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BACTERIAL PROFILE AND ANTIBIOTIC SUSCEPTIBILITY PATTERNS IN WOUND INFECTIONS AMONG SURGICAL PATIENTS: A CROSS-SECTIONAL STUDY

Original Article

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ABSTRACT

Background: Surgical wound infections remain a significant cause of postoperative morbidity, contributing to extended hospital stays and increased antimicrobial resistance. Understanding local bacterial profiles and antibiotic susceptibility is essential for guiding effective empirical treatment and reducing the burden of multidrug-resistant organisms.

Objective: To identify the most prevalent bacterial pathogens responsible for surgical wound infections and assess their antibiotic resistance patterns among hospitalized surgical patients.

Methods: A hospital-based cross-sectional study was conducted over six months in a tertiary care center. Wound swab samples were collected aseptically from 355 surgical patients with clinical signs of wound infection. Microbial culture and sensitivity testing were performed following Clinical and Laboratory Standards Institute (CLSI) guidelines. Data were analyzed using SPSS version 25 with significance set at $p<0.05$.

Results: Out of 355 patients, 271 (76.3%) had culture-positive wounds, yielding 305 bacterial isolates. The most common organisms were *Staphylococcus aureus* (28.7%), *Escherichia coli* (18.9%), and *Klebsiella spp.* (14.9%). *S. aureus* showed high resistance to ampicillin (85.3%) and ceftriaxone (72.5%) but remained largely sensitive to vancomycin (8.8% resistance). *E. coli* exhibited substantial resistance to ampicillin (91.0%) and ceftriaxone (78.2%), with lower resistance to meropenem (12.4%). Diabetic patients demonstrated significantly higher rates of multidrug-resistant isolates (74.2%) compared to non-diabetics (61.3%, $p=0.032$).

Conclusion: The study reveals a high burden of antibiotic-resistant pathogens in surgical wound infections, emphasizing the need for regular surveillance, localized antibiograms, and antimicrobial stewardship to optimize patient care and reduce resistance development.

Keywords: Anti-Bacterial Agents, Cross-Sectional Studies, Drug Resistance, Escherichia coli, Klebsiella, Surgical Wound Infection, Staphylococcus aureus.

INTRODUCTION

Wound infections are among the most common complications encountered in surgical patients, posing significant challenges to postoperative recovery and overall healthcare outcomes. These infections not only increase the length of hospital stays but also escalate healthcare costs and contribute to the growing global concern of antimicrobial resistance. Surgical site infections (SSIs) account for a substantial proportion of hospital-acquired infections, making their surveillance and management critical in the context of modern surgical care (1). The bacterial etiology of these infections is often diverse and can vary based on geographic location, hospital practices, and patient populations, necessitating localized studies to inform effective treatment protocols. The rise in multidrug-resistant organisms (MDROs) has further complicated the management of surgical wound infections (2). Empirical antibiotic treatment, though often necessary before culture results are available, runs the risk of being ineffective when guided by outdated or non-regional microbial data. Studies from various regions have identified Staphylococcus aureus, including methicillin-resistant strains (MRSA), Pseudomonas aeruginosa, Escherichia coli, and Klebsiella species as common culprits in wound infections (3). However, the resistance profiles of these organisms show notable variations, often shaped by patterns of antibiotic usage in specific clinical settings. Consequently, regular surveillance of local bacterial profiles and their susceptibility patterns is essential for tailoring effective empirical therapy and improving patient outcomes (4,5).

Moreover, the inappropriate or excessive use of antibiotics has accelerated the emergence of resistant strains, rendering formerly effective drugs obsolete. This has sparked a renewed focus on antimicrobial stewardship, where evidence-based prescribing is grounded in up-to-date microbiological data (6). The World Health Organization has consistently highlighted antimicrobial resistance as one of the top ten global public health threats, underscoring the importance of localized research in combating this issue. By identifying prevalent pathogens and understanding their resistance mechanisms, clinicians can make informed choices that not only enhance patient recovery but also contribute to broader public health efforts in curbing resistance (7,8). While multiple studies have explored bacterial profiles in wound infections across different parts of the world, there remains a gap in data specific to certain regions and hospital settings. The variability in microbial flora, driven by differences in surgical practices, hygiene standards, and antimicrobial usage, limits the generalizability of global data. Therefore, it becomes imperative to generate localized evidence to guide clinicians within a specific healthcare environment. This is particularly important in resource-limited settings where the lack of updated surveillance data can hinder appropriate clinical decision-making (9,10).

Furthermore, a detailed understanding of local bacterial trends aids in the development of hospital policies regarding infection prevention and control. It enables microbiologists and surgeons alike to anticipate changes in microbial patterns and to implement timely interventions. In addition, such knowledge supports ongoing training and education of healthcare workers, reinforcing the critical link between laboratory findings and bedside management (11,12). This study is grounded in the urgent need to bridge the existing knowledge gap surrounding the microbiological landscape of surgical wound infections within hospitalized populations. By employing a cross-sectional design, the investigation seeks to identify the most commonly isolated bacterial pathogens in surgical wound infections and to examine their antibiotic susceptibility profiles. The findings aim to inform more accurate empirical treatment strategies, reduce postoperative complications, and contribute to the global endeavor of mitigating antimicrobial resistance. With this rationale, the specific objective of the study is to identify the most common bacterial pathogens responsible for wound infections in surgical patients and to assess their patterns of antibiotic resistance within a hospital setting.

METHODS

This cross-sectional study was conducted in the surgical wards of a tertiary care teaching hospital over a period of six months. The primary objective was to identify the predominant bacterial pathogens involved in surgical wound infections and evaluate their patterns of antibiotic susceptibility. The study was designed to offer a snapshot of the microbial landscape during the defined period, providing critical insights into the organisms implicated in postoperative infections and their resistance profiles, thus guiding future empirical treatment protocols. The study population included patients who developed clinical signs of wound infection following surgical procedures and were admitted to the general surgery, orthopedics, and gynecology departments. Inclusion criteria required patients to be aged 18 years or older, to have undergone a surgical intervention during their hospital stay, and to present with signs suggestive of wound infection, such as localized redness, warmth, swelling, purulent discharge, or delayed wound healing. Patients who were already receiving antimicrobial therapy for other infections at the time of wound sampling, those with chronic wounds of non-surgical origin, and immunocompromised individuals such as those with HIV/AIDS or on long-term corticosteroid therapy were excluded to minimize confounding variables.

The sample size was determined using a single population proportion formula. Assuming a prevalence of wound infection at 30%, a 95% confidence level, and a 5% margin of error, the calculated minimum sample size was 323. To account for possible non-responses and laboratory exclusions, an additional 10% was added, making the final target sample size approximately 355 patients. Wound samples were collected aseptically using sterile cotton swabs from the deepest part of the wound after cleaning the surface with normal saline (2,3). In cases where pus was present, it was aspirated using sterile syringes. The samples were immediately transported to the microbiology laboratory for culture and sensitivity testing. Specimens were inoculated on blood agar and MacConkey agar and incubated aerobically at 37°C for 24 to 48 hours. Bacterial identification was performed using standard biochemical tests, including catalase, coagulase, indole, citrate utilization, triple sugar iron (TSI) agar tests, and others as per Clinical and Laboratory Standards Institute (CLSI) guidelines. Antibiotic susceptibility testing was carried out using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar. The selection of antibiotics for testing included commonly used agents such as ampicillin, ceftriaxone, ciprofloxacin, gentamicin, amikacin, meropenem, and vancomycin (12,13). The diameter of the zones of inhibition was measured and interpreted according to CLSI standards to classify bacterial isolates as sensitive, intermediate, or resistant.

The primary outcomes measured were the type and frequency of bacterial isolates and their respective susceptibility profiles. Data were recorded and managed using a standardized data collection sheet. Statistical analysis was performed using SPSS version 25. Descriptive statistics were used to present categorical variables as frequencies and percentages. For numerical data, mean and standard deviation were calculated. Since the data on bacterial prevalence and susceptibility patterns were normally distributed, the chi-square test was applied to assess associations between categorical variables such as type of bacteria and resistance patterns. A p-value of less than 0.05 was considered statistically significant. To ensure ethical compliance, the study received approval from the Institutional Review Board (IRB) of the participating hospital. Written informed consent was obtained from all participants or their legal guardians prior to enrollment. Confidentiality of patient information was strictly maintained, and all data were anonymized before analysis to preserve privacy. The methodological rigor of this study, combined with comprehensive microbiological testing and robust statistical analysis, provides a strong foundation for deriving clinically meaningful conclusions. By adhering to standardized laboratory procedures and ethical research practices, this study aims to generate reliable, reproducible data that can inform both local treatment guidelines and broader infection control strategies.

RESULTS

Out of the 355 surgical patients enrolled, 271 (76.3%) yielded positive bacterial growth from wound cultures. A total of 305 isolates were identified, with some wounds showing polymicrobial growth. Staphylococcus aureus was the most prevalent organism, accounting for 102 isolates (28.7%), followed by Escherichia coli (67 isolates, 18.9%), Klebsiella species (53 isolates, 14.9%), Pseudomonas aeruginosa (45 isolates, 12.7%), and Proteus species (26 isolates, 7.3%). A small proportion of isolates (3.4%) fell into the 'Others' category, including Acinetobacter baumannii and Enterococcus spp., as illustrated in the bar chart titled *"Distribution of Bacterial Isolates."* Among the S. aureus isolates, a significant proportion exhibited resistance to commonly used antibiotics. Ampicillin resistance was highest at 85.3%, followed by ceftriaxone (72.5%), ciprofloxacin (51.0%), and gentamicin (42.2%). Notably, vancomycin resistance was low at 8.8%, indicating its continued efficacy against S. aureus infections. This pattern suggests limited effectiveness of first-line agents and supports the ongoing reliance on glycopeptides for resistant strains.

E. coli isolates demonstrated an even more concerning resistance pattern. Resistance to ampicillin was observed in 91.0% of cases, while ceftriaxone and ciprofloxacin showed resistance rates of 78.2% and 66.1% respectively. Gentamicin resistance was recorded at 53.7%, whereas meropenem, a last-resort antibiotic, retained relatively high sensitivity, with only 12.4% of isolates resistant. These findings are visualized in the line graph labeled *"Antibiotic Resistance Patterns,"* comparing resistance percentages for both S. aureus and E. coli.The resistance profile of Klebsiella spp. revealed similarly high resistance to beta-lactams and fluoroquinolones, with over 70% of isolates resistant to ampicillin and over 60% resistant to ciprofloxacin and ceftriaxone. Resistance to carbapenems was less frequent (15.1%), though concerning. Pseudomonas aeruginosa showed marked resistance to ciprofloxacin (63.3%) and moderate resistance to meropenem (19.7%), but retained higher susceptibility to amikacin and piperacillin-tazobactam. There were no statistically significant differences in pathogen distribution between male and female patients ($p > 0.05$), nor were there notable associations between comorbid diabetes and specific bacterial profiles. However, patients with diabetes were more likely to harbor multidrug-resistant organisms, with a resistance rate of 74.2% compared to 61.3% in non-diabetics (p = 0.032). Overall, the results reveal a high burden of antimicrobial resistance among wound pathogens in surgical patients, with both Gram-positive and Gram-negative organisms demonstrating reduced susceptibility to commonly prescribed antibiotics. The data emphasize the need for continued surveillance and tailored empirical therapy based on local resistance trends.

Table 1: Demographics

Variable	Value
Total patients	355
Mean age (years)	47.3
Male (%)	198 (55.8%)
Female (%)	157 (44.2%)
Diabetic (%)	129 (36.3%)
Smokers (%)	76 (21.4%)

Table 2: Bacterial Isolates Frequency

Bacterial Species	Number of Isolates	Percentage (%)
Staphylococcus aureus	102	28.7
Escherichia coli	67	18.9
Klebsiella spp.	53	14.9
Pseudomonas aeruginosa	45	12.7
Proteus spp.	26	7.3
Others	12	3.4

Table 3: Antibiotic Resistance – Staphylococcus aureus

Antibiotic	Resistance (%)
Ampicillin	85.3
Ceftriaxone	72.5
Ciprofloxacin	51.0
Gentamicin	42.2
Vancomycin	8.8

Table 4: Antibiotic Resistance – Escherichia coli

Antibiotic	Resistance (%)
Ampicillin	91.0
Ceftriaxone	78.2
Ciprofloxacin	66.1
Gentamicin	53.7
Meropenem	12.4

Table 5: Multidrug Resistance in Diabetic vs Non-Diabetic Patients

Patient Group	MDR Organism Rate (%)	p-value
Diabetic (n=129)	74.2	0.032
Non-Diabetic (n=226)	61.3	—

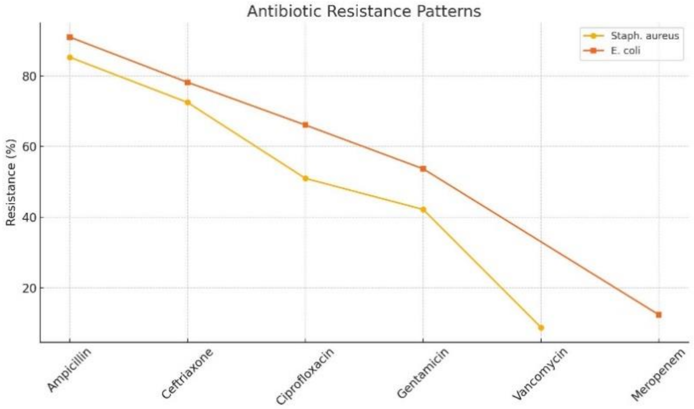

Figure 1 Antibiotic Resistance Patterns

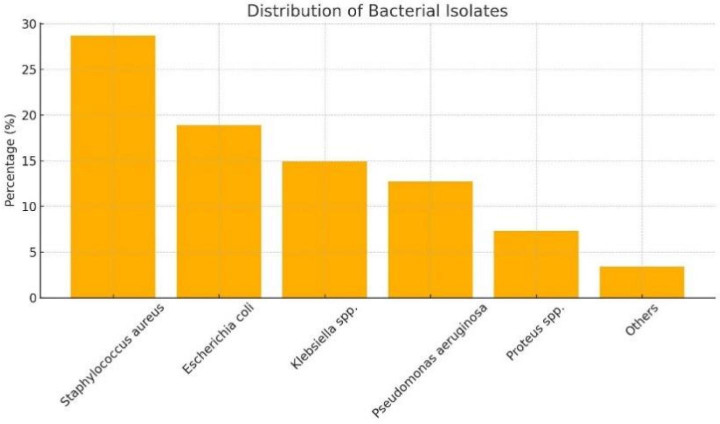

Figure 2 Distribution of Bacterial Isolates

DISCUSSION

The findings of this study offer a compelling insight into the current bacterial landscape of surgical wound infections and the accompanying antimicrobial resistance burden. The predominance of *Staphylococcus aureus*, *Escherichia coli*, and *Klebsiella* species aligns with global patterns, as consistently reported across multiple recent studies. However, the observed resistance trends underscore a growing clinical challenge, particularly in resource-limited settings where empirical antibiotic usage often proceeds without robust microbiological guidance. The high prevalence of *S. aureus* (28.7%) in this study reflects trends noted by a study, which identified this organism as the most dominant in surgical wounds in Nigeria, accounting for 37.3% of isolates. The low vancomycin resistance observed in our data corroborates findings by a study, which demonstrated that vancomycin remained effective against most Gram-positive isolates despite widespread resistance to beta-lactams and fluoroquinolones (14-16). This indicates that vancomycin continues to be a viable therapeutic option against *S. aureus*, particularly methicillin-resistant strains. Similarly, the resistance profiles of *E. coli* and *Klebsiella* spp. to ampicillin and third-generation cephalosporins mirror patterns documented by a study, where over 80% of *Klebsiella pneumoniae* isolates were resistant to ceftriaxone and meropenem (17,18). This resistance is particularly concerning in the context of empiric therapies, where third-generation cephalosporins are commonly deployed. The high levels of resistance in *Pseudomonas aeruginosa* to ciprofloxacin and meropenem observed here are also consistent with findings from a study, further highlighting the limitations of current antimicrobial protocols in managing Gram-negative pathogens (19,20).

The increased prevalence of multidrug-resistant organisms (MDROs) among diabetic patients is another critical observation. This correlates with trends noted by a study, which reported significantly higher resistance rates in patients with comorbid conditions, particularly diabetes. The metabolic and immune dysregulation in diabetic patients likely contributes to prolonged infection and broader antibiotic exposure, favoring resistance development (21,22). One of the strengths of this study lies in its comprehensive approach, combining clinical surveillance with microbiological confirmation and detailed antibiotic sensitivity profiling. The inclusion of a diverse patient demographic and polymicrobial wound presentations enhances the applicability of findings to real-world surgical settings. Moreover, the use of CLSI standards and robust statistical analysis strengthens the reliability of the results. Nonetheless, certain limitations should be acknowledged. Being a single-center study, the findings may not be generalizable to other institutions with different antibiotic policies or microbial flora. The cross-sectional design, while suitable for prevalence estimation, restricts the ability to infer causality or track resistance evolution over time. Additionally, the exclusion of anaerobic and fungal pathogens may have underestimated the true microbial burden in surgical wounds.

Future research should consider longitudinal multicenter studies to capture temporal trends and regional variability in antimicrobial resistance. Whole genome sequencing of resistant strains may also help identify molecular mechanisms underpinning resistance, offering insights for targeted therapy and infection control. Enhanced infection prevention strategies, including routine screening and decolonization protocols, particularly for high-risk patients such as those with diabetes, may help mitigate the burden of MDROs. In conclusion, this study underscores the alarming rate of antimicrobial resistance among surgical wound pathogens, emphasizing the urgency of implementing localized antibiograms, strict antimicrobial stewardship, and continuous microbial surveillance. The data support global calls for action on antimicrobial resistance and highlight the necessity for hospital-level policy adjustments to improve surgical outcomes and patient safety.

CONCLUSION

This study highlights the high prevalence of multidrug-resistant bacterial pathogens in surgical wound infections, with *Staphylococcus aureus* and *Escherichia coli* being the most common. The significant resistance to first-line antibiotics underscores the urgent need for routine culture-based surveillance, updated local antibiograms, and strengthened antimicrobial stewardship. These findings provide essential evidence to guide more effective, targeted empirical therapy and improve surgical outcomes.

AUTHOR CONTRIBUTION

Author	Contribution
Tahira Jamil	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Monishka Gurdino	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published
Shaista Hamid	Substantial Contribution to acquisition and interpretation of Data Has given Final Approval of the version to be published
Khizra Aleena	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Muhammad Israr*	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Amna Noor	Substantial Contribution to study design and Data Analysis Has given Final Approval of the version to be published
Amna Manahil	Contributed to study concept and Data collection Has given Final Approval of the version to be published

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