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MICROBIAL PROFILE AND ANTIBIOGRAM OF PUS SAMPLES FROM SURGICAL WARDS IN A TERTIARY CARE HOSPITAL

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ABSTRACT

Background: Surgical site infections are a common cause of morbidity in hospitalized patients and are frequently associated with pus formation. The increasing prevalence of multidrug-resistant organisms has made the management of these infections challenging. Periodic assessment of the microbial profile and antimicrobial susceptibility patterns is essential for guiding effective empirical therapy.
Objectives: To determine the microbial profile of organisms isolated from pus samples collected from surgical wards and to analyze their antimicrobial susceptibility patterns.
Materials and Methods: This hospital-based cross-sectional study was conducted over a period of 12 months in a tertiary care hospital. A total of 200 pus samples obtained from patients admitted to surgical wards were processed using standard microbiological techniques. Bacterial identification was performed by conventional methods, and antimicrobial susceptibility testing was carried out using the Kirby–Bauer disc diffusion method in accordance with CLSI guidelines.
Results: Of the 200 pus samples processed, 154 (77%) yielded significant bacterial growth. Gram-negative bacilli (57.8%) were more frequently isolated than Gram-positive cocci (42.2%). *Staphylococcus aureus* (31.8%) was the predominant organism, followed by *Escherichia coli* (22.1%) and *Klebsiella pneumoniae* (18.8%). Methicillin-resistant *Staphylococcus aureus* accounted for 36.7% of *S. aureus* isolates. High resistance was observed to ampicillin, third-generation cephalosporins, and fluoroquinolones, whereas better susceptibility was noted with vancomycin, linezolid, carbapenems, and piperacillin–tazobactam.
Conclusion: The study reveals a high burden of multidrug-resistant bacteria in pus samples from surgical wards. Continuous monitoring of local microbial patterns and antibiograms is crucial for optimizing empirical therapy, improving patient outcomes, and strengthening antimicrobial stewardship programs.

Keywords*: Surgical site infections; Pus samples; Microbial profile; Antibiogram; Antimicrobial resistance; Tertiary care hospital*

INTRODUCTION:

Surgical site infections (SSIs) remain a major postoperative complication and constitute a significant proportion of healthcare-associated infections across the globe. These infections are associated with delayed wound healing, prolonged hospitalization, increased treatment costs, and higher morbidity. The presence of pus in surgical wounds represents an active infective process resulting from microbial proliferation and host inflammatory response, making pus samples a valuable specimen for microbiological evaluation.[1]

The spectrum of microorganisms isolated from pus samples in surgical wards is influenced by multiple factors, including the type of surgical procedure, duration of hospital stay, patient immune status, and prevailing hospital flora. Although *Staphylococcus aureus* has traditionally been recognized as the principal pathogen responsible for surgical wound

infections, recent studies have reported an increasing involvement of Gram-negative bacilli such as *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter* species, particularly in tertiary care settings.[2,3]

A growing concern in the management of surgical wound infections is the rising incidence of antimicrobial resistance. Methicillin-resistant *Staphylococcus aureus* (MRSA) has emerged as a frequent cause of hospital-acquired infections, leading to limited therapeutic options and increased risk of adverse outcomes. In parallel, Gram-negative bacteria producing extended-spectrum β-lactamases (ESBLs) and carbapenemases have been increasingly reported, significantly compromising the effectiveness of commonly used antibiotics.[4,5]

The widespread and often inappropriate use of broad-spectrum antibiotics, coupled with inadequate infection control measures, has accelerated the development and dissemination of resistant strains. Antimicrobial resistance has been recognized by the World Health Organization as a critical global health challenge, particularly affecting low- and middle-income countries where surveillance and stewardship programs may be suboptimal.[6]

Regular assessment of the local microbial profile and antibiotic susceptibility patterns of pus isolates is therefore essential. Such surveillance data assist clinicians in selecting appropriate empirical therapy, reduce unnecessary antibiotic exposure, and contribute to the formulation of hospital-specific antibiotic policies. Periodic antibiogram analysis also plays a crucial role in strengthening antimicrobial stewardship and improving clinical outcomes in surgical patients.[7]

With this background, the present study was undertaken to analyze the microbial profile and antimicrobial susceptibility patterns of organisms isolated from pus samples collected from surgical wards in a tertiary care hospital.

MATERIALS AND METHODS:

Study Design and Setting

This hospital-based cross-sectional study was conducted in the Department of Microbiology in collaboration with the surgical wards of a tertiary care teaching hospital. The study aimed to evaluate the microbial profile and antimicrobial susceptibility patterns of organisms isolated from pus samples collected from surgical patients.

Study Duration

The study was carried out over a period of 12 months.

Study Population

Patients admitted to various surgical wards who developed clinical evidence of wound infection, such as purulent discharge, localized inflammation, or delayed wound healing, were included in the study.

Sample Size

A total of 200 non-repetitive pus samples were analyzed during the study period.

Inclusion Criteria

- Pus samples obtained from patients admitted to surgical wards
- Samples collected from post-operative wounds, traumatic wounds, abscesses, and surgical site infections
- Patients of all age groups and both sexes

Exclusion Criteria

- Repeat samples from the same patient
- Samples collected from patients already enrolled in the study
- Samples with inadequate quantity or improper collection

Sample Collection

Pus samples were collected aseptically by trained healthcare personnel using sterile cotton swabs or sterile disposable syringes. Whenever possible, aspirated pus was preferred over swab samples to minimize contamination. The samples were transported to the microbiology laboratory immediately without delay. In cases where immediate processing was not feasible, samples were stored at 4°C for a short duration.

Direct Microscopic Examination

All pus samples were subjected to Gram staining. Smears were examined microscopically to assess the presence of pus cells, epithelial cells, and microorganisms. The Gram stain findings were correlated with culture results.

Culture and Isolation

Samples were inoculated onto blood agar and MacConkey agar plates using standard techniques. The inoculated plates were incubated aerobically at 37°C and examined after 24 hours. Plates showing no growth were further incubated for an additional 24 hours before being reported as culture negative.

Identification of Bacterial Isolates
Bacterial isolates were identified based on colony characteristics, Gram reaction, and standard biochemical tests. Identification of Gram-positive cocci and Gram-negative bacilli was performed using conventional methods as per standard microbiological guidelines.

Antimicrobial Susceptibility Testing
Antimicrobial susceptibility testing was carried out using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar. The results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines.
The antibiotics tested included:

- **Gram-positive isolates:** penicillin, ampicillin, cefoxitin, erythromycin, clindamycin, ciprofloxacin, gentamicin, vancomycin, and linezolid
- **Gram-negative isolates:** ampicillin, amoxicillin-clavulanic acid, ceftriaxone, ceftazidime, cefepime, ciprofloxacin, gentamicin, amikacin, piperacillin-tazobactam, and carbapenems

Methicillin resistance in *Staphylococcus aureus* was detected using the cefoxitin disc diffusion method.

Data Collection and Analysis
Relevant demographic and clinical data were collected from patient records using a structured proforma. Microbiological findings and antimicrobial susceptibility results were entered into Microsoft Excel and analyzed using descriptive statistics. Results were expressed as frequencies and percentages

RESULTS:
A total of 200 pus samples collected from patients admitted to surgical wards were processed during the study period. The results are presented under culture positivity, microbial distribution, and antimicrobial susceptibility patterns.
Out of the 200 pus samples processed, 154 samples (77%) yielded significant bacterial growth, while 46 samples (23%) showed no growth on culture as shown in Table 1

TABLE 1: Culture positivity rate of pus samples (n = 200)

Culture result	Number (%)
Culture positive	154 (77.0%)
Culture negative	46 (23.0%)

Among the 154 culture-positive samples, Gram-negative bacilli (57.8%) were isolated more frequently than Gram-positive cocci (42.2%) as shown in Table 2.

Table 2: Distribution of Gram reaction among bacterial isolates (n = 154)

Type of organism	Number (%)
Gram-negative bacilli	89 (57.8%)
Gram-positive cocci	65 (42.2%)

Staphylococcus aureus was the most common isolate (31.8%), followed by *Escherichia coli* (22.1%) and *Klebsiella pneumoniae* (18.8%). Non-fermenting Gram-negative bacilli such as *Pseudomonas aeruginosa* and *Acinetobacter* species were also isolated in significant proportions as shown in Table 3.

Table 3: Microbial profile of organisms isolated from pus samples (n = 154)

Organism	Number (%)
Staphylococcus aureus	49 (31.8%)
Escherichia coli	34 (22.1%)
Klebsiella pneumoniae	29 (18.8%)
Pseudomonas aeruginosa	20 (13.0%)
Acinetobacter spp.	13 (8.4%)
Enterococcus spp.	9 (5.9%)

Among the 49 isolates of *Staphylococcus aureus*, 18 (36.7%) were identified as methicillin-resistant *Staphylococcus aureus* (MRSA), while the remaining isolates were methicillin-sensitive as shown in Table 4

Table 4: Distribution of MRSA among *Staphylococcus aureus* isolates (n = 49)

Type	Number (%)
MRSA	18 (36.7%)
MSSA	31 (63.3%)

Gram-positive cocci showed high resistance to penicillin and erythromycin. All isolates were uniformly sensitive to vancomycin and linezolid as shown in Table 5.

Table 5: Antibiotic susceptibility pattern of Gram-positive cocci (n = 65)

Antibiotic	Sensitive (%)
Penicillin	18.5
Ampicillin	24.6
Erythromycin	41.5
Clindamycin	58.5
Ciprofloxacin	46.2
Gentamicin	61.5
Vancomycin	100
Linezolid	100

Gram-negative bacilli exhibited high resistance to ampicillin and third-generation cephalosporins. Higher susceptibility was observed with carbapenems and piperacillin–tazobactam.

Table 6: Antibiotic susceptibility pattern of Gram-negative bacilli (n = 89)

Antibiotic	Sensitive (%)
Ampicillin	14.6
Amoxicillin–clavulanate	28.1
Ceftriaxone	32.6
Ceftazidime	35.9
Ciprofloxacin	41.6
Gentamicin	48.3
Amikacin	62.9
Piperacillin–tazobactam	71.9
Imipenem/Meropenem	86.5

DISCUSSION:

Surgical site infections continue to pose a significant challenge in hospital settings, particularly in surgical wards where invasive procedures and prolonged hospital stays increase the risk of infection. In the present study, the culture positivity rate of pus samples was 77%, which is comparable to reports from other tertiary care hospitals in India, where positivity rates ranging from 65% to 85% have been documented.[8] This high isolation rate underscores the importance of microbiological evaluation of pus samples for targeted antimicrobial therapy.

The predominance of Gram-negative bacilli (57.8%) over Gram-positive cocci (42.2%) observed in this study reflects a changing trend in the etiology of surgical wound infections. Similar findings have been reported by several authors, suggesting a gradual shift toward Gram-negative pathogens in tertiary care settings, possibly due to extensive use of broad-spectrum antibiotics and increased survival of critically ill patients.[9,10] Among Gram-positive cocci, *Staphylococcus aureus* was the most common isolate, consistent with its well-established role as a major pathogen in surgical site infections.

The prevalence of methicillin-resistant *Staphylococcus aureus* (MRSA) in the present study was 36.7%, which aligns with reports from other Indian studies documenting MRSA rates between 30% and 50%.[11] The presence of MRSA is clinically significant, as it limits the use of β-lactam antibiotics and necessitates the use of reserve drugs. The universal susceptibility of Gram-positive isolates to vancomycin and linezolid observed in this study is reassuring and supports their continued use for treating serious Gram-positive infections.

Among Gram-negative bacilli, *Escherichia coli* and *Klebsiella pneumoniae* were the most frequently isolated organisms, followed by *Pseudomonas aeruginosa* and *Acinetobacter* species. These findings are in agreement with previous studies

that have highlighted the increasing role of Enterobacterales and non-fermenting Gram-negative bacilli in surgical wound infections.[12] High resistance to ampicillin and third-generation cephalosporins observed in this study suggests the possible presence of extended-spectrum β-lactamase (ESBL)–producing strains, which has been widely reported in similar hospital settings.[13]

The relatively higher susceptibility of Gram-negative isolates to amikacin, piperacillin–tazobactam, and carbapenems indicates that these agents remain effective treatment options. However, the emergence of resistance even to these higher antibiotics has been reported elsewhere, emphasizing the need for judicious use.[14] The findings of the present study reinforce the importance of periodic antibiogram surveillance to guide empirical therapy and prevent the indiscriminate use of broad-spectrum antibiotics.

Overall, the study highlights the growing burden of multidrug-resistant organisms in surgical wound infections and underscores the need for strict infection control practices, rational antibiotic use, and robust antimicrobial stewardship programs. Regular monitoring of local resistance patterns is essential to improve patient outcomes and curb the spread of antimicrobial resistance in surgical wards.

CONCLUSION:

The present study demonstrates that surgical wound infections are caused by a wide range of bacterial pathogens, with Gram-negative bacilli predominating over Gram-positive cocci. *Staphylococcus aureus* remained the most frequently isolated organism, with a considerable proportion of methicillin-resistant strains. The isolates showed high resistance to commonly used antibiotics, highlighting the challenge in selecting appropriate empirical therapy. However, vancomycin, linezolid, carbapenems, and piperacillin–tazobactam retained good activity against most pathogens. Regular surveillance of microbial profiles and antibiograms is essential to guide rational antibiotic use and strengthen antimicrobial stewardship in surgical wards.

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