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A Four-Year Retrospective Study on Epidemiology, Bacteriology, and Antimicrobial Resistance of Bacterial Isolates from Burn Wounds in a Tertiary Care Hospital

Shagufta Roohi[1], Anjum Ara Mir[1*], Tufail Ahmed[1], Fakhri-Zehra Khaja[1], Tabish Qayoom[1], Nargis Bali[1]

[1]Sher-i-Kashmir Institute of Medical Sciences, Soura, Srinagar, Jammu and Kashmir, India

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***Correspondence**
Email: miranjum62@gmail.com
Tel: +919055205005
Fax: +911942403470

ABSTRACT

Introduction: Burn wound infections are a significant cause of morbidity and mortality among burn patients. Understanding of the prevalent bacterial etiologies and their antimicrobial susceptibility patterns within a healthcare facility is crucial for optimizing management strategies. **Methods**: This retrospective descriptive study was conducted over a four-year period at the Department of Microbiology in a tertiary care facility. We analyzed swab and pus samples collected from burn wound patients admitted to the Department of Plastic Surgery. Demographic data, including age and gender, were collected. Positive bacterial cultures underwent Gram staining and culture for identification. Biochemical tests were used for species-level identification. Antimicrobial susceptibility testing was performed using the disk diffusion method according to CLSI guidelines. Statistical analyses were carried out using SPSS software version 23 employing the chi-square test. **Results**: Out of 750 swab and pus samples analysed, 556 (74.1%) yielded positive bacterial cultures. Gram-negative bacteria predominated, accounting for 475 (85.4%) isolates, while 81 (14.6%) were Gram-positive. The most prevalent pathogens were *Pseudomonas aeruginosa* (175, 31.47%), *Klebsiella pneumoniae* (100, 17.99%), and *Acinetobacter baumannii* (68, 12.23%). Notably, 80.5% of *P. aeruginosa* isolates exhibited multidrug resistance (MDR). Among *Staphylococcus aureus* isolates, 37 (72.7%) were methicillin-resistant (MRSA). **Conclusions**: Among all isolates, *P. aeruginosa* was the most prevalent bacterial pathogen. *S. aureus* was the most prevalent Gram-positive organism. 72.7% of *S. aureus* isolates were MRSA. The high prevalence of multidrug-resistant *P. aeruginosa* and MRSA underscores the importance of implementing an antimicrobial stewardship program guided by local antibiograms.

INTRODUCTION

Burn injuries represent a significant global health burden, ranking as the fourth most common type of trauma worldwide. These injuries contribute to substantial mortality and morbidity, causing an estimated 26,500 annual deaths and 7.1 million injuries worldwide. Moreover, approximately 18 million disability-adjusted life years are lost globally due to burn injuries. In India alone, around seven million burn incidents occur each year [1, 2]. The majority of burn injuries result from exposure to heat, including hot liquids, solids, or fire. However, other causative agents such as friction, cold, radiation, chemicals, and electricity, can also cause burn injuries [3].

Burn patients are particularly susceptible to infections due to various factors, including the exposure of large body surface areas, immunocompromised state, invasive procedures performed in healthcare facilities, and prolonged hospital stays, which can disrupt the skin barrier and necessitate extended stays in the hospital [4, 5]. Previous research has established a statistically significant positive correlation between superficial bacterial contamination and sepsis in burn patients, highlighting contamination as a significant risk factor [4]. Among the numerous complications experienced by burn patients, infection stands out as the most common and severe.

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Burn wounds are initially sterile at the time of injury, but they become colonized by normal bacterial flora within the subsequent 72 hours. Initially, Gram-positive microorganisms predominate, but this trend is subsequently reversed, with Gram-negative bacteria emerging as the predominant pathogens by the second week post-injury. As the infection progresses, the bacteria proliferate at the wound site. They migrate along the sweat glands and hair follicles, eventually gaining access to the interface between the eschar and nonviable tissue [6].

Worldwide studies have identified *P. aeruginosa*, *Escherichia coli*, *A. baumannii*, *K. pneumoniae*, and *Proteus mirabilis* as the most common Gram-negative bacteria responsible for burn wound infections, with *P. aeruginosa* being the most frequent cause of sepsis [7]. The emergence of antibiotic resistance, particularly the development of resistance to multiple antibiotic classes, poses a significant challenge in the treatment of bacterial infections in both adult and pediatric patients, as it reduces the likelihood of adequate empirical coverage and increases the risk of unfavorable outcomes.

The treatment of multidrug-resistant Gram-negative bacterial (MDR-GNB) infections in critically ill patients has become a complex challenge, requiring dedicated expertise and up-to-date knowledge of the patient's medical history and the local microbiology epidemiology. This information is crucial for promptly recognizing the risk of MDR-GNB and identifying the most likely resistance mechanisms involved. Therefore, addressing these MDR-GNB infections demands a comprehensive, evidence-based approach [8].

MDR bacterial isolates can colonize and infect burn wounds, further prolonging hospital stays [9]. As bacterial infection is one of the most common complications of burns, the overuse of antibiotics to treat these infections has contributed to the alarming rise of antibiotic-resistant pathogens. To combat this trend, understanding the local epidemiology and antimicrobial susceptibility patterns is critical to prevent the indiscriminate use of antibiotics and guide appropriate treatment strategies. Analyzing hospital antibiogram data is essential for this purpose.

This four-year retrospective study aims to evaluate the distribution and antimicrobial resistance patterns of pathogens isolated from burn wound infections in a 1015-bed tertiary care hospital with a 32-bed burn unit, with the goal of analyzing the local epidemiology and resistance trends over this period will provide valuable insights to guide the development of an evidence-based antibiotic policy. Additionally, this study will assess the infection burden in this patient population.

MATERIAL AND METHODS

Sample collection. This four-year retrospective descriptive study was conducted in the Department of Microbiology at a tertiary care center from September 2018 to August 2022.

Inclusion criteria. We included all swab and pus samples conveniently collected from patients in the Burn Unit of the Department of Plastic Surgery and submitted to the Bacteriology laboratory.

Exclusion criteria. We excluded samples that were improperly labeled or repeat samples from the same patient within the study period.

Data validation and handling of missing data. Rigorous data validation procedures, including cross-checking data entries against predefined criteria, were applied to ensure the accuracy and consistency of the collected data. Additionally, strategies such as multiple imputation techniques were employed to handle missing data. Incomplete records were excluded only when absolutely necessary.

Isolation of bacteria. A total of 750 pus and swab samples were processed within 2 hours of receipt in the laboratory. The samples underwent inoculation on Sheep Blood Agar plates consisting of a blood agar base (HiMedia, India) supplemented with 5% sheep blood. Additionally, MacConkey agar (HiMedia, India) was employed. The culture plates were incubated at a temperature of 35 °C ± 2°C for 24 h. These incubators underwent regular calibration to ensure precise temperature control, and daily monitoring was conducted to verify the accuracy of the maintained temperatures.

Following Gram staining, the isolates were manually identified using conventional biochemical tests, including spot catalase, spot oxidase, carbohydrate fermentation, indole, Methyl Red, Phenyl Pyruvate, Triple Sugar Iron, citrate utilization, and urea hydrolysis tests. Gram-positive isolates were further tested using the catalase, slide coagulase, and tube coagulase tests. For catalase-negative Gram-positive cocci, identification relied on the Bile esculin test [10].

Antimicrobial susceptibility testing was conducted using the Kirby-Bauer disc diffusion method on Mueller-Hinton agar, following the Clinical and Laboratory Standards Institute (CLSI) guidelines. Detection of MRSA was performed using Cefoxitin as a surrogate marker [11]. For quality control, American Type Culture Collection (ATCC) strains of *S. aureus* (ATCC 25923), *E. coli* (ATCC 25922), and *P. aeruginosa* (ATCC 27853) were used as test control organisms every 15 days.

Ethical statement. Ethical clearance was obtained from the Sher-i-kashmir Institute of Medical Sciences Institutional Ethical Clearance Committee under the reference number RP 152/2022.

Statistical analysis. The collected data were consistently entered into WHONET, a freely available desktop Windows application endorsed and developed by the World Health Organization (WHO). WHONET serves as a comprehensive tool for the management and analysis of microbiology laboratory data, prioritizing

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antimicrobial resistance surveillance. This application was implemented in our laboratory during early 2018, and following multiple trial runs, it was fully integrated into our workflow by August 2018. The data on age were categorised into two categories (≤ 45 and >45 years). A chi-square test was employed to evaluate the association between culture positivity, age, and gender. Statistical analysis was conducted using SPSS software (Version 23). Statistical significance was defined at a threshold of $P<0.05$ to determine the presence of statistically significant associations or differences.

RESULTS

Demographic data. During the study period, a comprehensive analysis was conducted on a total of 750 pus and swab samples received at the laboratory. The patient population had a mean age of 40.73 years (range: 1-85 years), with a predominance of male patients (57.3%, n=430). The highest culture positivity was observed in patients under 45 years of age, accounting for 300 cases (53.9%) (Table 1). Of the 556 culture-positive isolates, 320 (57.5%) were from male patients and 236 (42.5%) were from female patients. (Table 2). No significant association was observed between various demographic factors, such as age and gender, and the bacterial isolates, as the *P*-values calculated by the chi-square test were 0.56 and 0.83, respectively.

Table 1. Distribution of culture-positive and culture-negative isolates by age group

Age	No. of culture positive isolates (%)	No. of culture negative isolates (%)	*P*-value
≤ 45 years	300 (53.9)	100 (51.5)	0.56
>45 years	256 (46.1)	94 (48.5)	Chi-Square: 0.335
Total	556 (100)	194 (100)	

Table 2. Distribution of culture-positive and culture-negative isolates by gender

Gender	No. of culture positive isolates (%)	No. of culture negative isolates (%)	*P*-value
Male	320 (57.5)	110 (56.7)	0.83
Female	236 (42.5)	84 (43.3)	Chi-square :0.042
Total	556 (100)	194 (100)	

Table 3. Bacterial isolates from burn unit patients (September 2018–August 2022)

Organism	Number of isolates (n)	(%)
P. aeruginosa	175	31.47
Klebsiella pneumoniae	100	17.99
Acinetobacter baumannii	68	12.23
Escherichia coli	67	12.05
Staphylococcus aureus	51	9.17
Proteus mirabilis	36	6.47
CoNS	20	3.60
Proteus vulgaris	9	1.62
Acinetobacter lwoffii	9	1.62
Enterococcus faecalis	6	1.08
Providencia sp.	5	0.90
Enterococcus faecium	4	0.72
Citrobacter freundii	2	0.36
Klebsiella oxytoca	2	0.36
Morganella sp.	2	0.36
Total	556	100

Bacterial isolation. The swab culture positivity rate was 74.1% (n=556). Among the culture-positive samples, 85.4% (n=475) were Gram-negative organisms, while 14.6% (n=81) were Gram-positive bacteria. The most prevalent Gram-negative isolate was *P. aeruginosa* (n=175), followed by *K. pneumoniae* (n=100), *A. baumannii* (n=100), *E. coli* (n=100), *P. mirabilis* (n=50), *Proteus vulgaris* (n=25), *Acinetobacter lwoffii* (n=10), *Providencia* spp. (n=5), *Citrobacter* spp. (n=5), *Klebsiella oxytoca* (n=3), and *Morganella* spp. (n=2). Among the Gram-positive isolates, *S. aureus* (n=51) was the most frequently isolated, followed by coagulase-negative staphylococci (CoNS) (n=20), *Enterococcus faecalis* (n=5), and *Enterococcus faecium* (n=5) (Table 3).

Antibacterial susceptibility testing. The susceptibility patterns of the bacterial isolates are presented in Tables 4

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and 5. The antimicrobial susceptibility testing revealed that 72.7% of the *S. aureus* isolates were methicillin-resistant (MRSA), and 87.5% of the CoNS isolates were methicillin-resistant (MRCoNS). All *E. faecalis* isolates were susceptible to ampicillin, penicillin, vancomycin, teicoplanin, and linezolid.

Among the Gram negative bacteria, *P. aeruginosa* exhibited a high degree of antimicrobial resistance, with various phenotypic resistance patterns observed (Table 6). Of the 175 *P. aeruginosa* isolates, 141 (80.6%) were classified as MDR based on their resistance to three or more antimicrobial classes. The highest resistance rate was observed for ticarcillin-clavulanate (n=104, 59.4%), followed by cefepime (n=104, 59.4%), piperacillin-tazobactam (n=49, 28.0%), aminoglycosides (amikacin, gentamicin, or tobramycin; n=31, 17.7%), fluoroquinolones (ciprofloxacin or levofloxacin; n=28, 16.0%), and carbapenems (imipenem or meropenem; n=29, 16.6%). Notably, all *P. aeruginosa* isolates were susceptible to polymyxin B.

Table 4. Percentage susceptibility of Gram-positive isolates to antibiotics (September 2018–August 2022)

Organism	Ampicillin	Cefoxitin	Clindamycin	Erythromycin	Linezolid	Penicillin	Teicoplanin	Vancomycin
Enterococcus faecalis (n=6)	100	ND	ND	ND	100	100	100	100
Enterococcus faecium (n=4)	100	ND	ND	ND	100	0	100	100
Staphylococcus aureus (n=51)	ND	27.3	51.5	17.6	100	0	100	100
Staphylococcus, coagulase-negative (n=20)	ND	12.5	41.7	10	100	20	100	100

Note: ND = not determined; antibiotics not recommended to be tested by CLSI for the specific bacteria.

Table 5. Percentage susceptibility of Gram-negative isolates to antibiotics during the study period

	Beta-Lactams/ Beta-Lactam Inhibitor Combinations								Aminoglycosides			Carbapenems		Fluoroquinolones		Misc.				
Organism	Cefepime	Cefotaxime	Ceftazidime	Ceftriaxone	Amoxicillin-clavulanate	Piperacillin-tazobactam	Ticarcillin-clavulanate	Cefoperazone-sulbactam	Amikacin	Gentamicin	Tobramycin	Imipenem	Meropenem	Levofloxacin	Ciprofloxacin	Polymyxin B	Aztreonam	Tetracycline	Tigecycline	Cotrimoxazole
Acinetobacter baumannii (n=68)	12.5	ND	10.5	3.8	ND	15.8	0	8.3	9.8	11.8	12.5	13.2	18.9	15	7.5	100	ND	0	0	0
Acinetobacter lwoffii (n=9)	ND	ND	ND	ND	ND	0	ND	100	0	0	ND	ND	100	0	0	100	ND	100	ND	ND
Citrobacter freundii (n=2)	0	0	0	0	0	0	ND	ND	100	100	ND	0	100	0	ND	100	ND	ND	ND	ND
Escherichia coli (n=67)	0	0	6.3	7.1	0	41.5	ND	41.7	63.4	52.6	66.7	5	62.5	5.1	5.4	100	13.6	55.6	0	100
Klebsiella oxytoca (n=2)	ND	ND	ND	ND	ND	0	ND	0	0	0	ND	0	0	ND	0	100	ND	ND	0	ND
Klebsiella Pneumoniae (n=100)	12.2	8.5	15.4	10.6	3.4	25.4	ND	23.9	21.4	20.6	13.3	13.2	31.3	15.7	10.8	100	10.5	50	0	0
Morganella spp. (n=2)	ND	ND	ND	0	ND	0	ND	0	ND	ND	0	0	0	0	0	0	ND	0	ND	ND
Proteus mirabilis (n=36)	45	27.3	25	31.6	0	83.3	100	62.5	36	38.1	21.1	64	91.3	60	54.5	0	55.6	0	0	0
Proteus vulgaris (n=9)	66.7	75	100	75	0	75	-	0	50	60	100	60	80	80	50	0	100	0	0	ND
Providencia spp. (n=5)	0	0	ND	0	ND	0	ND	0	0	0	ND	100	100	0	ND	0	ND	ND	ND	ND

Note: ND = Not determined. This indicates that the antibiotic susceptibility was not determined either because the antibiotic discs were unavailable or because CLSI guidelines do not recommend testing for that specific bacterium.

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Table 6. Resistance profiles of *P. aeruginosa* isolates

Antibiogram patterns and susceptibility rates of *P. aeruginosa* isolates							
Antibiotype	**Susceptibility pattern**						**N= 175**
	FEP	CAZ	TZP	LVX/CIP	AMK/GEN/TOB	MEM/IPM	
I	S	S	S	S	S	S	17
II	S	S	S	S	R	S	2
III	S	R	S	S	S	S	2
IV	S	S	S	R	R	R	2
V	R	R	S	S	S	S	2
VI	S	S	S	R	R	S	2
VII	S	R	S	S	S	R	4
VIII	S	S	S	R	S	R	5
IX	R	S	R	S	S	S	1
X	S	S	R	R	R	R	44
XI	R	R	S	S	R	S	2
XII	S	R	R	R	R	R	29
XIII	R	S	S	R	R	R	14
XIV	R	S	R	R	R	R	14
XV	R	R	R	R	R	R	32
XVI	S	R	R	R	R	S	3

Note: FEP = Cefepime; CAZ = Ceftazidime; TZP = Piperacillin-Tazobactam; LVX = Levofloxacin; CIP = Ciprofloxacin; AMK = Amikacin; GEN = Gentamicin; TOB = Tobramycin; IPM = Imipenem; MEM = Meropenem; S = Sensitive; R = Resistant.

DISCUSSION

Burn injuries compromise the immune system and host defense mechanisms, predisposing patients to infections. Advancements in patient care have led to infections surpassing non-infectious complications [12]. Several environmental, patient-related, and treatment-related factors contribute to the development of infections [13]. A thorough physical examination, biomarker detection, and microbiology culture are essential components for diagnosing and managing these injuries. Effective infection control necessitates the use of appropriate antibiotics and proper wound care [14]. *P. aeruginosa*, originating from the patient's endogenous gastrointestinal flora and/or environmental sources, is the most common cause of burn wound infections [15]. This opportunistic pathogen has been extensively studied in terms of its transmission ability and resistance patterns, as it has been identified as a prevalent agent in burn hospitals [16].

Our study provides an epidemiological evaluation of bacterial isolates from hospitalized burn patients, including demographic variables, and presents a comprehensive picture of the involved pathogens and their antimicrobial susceptibility patterns.

The mean age of patients in our study was 40.73 years, which aligns with societal patterns where adults in this age group bear responsibilities both at home and outside. In contrast, Lamichhane *et al*. (2019) found that the majority of admitted patients were between 21 and 30 years of age [17], while Emami *et al*. (2020) reported a mean age of 28.79±21.48 years [18]. These discrepancies may be attributed to variations in the study populations and settings.

Consistent with findings from Lam *et al*. (2019), where 72.8% of 5,061 patients admitted with varying degrees of burns over three years were males [19], and a WHO survey showing 62% of 6,431 burn patients were males [20], our study found a predominance of male patients. This finding aligns with the general trend of male predominance in burn injuries reported in various studies. However, AbuIbaid *et al*. (2022) reported a higher proportion of female patients (69.4%) compared to males (30.6%) [21]. This discrepancy might be attributed to regional or sociocultural factors influencing burn incidence and healthcare-seeking behaviors. The higher risk of sustaining burn injuries in males obsreved in our study and other similar settings can be attributed to increased occupational exposure to hazardous environments [4]. Additionally, in lower- and middle-income countries, females may have limited access to surgical care due to social stigma and the need for male accompaniment when seeking healthcare [20].

The swab culture positivity rate in our study was 74.1%, which falls within the range reported by other studies, such as 68.5% by Chaudhary *et al*. (2019) [4], 84% by Padmaja *et al*. (2023) [22-23], and 88.23% by Datta *et al*. (2016) [24]. This variation could be due to differences in study populations, sample collection methods, or antibiotic usage patterns. For instance, the relatively lower positivity rate in our study could be due to the collection of specimens for culture after the initiation of antibiotics.

The most commonly isolated Gram-negative bacteria were *P. aeruginosa*, *K. pneumoniae*, *A. baumannii*, and *E. coli*. This finding is consistent with previous studies by Gupta *et al*. (2019) and Garg *et al*. (2019), which also identified *P. aeruginosa* as the most prevalent Gram-negative organism in burn wound infections [5, 25-27]. These pathogens are highly prevalent due to their ability to thrive in moist environments, allowing them to persist in hospital settings [5]. *P. aeruginosa*, in particular, is

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predisposed to cause infections in burn patients due to factors such as the activation of quorum-sensing systems, production of pigments like pyoverdine and pyocyanin, elastase activity, and rhamnolipid biosynthesis [28]. Moreover, *P. aeruginosa* poses a significant threat due to its intrinsic resistance to antimicrobials like sulfonamides, ampicillin, first- and second-generation cephalosporins, chloramphenicol, and tetracycline, as well as its propensity to develop acquired resistance, which further limits treatment options. Plasmids are key transferable genetic agents that contribute to antibiotic resistance. Studies reveal that the majority of *P. aeruginosa* isolates contain plasmids harboring at least one resistance gene [17, 29]. The ability of *P. aeruginosa* to thrive in moist environments and readily acquire resistance genes enables its persistence in hospital settings, making it a leading cause of infections in hospitalized burn patients [1].

We constructed an antibiogram for *P. aeruginosa* isolates and identified 16 distinct resistance patterns among the 175 isolates. Notably, a substantial number of isolates clustered into common antibiotypes, with 44 isolates in antibiotype X, 32 in antibiotype XV, and 29 in antibiotype XII. This clustering suggests a common source of these infections and highlights the importance of adhering to proper infection control practices to prevent the spread of such infections.

Multidrug-resistant (MDR) *P. aeruginosa* was defined as isolates non-susceptible to at least one agent in three or more antimicrobial categories including antipseudomonal carbapenems, cephalosporins, fluoroquinolones, penicillins with β-lactamase inhibitors, monobactams, phosphonic acids, and polymyxins [30]. MDR phenotypes were observed in antibiotypes IV and X-XVI, with 141 (80.5%) isolates classified as MDR. The highest resistance rates were observed against ticarcillin-clavulanate (59.4%), followed by cefepime (59.4%), piperacillin-tazobactam (28.0%), aminoglycosides (amikacin, gentamicin, tobramycin; 17.7%), fluoroquinolones (ciprofloxacin, levofloxacin; 16.0%), and carbapenems (imipenem, meropenem; 16.6%). Notably, all of the isolates were susceptible to polymyxin B, which is consistent with the findings of Padmaja *et al*. (2023) [22].

The prevalence of MDR *P. aeruginosa* in our study (80.6%) was higher than that reported by Kaita *et al*. (2022) (35.1%) [27], but comparable to the findings of Dawra *et al*. (2017) (85.45%) and Kabanangi *et al*. (2021) (79.2%) [30-32]. In contrast, Zampar *et al*. (2017) reported a lower MDR rate of 13% [33], while Bhat *et al*. (2015) found 76.8% of *P. aeruginosa* isolates to be MDR [34]. This variability in MDR *P. aeruginosa* prevalence across studies highlights the importance of local surveillance to guide treatment decisions. The lack of resistance to polymyxin B aligns with other studies [17, 26, 35], suggesting that polymyxin B remains a viable treatment option, as the majority of carbapenem-resistant *P. aeruginosa* strains are susceptible to this antibiotic. However, it is crucial to note that polymyxin B resistance rates may vary geographically, with a relatively high rate of 53% reported in Singapore [36]. Factors influencing polymyxin B resistance include exposure to the antibiotic, inappropriate use of other antibacterials such as carbapenems, and resistance transmission via plasmids [36].

The high prevalence of MDR *P. aeruginosa* strains in our study can be attributed to factors such as the prolonged and combined use of broad-spectrum antibiotics, increased invasive procedures, and extended hospital stays [5, 14, 37].

The findings of the current study revealed that 72.7% of the *S. aureus* isolates were MRSA. This high prevalence of MRSA is consistent with the results reported in several previous studies conducted in similar settings [38-40]. However, other studies have reported lower MRSA prevalence rates [18, 26].

The high MRSA incidence observed in our study setting may be attributed to various factors. Studies from India have highlighted that inadequate hospital hygiene practices, as well as the prevalence of socioeconomically disadvantaged patient populations with poor sanitation, malnutrition, and suboptimal personal hygiene, can contribute to the high burden of MRSA infections in such healthcare facilities [41]. In contrast, developed regions like the Middle East and Europe tend to exhibit lower MRSA incidence, possibly owing to more rigorous MRSA surveillance and treatment protocols implemented in these settings [42].

This study has several limitations that should be considered when interpreting the findings. First, the retrospective nature of the study design precluded the collection of data on the use of invasive devices and the specific antimicrobials administered to the patients, as these were not within the scope of the current investigation. Second, environmental samples were not collected due to the retrospective nature of the study, which could have provided valuable insights into the potential sources and transmission dynamics of the identified bacterial isolates.

Moreover, due to financial constraints, molecular characterization of the bacterial isolates was not performed. Such molecular typing techniques could have helped establish the genetic relatedness among the isolates and potentially identified common sources of infection. Information on the environmental reservoirs harboring MDR *P. aeruginosa* strains and their role in the circulation of these pathogens within the healthcare facility would have been valuable for informing targeted infection control strategies.

In conclusion, the findings of this four-year retrospective study provide valuable insights into the epidemiology, bacteriology, and antimicrobial resistance patterns of bacterial isolates from burn wound infections

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in the study setting. These results can serve as a valuable reference to guide the empirical antibiotic treatment of burn patients before the availability of antibiotic susceptibility data. This information can also aid in the effective implementation of antimicrobial stewardship programs, a crucial component of evidence-based clinical practice guidelines for the prevention of multidrug-resistant bacterial infections in burn care settings.

The high prevalence of MRSA observed in this study underscores the need for the development and implementation of diverse programs and policies aimed at enhancing infection surveillance and optimizing antibiotic usage. Additionally, the strict enforcement of hand hygiene protocols and environmental disinfection practices is essential to mitigate the transmission of multidrug-resistant pathogens in burn care facilities.

Further research, including molecular typing of the bacterial isolates and the processing of environmental samples, is warranted to investigate the genetic relatedness among the isolates and identify potential common sources of infection. Such comprehensive investigations can provide valuable insights for the formulation of targeted infection prevention and control strategies in burn care settings.

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CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest associated with this manuscript.

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