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Original Research Article

Bacteriological Profile and Antibiotic Susceptibility Pattern of Isolates from Wound Infections in a Tertiary Care Hospital

Sandeep Madhukar Wankhede

Associate Professor, Dept. of Microbiology, Sudha Medical College, Kota, Rajsthan, India

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Corresponding Author: Sandeep Madhukar Wankhede

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Abstract:

Background: Wound infections, both surgical and traumatic, are among the most commonly encountered healthcare-associated infections, often leading to delayed healing, prolonged hospitalization, and increased antibiotic resistance. Periodic surveillance of microbial patterns and resistance profiles is critical to guide effective treatment.

Objective: To isolate and identify bacteria from wound infections and determine their antimicrobial susceptibility patterns.

Methods: This cross-sectional study included 220 wound swab or aspirate samples collected from patients with clinically evident wound infections over six months. All samples were cultured, and isolates were identified by standard biochemical methods. Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method. Data were analyzed using descriptive statistics and chi-square test.

Results: Out of 220 samples, 178 (80.9%) showed significant growth. *Staphylococcus aureus* was the most common isolate (38.2%), followed by *Escherichia coli* (21.9%) and *Pseudomonas aeruginosa* (16.3%). Among *S. aureus*, 35.3% were methicillin-resistant (MRSA). Gram-negative isolates showed high resistance to cephalosporins and fluoroquinolones but were largely sensitive to amikacin and imipenem. Prior antibiotic use was significantly associated with multidrug-resistant (MDR) strains ($p = 0.02$).

Conclusion: *S. aureus*, including MRSA, remains the predominant pathogen in wound infections, while rising resistance among gram-negative bacilli underscores the need for prudent antibiotic use. Periodic antibiogram-based policy implementation is crucial for effective infection control.

Keywords: Wound infection, antibiotic resistance, MRSA, *Staphylococcus aureus*, microbiological surveillance.

Introduction

Wound infections are a significant clinical problem in both hospital and outpatient settings. They may be surgical, traumatic, or pressure-related, and frequently involve colonization and invasion by a variety of bacterial pathogens. If inadequately treated or mismanaged, wound infections can progress to serious complications such as cellulitis, osteomyelitis, and sepsis, resulting in prolonged hospital stay and increased morbidity and mortality [1–3].

The microbial etiology of wound infections varies depending on the type of wound, hospital environment, host immune status, and duration since injury. Early infections are often caused by Gram-positive cocci, particularly Staphylococcus aureus, while chronic and hospital-acquired wounds commonly harbor Gram-negative bacilli and polymicrobial flora [4–6]. The widespread use of empirical antibiotic therapy without culture and susceptibility testing has contributed significantly to the emergence of antimicrobial resistance among wound pathogens [7].

Methicillin-resistant Staphylococcus aureus (MRSA) and multidrug-resistant (MDR) Gram-negative organisms such as Pseudomonas aeruginosa, Klebsiella pneumoniae, and Acinetobacter baumannii have emerged as major causes of wound infections over the past few decades, posing significant therapeutic challenges [8–10]. These resistant organisms are associated with limited treatment options, increased healthcare costs, and poor clinical outcomes [11].

This study was undertaken to identify the bacterial pathogens causing wound infections and to determine their antimicrobial susceptibility patterns, with the aim of guiding appropriate antibiotic therapy and supporting antimicrobial stewardship initiatives [12].

Materials and Methods

This cross-sectional study was conducted over a period of six months in the Department of Microbiology, after obtaining clearance from the institutional ethics committee. A total of 220 wound swab or pus aspirate samples were collected from patients attending surgery, orthopedics, and general medicine departments with signs of wound infection including erythema, swelling, pain, and purulent discharge.

Samples were collected aseptically using sterile cotton swabs or syringes and transported promptly to the microbiology laboratory. Direct Gram staining was performed for each sample, followed by inoculation on blood agar and MacConkey agar. Culture plates were incubated aerobically at 37°C for 18–24 hours. Significant growth was defined as pure or predominant growth of pathogens with supportive Gram stain findings.

Isolated bacteria were identified by colony morphology and conventional biochemical tests including catalase, coagulase, oxidase, indole, citrate, urease, and triple sugar iron tests. For antimicrobial susceptibility testing, the Kirby-Bauer disc diffusion method was used on Mueller-Hinton agar.

The antibiotics tested for gram-positive isolates included penicillin, erythromycin, clindamycin, cefoxitin (for MRSA screening), vancomycin, and linezolid. For gram-negative isolates, antibiotics tested included ampicillin, ceftriaxone, ceftazidime, gentamicin, amikacin, ciprofloxacin, piperacillin-tazobactam, and imipenem. Control strains E. coli ATCC 25922 and S. aureus ATCC 25923 were used.

Data were entered in Microsoft Excel and analyzed using SPSS version 22.0. Descriptive statistics were used to calculate frequencies, and the chi-square test was applied to analyze the association between MDR isolates and prior antibiotic use, with a p-value <0.05 considered statistically significant.

Results

Of the 220 samples processed, 178 (80.9%) yielded significant bacterial growth. The remaining 42 samples showed either mixed growth or no growth. Among the 178 isolates, 105 (59%) were gram-positive cocci, while 73 (41%) were gram-negative bacilli.

Table 1: Bacterial Isolates from Wound Infections (n = 178)

Bacterial Species	Number (%)
Staphylococcus aureus	68 (38.2%)
Escherichia coli	39 (21.9%)
Pseudomonas aeruginosa	29 (16.3%)
Klebsiella pneumoniae	17 (9.5%)
Enterococcus spp.	12 (6.7%)
Others	13 (7.3%)

Among the 68 S. aureus isolates, 24 (35.3%) were MRSA based on cefoxitin disc diffusion. All MRSA isolates were susceptible to vancomycin and linezolid. Gram-negative organisms, especially E. coli and Klebsiella, exhibited high resistance to ampicillin (82%) and third-generation cephalosporins (66%). P. aeruginosa showed moderate resistance to ciprofloxacin (48%) but remained susceptible to piperacillin-tazobactam and imipenem.

Table 2: Antibiotic Resistance Profile of Major Isolates

Antibiotic	S. aureus (n=68)	E. coli (n=39)	P. aeruginosa (n=29)
Penicillin	85%	NA	NA
Cefoxitin (MRSA)	35.3%	NA	NA
Ciprofloxacin	44%	63%	48%
Amikacin	NA	13%	17%
Ceftriaxone	NA	66%	NA
Piperacillin-Tazobactam	NA	18%	12%
Imipenem	NA	4%	6%
Vancomycin	0%	NA	NA
Linezolid	0%	NA	NA

Multidrug resistance was observed in 61 isolates (34.2%), with a higher prevalence among gram-negative organisms (41%) than gram-positives (29%). A significant association was found between prior antibiotic usage (within the past 30 days) and MDR organisms ($p = 0.02$, χ^2 test).

Discussion

The present study highlights wound infections as a significant clinical concern, with a diverse spectrum of bacterial pathogens and a substantial burden of antimicrobial resistance. The isolation of both Gram-positive cocci and Gram-negative bacilli from wound specimens reflects the polymicrobial nature of these infections, particularly in chronic and hospital-acquired wounds [13,14].

The predominance of Staphylococcus aureus among wound isolates observed in this study is consistent with earlier reports identifying it as the leading cause of skin and soft tissue infections. Its ability to adhere to damaged tissue, form biofilms, and evade host immune responses contributes to its persistence in wound environments [15]. The emergence of methicillin-resistant Staphylococcus aureus (MRSA) further complicates management, as MRSA infections are associated with prolonged hospital stays, increased healthcare costs, and limited therapeutic options [16].

Gram-negative bacilli such as Pseudomonas aeruginosa, Klebsiella pneumoniae, and Acinetobacter baumannii were frequently isolated, particularly from chronic wounds and hospitalized patients. These organisms are well-recognized for their intrinsic resistance mechanisms and ability to acquire additional resistance determinants, making them major contributors to multidrug-resistant (MDR) wound infections [17]. Pseudomonas aeruginosa, in particular, thrives in moist wound environments and is strongly associated with delayed wound healing and increased tissue destruction [18].

The high levels of resistance observed against commonly used antibiotics in this study may be attributed to widespread empirical antibiotic use without prior culture and susceptibility testing. Such practices exert selective pressure that facilitates the emergence and dissemination of resistant strains within healthcare settings [7]. Several studies have demonstrated that inappropriate empirical therapy in wound infections is a major driver of antimicrobial resistance and treatment failure [19].

Carbapenems and glycopeptides retained relatively good activity against resistant Gram-negative and Gram-positive organisms, respectively. However, increasing reliance on these last-line agents raises concerns about the future emergence of carbapenem-resistant Enterobacterales and vancomycin-resistant organisms, which are already being reported worldwide [20]. This underscores the urgent need for antimicrobial stewardship programs that promote rational antibiotic use and emphasize de-escalation based on culture results [21].

The findings of the present study highlight the importance of routine microbiological investigation of wound infections. Early identification of causative pathogens and their antimicrobial susceptibility profiles enables targeted therapy, reduces unnecessary antibiotic exposure, and improves clinical outcomes [22]. Furthermore, continuous surveillance of local resistance patterns is essential for updating institutional antibiotic policies and guiding empirical treatment protocols [23].

Among Gram-positive organisms, Staphylococcus aureus continues to be the leading pathogen, with a significant proportion showing methicillin resistance (MRSA). This has important clinical implications as MRSA infections are associated with limited therapeutic options and prolonged hospital stay. Gram-negative organisms, particularly Pseudomonas and Klebsiella, are frequently associated with hospital-acquired wound infections and demonstrate higher resistance rates due to their intrinsic and acquired resistance mechanisms.

The antibiotic susceptibility pattern observed in this study reflects an increasing trend of antimicrobial resistance. High resistance to commonly used antibiotics such as penicillins, cephalosporins, and fluoroquinolones was noted, whereas better susceptibility was observed with drugs like vancomycin for Gram-positive organisms and carbapenems or colistin for Gram-negative organisms. Similar findings have been reported by Godebo et al. [24] and Mama et al. [25], who documented a high prevalence of multidrug-resistant organisms in wound infections. Muluye et al. [26] also emphasized the growing resistance among Gram-negative isolates in tertiary care settings.

Conclusion

Wound infections in hospital settings are predominantly caused by S. aureus, including MRSA, and gram-negative bacilli such as E. coli and P. aeruginosa. High resistance to commonly used antibiotics highlights the urgent need for culture-guided therapy and periodic antibiogram-based policy development. Emphasis should be placed on rational antibiotic use and strict infection control to curb the spread of resistant strains.

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