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Research Article

Bacterial Isolates and their Antimicrobial Susceptibility Patterns of Wound Infections among Patients in Surgery Department of Tertiary Health Care Centre

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ABSTRACT

Introduction: Wound infections are an important cause of delayed healing and morbidity among surgical patients, and increasing antimicrobial resistance complicates their management. Identification of bacterial pathogens and determination of their antimicrobial susceptibility patterns are important for appropriate antimicrobial selection.

Aim: To determine the bacterial profile and antimicrobial susceptibility patterns of wound infections among patients attending the Surgery Department of a tertiary healthcare centre.

Methods: A retrospective study is done among clinical samples obtained from both inpatients and outpatients attending Surgery Department of National Institute of Medical Sciences and Research, Nims University Rajasthan, Jaipur from February 2026 to July 2026. The isolates were identified and their antibiotic sensitivity was determined following the standard protocol and CLSI guidelines.

Results: A total of 348 bacterial isolates were included in the analysis. Gram-negative organisms predominated, accounting for 67.2%, while Gram-positive organisms accounted for 32.8%. Staphylococcus spp. was the most frequently isolated organism (28.4%), followed by Escherichia coli (23.3%), Klebsiella pneumoniae (12.9%), and Pseudomonas spp. (7.8%). Most isolates were recovered as single-organism infections (91.38%), while multiple microbial isolates accounted for 8.62%. Wound swabs constituted the majority of specimens (66.4%). High resistance was observed among Staphylococcus spp. to penicillin (72.7%), E. coli to ampicillin and ciprofloxacin (81.4% each), K. pneumoniae to ampicillin (86.6%), and Pseudomonas spp. to cefepime and cefoperazone-sulbactam (66.6% each). Relatively high susceptibility was observed to amikacin among E. coli (85.1%) and to gentamicin among K. pneumoniae (66.6%) and Pseudomonas spp. (77.7%).

Conclusion: The study demonstrated a diverse bacterial profile among wound infections, with Gram-negative organisms predominating and substantial resistance to several commonly used antimicrobials. The variation in susceptibility among bacterial species highlights the importance of bacterial identification and antimicrobial susceptibility testing for appropriate management of wound infections in the study setting.

INTRODUCION

Infectious diseases nevertheless remain an essential cause of morbidity and mortality among humans, particularly in developing countries. Various species of microorganism live on human skin, gastrointestinal tract, in the nasopharynx and different parts of the body with much less capacity for causing disease due to first line protection in the body. Skin abrasions because of surgical procedure, trauma, burns, diseases, lack of nutritions and different factors have an effect on this primary line of protection and results in infections [1]. As wound infections are largely hospital acquired and the infecting pathogens now no longer only differ from country to country, however additionally range from one hospital to another within the same country [2].

The primary characteristic of intact skin is to control microbial populations that stay in the skin floor and to prevent underlying tissue from becoming colonized and invaded through potential pathogens [3]. Since wound colonization is maximum often poly-microbial, concerning numerous microorganisms which are probably pathogenic, any wound without primary care is susceptible for getting infected. [4]. Infection in wound constitutes a prime barrier to healing and may have an unfavorable effect on the patient's quality of life as well as on the healing rate of the wound. Infected wounds are probably to be more painful, hypersensitive and odorous, resulting in increased pain and inconvenience for the patient [5]. The typical organisms which have been associated with wound infection include Staphylococcus aureus (S. aureus) which from various research had been discovered to account for 20-40% and Pseudomonas aeruginosa (P. aeruginosa) 5-15% of the nosocomial infection, with infection especially following surgical treatment and burns. Other pathogens which include Enterococci and members of the Enterobacteriaceae were implicated, especially in immune compromised patients and following abdominal surgery [6]. Wound healing needs a very good healthy environment so that the normal physiological process will result in a normal healing process with minimum scar formation. One of the maximum crucial strategies to maintain the process of healing ongoing is to sterilize the damaged tissue from any microbial contamination [7].

Wounds presented by patients range from one setting to some other, starting from acute surgical wounds, traumatic wounds along with those that arise following an accident, burn wounds or chronic wounds consisting of diabetic foot, leg and pressure ulcers. All wounds are infected with microorganisms which can be a part of the saprophytic microflora of the skin and the amount of those microorganisms range from one wound to another [9]. Some essential elements such as origin, body location, size and duration of the wound need to be taken into consideration in the wound control due to their effect on wound colonisation and contamination [10]. Microbial colonisation of wounds is characterized by the presence of multiplying microorganisms at the surface of a wound, however without an immune reaction from the host [11,12] and without a related clinical signs and symptoms. Differently, wound contamination relies upon at the pathogenicity and virulence of the microorganisms and at the immune competency of the host, and it is decided by the presence of clinical signs of contamination along with erythema, pain, tenderness, heat, oedema, cellulites and abscess/

Despite advances in control of infections, wound infections have now no longer completely prevented because of the problem of drug resistance [16]. The vast makes use of antibiotics, together with the duration of time over which they were available, have brought about primary issues of resistant organisms contributing to morbidity and mortality [17]. Knowledge of the causative agents of wound infection has confirmed to be beneficial in the choice of appropriate antimicrobial therapy and on infection control measures taken in health institutions [18]. Therefore, the present study aimed to assess the important causative agents of microorganism and their antibiotic susceptibility patterns which can be imperative because it guides the selection of an effective regimen for the treatment.

METHODS

A Retrospective study was Conducted among clinical samples obtained from both inpatients and outpatients attending Surgery Department of the National Institute of Medical Sciences and Research, Nims University Rajasthan, Jaipur. Exudative samples from patients were collected During the Period from February 2026 to July 2026. All individuals who provide pus and/or wound discharge samples at National Institute of Medical Sciences and Research (NIMS&R) Hospital during the Study Period were included as Participants. Socio-demographic Details and Laboratory Findings were collected from the Hospital Microbiology Laboratory Registration Records by using a Standard Data Collection format after ensuring the completeness of the Available data.

All wound swabs and Pus / discharge Samples were collected aseptically using sterile swabs and processed according to standard Microbiological Procedures. Samples were Subjected to microscopic examination following Gram staining and inoculated onto appropriate Culture media, including blood agar, chocolate agar, and MacConkey agar medium using calibrated loops. Biochemical testing is done for identification of Bacterial isolates and antimicrobial susceptibility testing was performed by Kirby-Bauer Disk diffusion method or using an Automated Method by VITEK 2 COMPACT system. All antibiotic discs were from HIMEDIA (Mumbai, India). Quality control of media and discs was done using ATCC control strains. Antimicrobial susceptibility testing was done for the following drugs Penicillins –Ampicillin (10), Beta-lactam + Beta-lactam inhibitors – Piperacillin + Tazobactam (100/10), Cefoperazone + sulbactam (75/30), cephalosporins – Cefotaxime (30), Cefixime , Ceftriaxone (30), Carbapenems – Ertapenem (10mcg), Meropenem (10mcg), Imipenem (10mcg), Aminoglycosides - Gentamicin (10mcg), Quinolones - Ofloxacin (5mg), Ciprofloxacin (5mcg), Polypeptide antibiotics – Colistin (10mcg), Cotrimoxazole (25) and Tigecycline (15mcg) . The screening for ESBL detection was performed by antimicrobial susceptibility tests using Ceftazidime and Cefotaxime, with or without Clavulanic Acid, as per standard Procedures. The distribution of the bacterial isolates, Antimicrobial Susceptibility Patterns, antimicrobial resistance and ESBL-production were expressed as percentages. The study was approved by the Institutional Research Board and Ethical Committee of the Hospital. The collected data were entered into Microsoft Excel and subsequently Analyzed using SPSS Version 20 Software. Odds ratio and Chi-square test were employed. P-value was considered statistically significant.

Table 1. Distribution of Study Population According to Gender

	FREQUENCY	PERCENTAGE
MALE	234	67.2
FEMALE	114	32.8

Table 2. Distribution of Study Population According to Age

	FREQUENCY	PERCENTAGE
LESS THAN 18 YEARS	6	1.7
18-25 YEARS	21	6.0
26-44 YEARS	105	30.2
45-60 YEARS	123	35.3
61-75 YEARS	90	25.9
76-90 YEARS	3	0.9

Table 3. Distribution of Study Population According to Organism

	FREQUENCY	PERCENTAGE
GRAM POSITIVE	114	32.8
GRAM NEGATIVE	234	67.2
TOAL	348	100

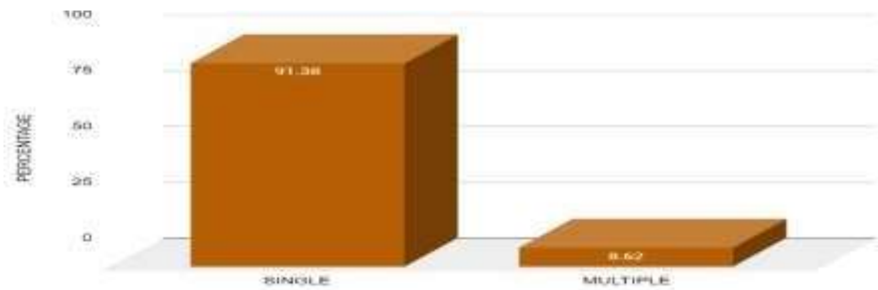

Fig. 1 Distribution of Single and Multiple Microbial Isolates from Samples

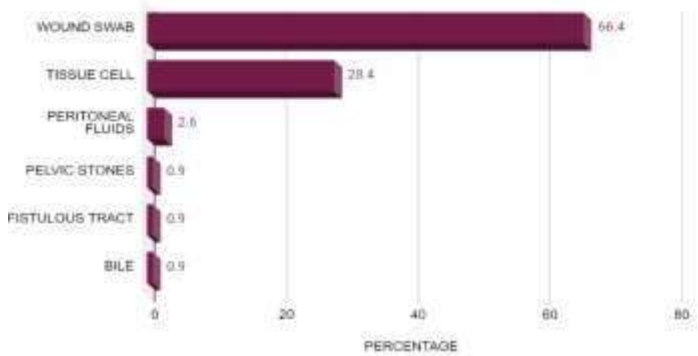

Fig. 2 Distribution of Study Population According to Specimen

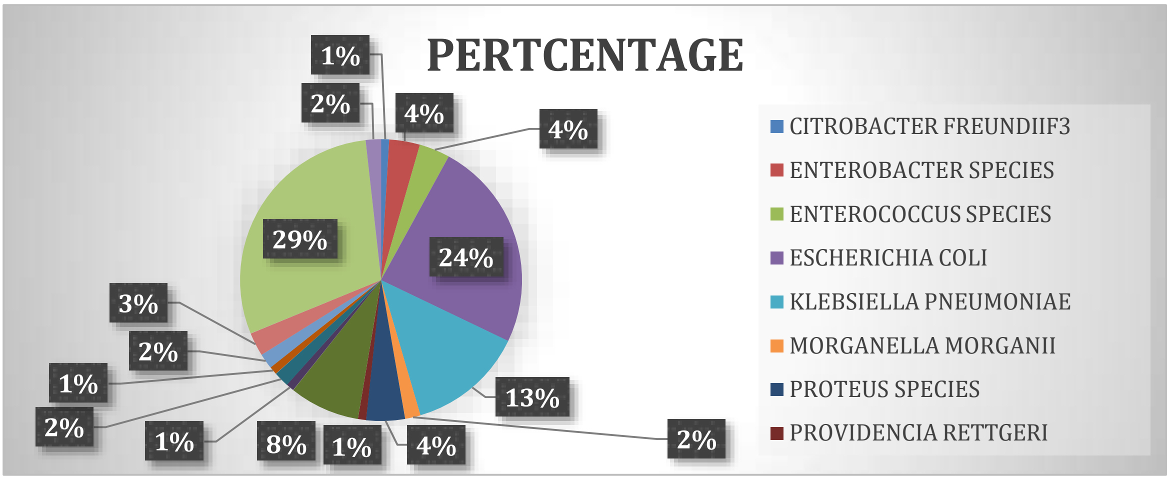

Fig.3 Distribution of Study Population According to Organism Type

Table 4. Antibiogram of Staphylococcus Species, Escherichia Coli, Klebseilla Pnemoniae and Pseudomonas Species

ANTIBIOTICS	Staphylococcus species (n=99)		Escherichia coli (n=81)		Klebsiella pneumoniae (n=45)		Pseudomonas species (n=27)	
	R	S	R	S	R	S	R	S
AMPICILLIN %	6.0	9.0	81.4	3.7	86.6	0.0	0.0	11.1
PIPERACILLIN TAZOBACTAM %	0.0	0.0	48.1	33.3	40.0	53.3	55.5	22.2
CIPROFLOXACIN %	51.5	30.3	81.4	7.4	53.3	33.3	55.5	33.3
CEFOPERAZONE SULBACTAM %	0.0	0.0	22.2	48.1	40.0	53.3	66.6	22.2
CEFEPIME %	0.0	0.0	55.5	18.5	53.3	40.0	66.6	22.2
AMIKACIN %	0.0	0.0	3.7	85.1	33.3	46.6	11.1	55.5
CEFATAXIME %	0.0	3.0	44.4	11.1	40.0	20.0	0.0	0.0
CEFIXIME %	0.0	0.0	18.5	3.7	26.6	6.6	11.1	0.0
GENTAMICIN %	24.2	63.3	18.5	74.0	33.3	66.6	22.2	77.7
COTRIMOXAZOLE %	42.4	51.5	70.3	18.5	40.0	53.3	22.2	0.0
COLISTIN %	0.0	0.0	3.7	3.7	6.6	6.6	0.0	0.0
IMIPENEM %	0.0	0.0	22.2	40.7	33.3	6.6	22.2	44.4
ERTAPENEM %	0.0	0.0	11.1	48.1	33.3	0.0	11.1	0.0
MEROPENEM %	3.0	0.0	14.8	59.2	40.0	13.3	11.1	55.5
VANCOMYCIN %	3.0	54.5	0.0	3.70	0.0	0.0	0.0	0.0
LINEZOLID %	9.9	60.6	0.0	3.7	0.0	0.0	0.0	0.0
CLOXACILLIN %	27.2	27.2	0.0	0.0	0.0	0.0	0.0	0.0
PENICILLIN %	72.7	6.0	3.7	0.0	0.0	0.0	0.0	0.0
CEFAZOLIN %	15.1	9.0	0.0	0.0	0.0	0.0	0.0	0.0
COFOXITIN %	6.0	-	0.0	-	6.6	-	11.1	-
DORIPENEM %	-	0.0	-	0.0	-	0.0	-	11.1
FOSFOMYCIN %	-	3.0	-	0.0	-	0.0	-	0.0
TIGECYCLINE %	9.0	72.7	0.0	11.1	0.0	6.6	0.0	0.0
ERYTHROMYCIN %	51.5	42.4	0.0	0.0	0.0	0.0	0.0	0.0
CLINDAMYCIN %	33.3	51.5	0.0	0.0	0.0	0.0	0.0	0.0
OFLOXACIN %	21.2	-	7.4	-	0.0	-	22.2	0.0
CEFTRIAXONE %	0.0	-	0.0	-	13.3	-	0.0	0.0

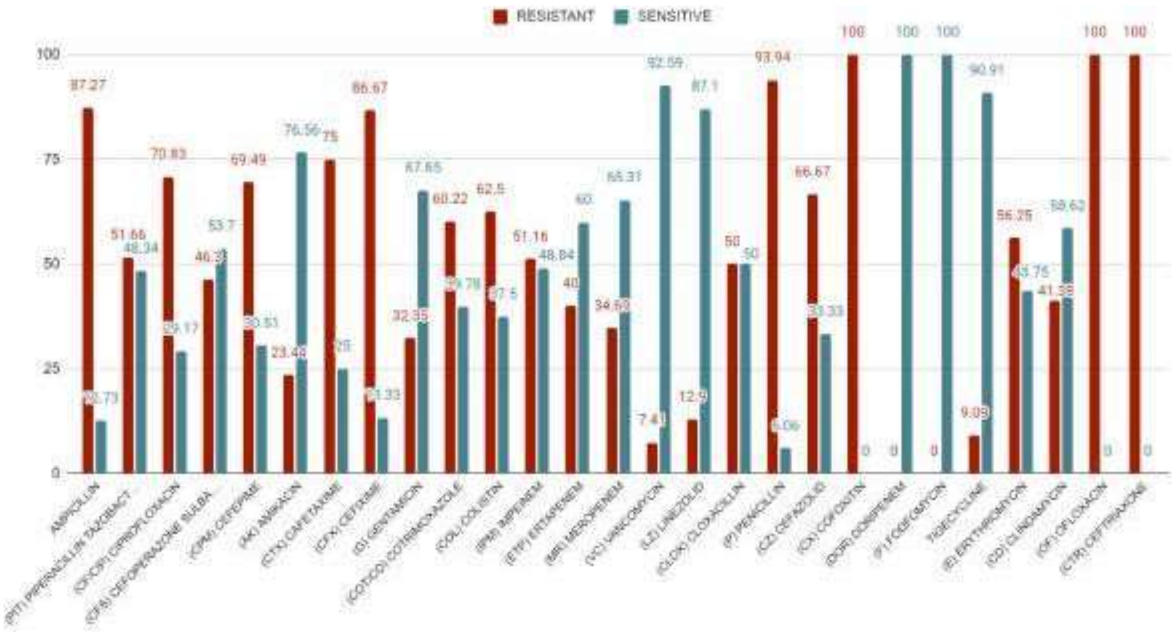

Fig. 4 Distribution of Antibiotic Resistance and Sensitivity.

RESULT

A total of 348 study participants/samples were included in the analysis. The demographic and microbiological characteristics of the study population are presented in Tables 1–3 and Figures 1–4.

As shown in Table 1, males constituted the majority of the study population, with 234 (67.2%) participants, whereas females accounted for 114 (32.8%). Thus, males represented approximately two-thirds of the study population. The age distribution of the study population is presented in Table 2. The largest proportion of participants belonged to the 45–60-year age group, comprising 123 (35.3%) of the study population. This was followed by participants aged 26–44 years, with 105 (30.2%), and those aged 61–75 years, with 90 (25.9%). Participants aged 18–25 years accounted for 21 (6.0%), while those aged less than 18 years accounted for 6 (1.7%). The smallest proportion was observed among participants aged 76–90 years, comprising 3 (0.9%).

According to Table 3, gram-negative organisms accounted for 234 (67.2%) of the isolates, while gram-positive organisms accounted for 114 (32.8%). Thus, gram-negative organisms constituted the larger proportion of the organisms identified in the study population. As illustrated in Figure 1, the majority of samples yielded a single microbial isolate (91.38%), whereas 8.62% yielded multiple microbial isolates. Therefore, single-isolate samples constituted the predominant pattern among the samples examined. The distribution of the study population according to specimen type is shown in Figure 2. Wound swabs constituted the predominant specimen type, accounting for 66.4% of the samples, followed by tissue cell specimens (28.4%). Peritoneal fluid accounted for 2.6%, while pelvic stones, fistulous tract specimens, and bile each accounted for 0.9% of the specimens.

The distribution of bacterial isolates according to organism type is presented in Figure 3. A total of 17 organism categories were represented. Staphylococcus species constituted the largest proportion of isolates, accounting for 28.4%, followed by Escherichia coli (23.3%) and Klebsiella pneumoniae (12.9%). Pseudomonas species accounted for 7.8% of the isolates, while Proteus species represented 4.3%. Other organisms were present in smaller proportions, including Acinetobacter species (3.4%), Enterobacter species (3.4%), Enterococcus species (3.4%), and Sphingomonas paucimobilis (2.6%). Morganella morganii, Raoultella ornithinolytica, and Serratia fonticola each accounted for 1.7% of the isolates. Citrobacter freundii, Providencia rettgeri, Ralstonia pickettii, and Salmonella species each represented 0.9%. Streptococcus species accounted for 1.7%. Overall, the distribution was dominated by Staphylococcus species and Escherichia coli, which together accounted for 51.7% of the isolates.

The antibiotic resistance and sensitivity patterns of the major bacterial isolates are presented in Table 4 . The analysis included Staphylococcus species (n=99), Escherichia coli (n=81), Klebsiella pneumoniae (n=45), and Pseudomonas species (n=27). Among Staphylococcus species, the highest resistance was observed to penicillin (72.7%), followed by erythromycin (51.5%), co-trimoxazole (42.4%), and clindamycin (33.3%). Sensitivity was highest to tigecycline (72.7%), followed by gentamicin (63.6%), linezolid (60.6%), and vancomycin (54.5%). For E. coli, the highest resistance was observed to ampicillin (81.4%) and ciprofloxacin (81.4%), followed by co-trimoxazole (70.3%) and cefepime (55.5%). The highest sensitivity was observed to amikacin (85.1%), followed by gentamicin (74.0%), meropenem (59.2%), and ertapenem (48.1%). Among K. pneumoniae, resistance was highest to ampicillin (86.6%), followed by ciprofloxacin (53.3%) and cefepime (53.3%). Sensitivity was highest to gentamicin (66.6%), while sensitivity to piperacillin-tazobactam and cefoperazone-sulbactam was 53.3% each. For Pseudomonas species, the highest resistance was observed to cefoperazone-sulbactam (66.6%) and cefepime (66.6%), followed by piperacillin-tazobactam (55.5%) and ciprofloxacin (55.5%). The highest sensitivity was observed to gentamicin (77.7%), followed by amikacin (55.5%) and meropenem (55.5%). Overall, the resistance profile varied across the bacterial species. Ampicillin resistance was particularly high among E. coli (81.4%) and K. pneumoniae (86.6%), while penicillin resistance was highest among Staphylococcus species (72.7%). Among the tested agents, amikacin and gentamicin demonstrated relatively high sensitivity against the gram-negative isolates, although the sensitivity varied according to bacterial species.

The antibiotic susceptibility pattern showed considerable variation among the tested antibiotics. Resistance was highest for ampicillin (87.27%), cefepime (86.67%), and penicillin (93.94%), while high sensitivity was observed for vancomycin (92.59%), linezolid (87.1%), and tigecycline (90.91%). Overall, the figure demonstrates variable resistance and sensitivity patterns across the antibiotics tested

DISCUSSION

The present study found that Gram-negative organisms predominated among wound isolates, accounting for 67.2%, while Gram-positive organisms accounted for 32.8%. Staphylococcus species were the most frequently isolated individual organisms (28.4%), followed by Escherichia coli (23.3%), Klebsiella pneumoniae (12.9%), and Pseudomonas species (7.8%). The predominance of Gram-negative organisms is consistent with the findings of Shrestha et al., who reported 50.8% Gram-negative isolates from soft-tissue infections.[23] However, it differs from the study by Muluye et al. in Gondar, where Gram-positive organisms predominated.[22]

The high proportion of Staphylococcus species in the present study is comparable with previous wound-infection studies in which Staphylococcus aureus was among the predominant isolates. Shrestha et al. reported S. aureus as the most common isolate (47%),[23] while Muluye et al. reported 32.9%.[22] The present study also showed substantial representation of E. coli and K. pneumoniae, findings broadly comparable with those reported by Shrestha et al.[23]

The antimicrobial susceptibility pattern demonstrated considerable variation among bacterial species. High resistance was observed to penicillin among Staphylococcus species (72.7%), ampicillin among E. coli (81.4%) and K. pneumoniae (86.6%), and cefepime among Pseudomonas species (66.6%). Similar high resistance to commonly used antibiotics has been reported in previous Ethiopian studies.[20,22] Mulu et al. reported high ampicillin resistance among E. coli (87%),[20] which is comparable to the present finding.

Conversely, relatively high susceptibility was observed to amikacin among E. coli (85.1%), gentamicin among K. pneumoniae (66.6%) and Pseudomonas species (77.7%), and selected agents against Staphylococcus species. Shrestha et al. similarly reported high susceptibility of E. coli to amikacin.[23] Differences between studies may reflect variations in study populations, bacterial distribution, antimicrobial exposure, geographical setting, and laboratory methods.[20,22,23]

Overall, the findings demonstrate a diverse bacterial profile and substantial antimicrobial resistance among wound isolates. The observed variation in susceptibility emphasizes the importance of local antimicrobial susceptibility testing when guiding treatment of wound infections.[17,18]

CONCLUSION

In this study, most of the bacterial isolates were obtained as single-organism (monomicrobial) infections, with Gram-negative bacteria predominating over Gram-positive bacteria. Male patients constituted a larger proportion of the study population, while the highest proportion of patients was observed in the 45–60-year age group. Staphylococcus spp. was the predominant bacterial isolate, followed by Escherichia coli and Klebsiella pneumoniae. The antimicrobial susceptibility pattern showed considerable variation among the bacterial isolates, with high resistance to ampicillin observed in Staphylococcus spp., whereas vancomycin showed 100% susceptibility among the tested Staphylococcus isolates. Among the Gram-negative organisms, relatively high susceptibility to amikacin was observed, particularly among E. coli. These findings provide useful information on the local distribution of wound pathogens and their antimicrobial susceptibility patterns and may assist in selecting appropriate antimicrobial therapy for wound infections.

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