Colorectal Surgery	2	1	0	1	2	0	0
Transplant Surgery	1	0	0	0	0	1	1

guide infection control measures and antimicrobial stewardship strategies to optimize patient care.

Distribution and prevalence of Healthcare-Associated Infections (HAI) in the trauma and surgical intensive care units across various departments

The comprehensive analysis of Healthcare-Associated Infections (HAIs) within the Trauma Intensive Care Unit (TICU) and Surgical Intensive Care Unit (SICU) provides detailed insights into infection prevalence and distribution based on patient stay duration and specialty. In the TICU, Trauma Surgery, with the highest patient count of 3, showed relatively low infection rates, with 2 out of 3 patients staying less than 5 days and 2 out of 3 staying 5-10 days remaining infection-free. Orthopedic Surgery had a perfect infection-free record for stays under 5 days, and 2 out of 3 patients in the 5-10 days category were also infection-free. Conversely, Emergency Medicine reported 2 infections among 2 patients staying less than 5 days and 1 infection out of 2 patients in the 5-10 days group, indicating a higher infection rate for shorter stays. Neurosurgery had a more mixed pattern with infections in both stay categories. In the SICU, General Surgery, with the highest patient volume (20 cases), demonstrated a progressive decrease in infection rates with longer stays, with no infections reported beyond 10 days. Cardiothoracic Surgery, where most patients stayed less than 5 days, reported no infections in this category. Vascular Surgery had a balanced patient distribution across stay categories, with infections predominantly in the 5-10 days group. Urology and Gynecologic Surgery, with lower patient counts, reported infections primarily in shorter stays, with no infections in longer stays. Plastic and Reconstructive Surgery experienced infections in both short and long stay categories, suggesting a need for enhanced infection control measures. Overall, this detailed data highlights significant variability in infection rates across different departments and stay durations, underscoring the necessity for tailored infection prevention strategies and continuous monitoring to effectively manage and reduce HAIs in both the TICU and SICU settings.

DISCUSSION

Multidrug-resistant (MDR) organisms are a global concern in Intensive Care Units (ICUs), presenting significant challenges in disease management and being linked to elevated mortality rates[16]. The financial burden associated with treating these infections is substantial, driven by the need for more costly therapies to combat resistant pathogens.

Table 3 illustrates the demographic characteristics of patients who acquired nosocomial infections in the Trauma and Surgical Intensive Care Units (TICU and SICU). The data reveals that healthcare-associated infections are notably more prevalent among younger patients, with the 18-29 age group accounting for the highest proportion of infections at 36.42%. This trend persists across subsequent age groups but diminishes with increasing age. Additionally, a consistent gender disparity is observed, with male patients experiencing a higher prevalence of infections across all age categories. Specifically, in the 18-29 age group, 64.28% of the infected patients are male, compared to 35.71% female. This disparity is likely due to the larger number of injuries in this age group, with males being more frequently exposed to accidents, potentially due to the nature of their work. It has been reported that men are three times more susceptible to fatal road accidents compared to women[17].

These findings underscore the importance of implementing targeted infection prevention and control strategies tailored to address the unique demographic vulnerabilities observed in the TICU and SICU. Enhanced surveillance, strict adherence to hand hygiene protocols, and robust antimicrobial stewardship programs are crucial in mitigating the incidence of nosocomial infections and improving patient outcomes[18]. Further research is warranted to explore the underlying factors contributing to these demographic disparities and to evaluate the efficacy of targeted prevention measures in reducing the burden of hospital-acquired infections[19,20].

The presented data provides valuable insights into the microbial landscape of clinical specimens, highlighting prevalent pathogens and their distribution across various sample types. Notably, *Klebsiella pneumoniae* and *Escherichia coli* exhibited exceptionally high frequencies of multidrug resistance (MDR). Specifically, 92.59% of *K. pneumoniae* isolates and all *E. coli* isolates were MDR, consistent with previous reports that identified these pathogens as multidrug-resistant[21].

K. pneumoniae emerged as the predominant organism in this study, particularly in sputum samples, which aligns with its known association with respiratory tract infections, including pneumonia and bronchitis. These findings are consistent with those of previous studies, which identified *K. pneumoniae* as the most prevalent pathogen, accounting for 49.9% of total cases[22]. The detection of *K. pneumoniae* in blood and urine samples further indicates its potential to cause systemic and urinary tract infections, respectively, a pattern also observed in Neonatal and Pediatric Intensive Care Units[23].

The detection of *Candida albicans* predominantly in sputum and urine specimens underscores the importance of fungal surveillance in clinical settings. Although *C. albicans* is commonly found as a commensal organism in humans, it can become pathogenic under certain conditions, leading to infections such as candidiasis[24]. The predominance of *C. albicans* in sputum samples suggests the possibility of respiratory candidiasis, particularly in immunocompromised individuals or those with underlying respiratory conditions. This observation aligns with previous findings that highlighted the significance of *C. albicans* as a primary cause of respiratory tract invasive fungal infections (IFIs)[25].

Finally, *Pseudomonas aeruginosa*, a versatile opportunistic pathogen, was notably prevalent in sputum samples, further emphasizing the need for vigilant monitoring and targeted antimicrobial strategies in managing infections caused by this organism.

Pseudomonas aeruginosa is notorious for its intrinsic resistance to many antibiotics and its ability to cause a broad spectrum of infections, particularly in immunocompromised patients and those with cystic fibrosis. The presence of *P. aeruginosa* in blood and urine samples further emphasizes its clinical significance and the necessity for vigilant monitoring and targeted therapeutic interventions. This observation aligns with reports indicating that *P. aeruginosa* is a prevalent pathogen in individuals with cystic fibrosis, contributing to increased morbidity and mortality[26].

The high prevalence of *Escherichia coli* in urine samples is indicative of urinary tract infections (UTIs), which are among the most common bacterial infections encountered in clinical practice. The predominance of *E. coli* in UTIs underscores the critical importance of appropriate diagnostic methods, antimicrobial stewardship, and infection prevention strategies to manage and reduce the burden of UTIs. Additionally, the detection of *Staphylococcus aureus* (MRSA) and *Enterobacter* species in specimens, although in smaller numbers, highlights the ongoing challenges posed by antibiotic-resistant bacteria in healthcare settings. *Enterobacter* species, including *Enterobacter cloacae* and *Enterobacter aerogenes*, are opportunistic pathogens known to cause a range of infections, such as respiratory and urinary tract infections. The predominance of *Enterobacter* species in urine samples in this study warrants further investigation into the underlying risk factors and resistance patterns associated with these infections.

The identification of *Acinetobacter baumannii* predominantly in sputum samples is concerning given its increasing recognition as a major nosocomial pathogen with elevated levels of antibiotic resistance. The presence of *A. baumannii* in clinical specimens highlights the significance of stringent infection control measures, antimicrobial stewardship, and continuous surveillance to prevent and manage infections caused by this multidrug-resistant organism.

The detection of *Aspergillus* and *Fusarium* fungi in the specimens underscores the importance of considering fungal infections in differential diagnoses, particularly in immunocompromised patients or those with underlying respiratory conditions. Similar findings have been reported, noting that the rise of rare yet medically significant fungal infections is contributing to increased morbidity and mortality[27]. These fungi can lead to a variety of infections, ranging from superficial skin conditions to more severe invasive and disseminated diseases, necessitating early detection, appropriate antifungal therapy, and supportive care.

Overall, the diverse distribution of microorganisms identified in this study highlights the complex nature of healthcare-associated infections and underscores the importance of comprehensive microbial surveillance, targeted diagnostic approaches, and multidisciplinary interventions to guide effective treatment strategies, optimize patient outcomes, and minimize the spread of antimicrobial resistance.

The results of this study reveal a concerning prevalence of multidrug-resistant (MDR) organisms across various microbial species, posing significant challenges to clinical management and patient outcomes. In our study, the prevalence of MDR healthcare-associated infections (HAIs) was 88.89%, consistent with a reported prevalence of 85.8% in ICUs at Beni-Suef University Hospital[23]. Differences in sample size, demographics, and adherence to infection control protocols may account for variations[28].

Klebsiella pneumoniae emerged as the most predominant MDR organism, with 52% of isolates exhibiting multidrug resistance. This finding aligns with both national and international studies reporting *K. pneumoniae* as a predominant pathogen in ICUs[29]. The high prevalence of *K. pneumoniae* emphasizes the increasing difficulty in treating infections caused by this bacterium[30]. Its widespread resistance to multiple antibiotics, including carbapenems, underscores the urgent need for enhanced surveillance and the development of alternative treatment strategie[31]. Similarly, *E. coli*, another common pathogen, exhibited a complete resistance profile, complicating the therapeutic landscape. The complete resistance observed in *S. aureus* (MRSA) and *Enterobacter* species further accentuates the severity of the MDR crisis, given the significant clinical implications of MRSA infections and the opportunistic nature of *Enterobacter* species.

Although less predominant than *K. pneumoniae*, *P. aeruginosa* demonstrated a notable resistance profile. Given its intrinsic resistance to many commonly used antibiotics and its ability to acquire additional resistance mechanisms, the presence of MDR *P. aeruginosa* strains raises concerns about the management of infections caused by this versatile pathogen.

Interestingly, while *Candida albicans* and *A. baumannii* exhibited lower MDR prevalence rates compared to *K. pneumoniae* and *E. coli*, the presence of MDR strains in all examined isolates underscores the need for vigilance and continuous monitoring. *C. albicans*, a common commensal organism in humans, can become pathogenic under certain conditions, leading to infections such as candidiasis. The complete resistance observed in *A. baumannii* isolates is particularly concerning, given its increasing recognition as a major nosocomial pathogen with high levels of antibiotic resistance. These findings are in accordance with previous studies reporting on the virulence factors and resistance properties of *A. baumannii* as a concerning hospital-acquired pathogen[32].

The comparative analysis between the TICU and SICU provides valuable insights into the microbial epidemiology within these critical care settings. Overall, these findings underscore the importance of tailored, specialty-specific infection prevention strategies and continuous monitoring to mitigate the risk of HAIs and improve patient outcomes in the SICU. Our study highlights the high prevalence of MDR organisms in trauma and surgical ICUs, emphasizing the necessity for robust infection control measures, prudent antibiotic use, and continuous surveillance to improve patient outcomes and reduce healthcare costs.

CONCLUSION

Based on this observational study, it can be inferred that hospital-acquired infections are a significant concern in intensive care units, with an alarmingly high prevalence of multidrug-resistant organisms (MDROs) at 88.89% among TICU and SICU patients. The most frequently isolated MDROs included *Klebsiella*, CONS, *Candida*, and *Pseudomonas* species, with Gram-negative organisms being more prevalent than Gram-positive ones. The escalating rates of antimicrobial resistance, even against newer antibiotic classes, underscore the urgent need for rigorous infection control measures. To effectively address these challenges, our findings suggest several practical recommendations. First, enhancing routine microbial surveillance within ICUs is essential for early detection and timely intervention. Second, implementing strict adherence to infection control protocols, including hand hygiene, environmental cleaning, and isolation practices, can significantly reduce the transmission of MDROs. Third, developing and enforcing targeted antimicrobial stewardship programs that emphasize the judicious use of antibiotics will be crucial in curbing the spread of resistance. In conclusion, our study provides a comprehensive overview of the microbial landscape within TICU and SICU, emphasizing the need for continuous surveillance, robust infection control practices, and focused antimicrobial stewardship strategies. Future studies should prioritize the molecular epidemiology and resistance mechanisms of these organisms to develop tailored interventions that effectively combat the growing threat of MDROs in critical care settings. Additionally, exploring the implementation of rapid diagnostic technologies and the role of interdisciplinary teams in infection prevention could further enhance patient outcomes and reduce healthcare-associated infections.

Future Recommendations

Given the growing challenge of MDROs, exploring the role of non-antibiotic antimicrobials presents a promising avenue for future research and clinical practice. Non-antibiotic antimicrobials, including bacteriophages, antimicrobial peptides, and silver compounds, offer alternative mechanisms to combat infections and could potentially reduce reliance on traditional antibiotics. Integrating these agents into infection control strategies might not only help in managing resistant infections but also provide novel solutions to complement existing antimicrobial treatments. Their development and application could play a crucial role in mitigating the impact of antimicrobial resistance and improving patient outcomes in critical care settings.

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Conflicts of Interest

The authors do not have any conflict of interest.

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Data Availability Statement

This statement does not apply to this article.

Ethics Statement

The study was approved by the ethical committee of approval from the Faculty of Medicine Beni Suef University Research Ethical Committee.

Informed Consent Statement

This study did not involve human participants, and therefore, informed consent was not required.

Author Contributions

Conceptualization, Moaz Beni Melhem. and Wael N. Hozzein.; Methodology, Moaz Beni Melhem. and Aya I. Tagyan.; Validation, Manal M. Yasser; Formal analysis, Aya I. Tagyan.;

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