

PREVALENCE OF ORGANISMS ISOLATED FROM PUS & SWAB & THEIR ANTIBIOTIC SUSCEPTIBILITY PATTERN

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Received : 08/02/2025
 Received in revised form : 01/04/2025
 Accepted : 16/04/2025

Keywords:

Antibiotic Susceptibility Pattern,
 Isolates, Staphylococcus, Escherichia coli.

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DOI: 10.47009/jamp.2025.7.2.195

Source of Support: Nil,
 Conflict of Interest: None declared

Int J Acad Med Pharm
 2025; 7 (2); 969-973

**Abstract**

Background: The presence of pathogenic bacteria in the wound does not imply infection. Infection occurs when one or more than one contaminant evades the host defenses, replicating in large numbers, attacks, and harms the host tissue. Different microbial organisms can infect wounds. They are likely *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Klebsiella* spp, *Acinetobacter* spp, *Escherichia coli*, *Proteus* spp, and *Enterobacter* spp. **Materials and Methods:** This study was included 170 cases of pus and swab from the out and in patients. This study was conducted in Department This study was conducted in Mediinn Diagnostics Private Limited, Belur, Howrah. The duration of study was over a period of one year. **Result:** Out of 170 clinical specimens, pus cultures (63.5%) were more commonly collected than wound swabs (36.5%), and also showed a higher microbial growth rate (59.3% vs. 19.3%). Of the 76 specimens with growth, gram-negative bacteria (71.1%) were more prevalent than gram-positive (28.9%). *Escherichia coli* was the most frequently isolated organism (31.5%), followed by *Staphylococcus aureus* (18.4%) and *Pseudomonas* spp. (17.1%). **Conclusion:** This study concludes that there are very limited treatment options available for the resistant bacteria. So, early detection and appropriate antibiotic application remain a significant priority in controlling the development and spread of multidrug resistant organisms.

INTRODUCTION

A wound is defined as a disruption in the skin's protective barrier and a loss of epithelial continuity, which may occur with or without the loss of underlying connective tissue.^[1] Various microorganisms can cause wound infections, making it one of the most frequent healthcare-associated infections, often leading to prolonged hospital stays and increased medical expenses.^[1] Diabetes is a prevalent comorbidity that contributes to the development of wound infections.^[2] Notably, diabetic wound infections are often polymicrobial, characterized by higher bacterial loads and a greater likelihood of colonization by antimicrobial-resistant organisms compared to non-diabetic cases.^[2,3] The mere presence of pathogenic bacteria in a wound does not necessarily indicate an infection. Infection arises when one or more pathogens evade the host's immune response, proliferate extensively, and cause tissue damage. A wide range of microorganisms can infect wounds, including *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Klebsiella* spp., *Acinetobacter* spp., *Escherichia coli*, *Proteus* spp., and *Enterobacter* spp.^[4-6]

Complications from wound infections are commonly linked to inadequate hospital management and poor aseptic practices during surgical and other medical procedures. These infections are among the most frequently acquired in healthcare settings, significantly contributing to prolonged hospitalizations, increased healthcare costs, and elevated morbidity and mortality rates, particularly in developing countries.^[7-9] Additionally, regional and local differences exist in the types of microorganisms responsible for wound infections. Therefore, it is essential for clinicians to understand the prevalent pathogens and their antimicrobial resistance patterns within their specific region.^[10]

This study was undertaken to identify the bacterial pathogens associated with wound infections and to assess their resistance profiles against commonly prescribed antibiotics in patients with wound infections.

MATERIALS AND METHODS

Study Population: This study was included 170 cases of pus and swab from the out and in patients.

Study Area: This study was conducted in Mediinn Diagnostics Private Limited, Belur, Howrah.

Study Duration: The duration of study was over a period of one year.

Data collection: Samples were inoculated onto blood agar and MacConkey agar media, then incubated aerobically at 37°C for 24 hours. For the isolation and identification of bacteria, the culture plates were examined for bacterial growth. The organisms were identified based on colony morphology, hemolysis patterns, pigment production, Gram staining, and various biochemical tests. Antimicrobial susceptibility testing was performed according to Clinical and Laboratory Standards Institute (CLSI) guidelines.

Data analysis: Data were analyzed by using Microsoft excel.

RESULTS

Out of 170 clinical specimens, pus cultures (63.5%) were more commonly collected than wound swabs (36.5%), and also showed a higher microbial growth rate (59.3% vs. 19.3%). Of the 76 specimens with growth, gram-negative bacteria (71.1%) were more

prevalent than gram-positive (28.9%). *Escherichia coli* was the most frequently isolated organism (31.5%), followed by *Staphylococcus aureus* (18.4%) and *Pseudomonas* spp. (17.1%). Antibiotic susceptibility testing (AST) revealed that *Enterococcus* spp. showed high sensitivity to most antibiotics. *E. coli* exhibited multidrug resistance, especially to fluoroquinolones and cephalosporins, but remained susceptible to chloramphenicol and amikacin. *Proteus* spp. showed good sensitivity to several antibiotics including fluoroquinolones and cephalosporins. *Staphylococcus* spp. had notable resistance, suggesting MRSA presence, but showed high sensitivity to linezolid and daptomycin. *Klebsiella* spp. showed resistance to multiple antibiotics but responded better to chloramphenicol and amikacin. *Pseudomonas* spp. demonstrated variable resistance, with carbapenems and piperacillin-tazobactam being more effective. *Acinetobacter* spp. showed resistance to nearly all tested drugs, highlighting its multidrug-resistant nature. Coagulase-negative staphylococci (CoNS) were largely susceptible to linezolid, gentamicin, and doxycycline, showing a favorable resistance profile.

Table 1: Distribution of cases according to specimen.

Specimen	Number	Percentage
Pus culture	108	63.5%
Wound swab	62	36.5%
Total	170	100%

Table 2: Distribution of cases according to growth in specimen

Specimen	Growth	No Growth	Total
Pus culture	64	44	108
Wound swab	12	50	62
Total	76	94	170

Table 3: Distribution of cases according to Bacteria

Organism	Number	Percentage
Gram positive bacteria	22	28.9%
Gram negative bacteria	54	71.1%
Total	76	100%

Table 4: Distribution of cases according to isolates

Isolates	Number	Percentage
<i>Pseudomonas</i> spp.	13	17.1%
<i>Escherichia coli</i>	24	31.5%
<i>Klebsiella</i> spp.	5	6.5%
<i>Proteus</i> spp.	8	10.5%
<i>Acinetobacter</i> spp.	2	2.6%
<i>Staphylococcus aureus</i>	14	18.4%
CoNS	8	10.5%
<i>Enterococci</i> spp.	2	2.6%
Total	76	100%

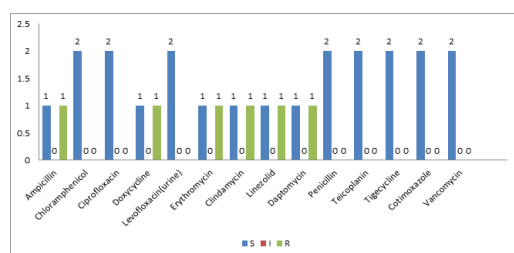


Figure 1: Antibiotic susceptibility pattern of *Enterococcus* spp.

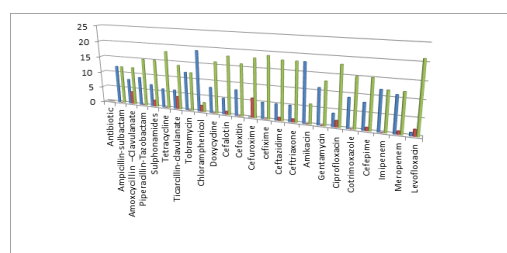


Figure 2: Antibiotic susceptibility pattern of *Escherichia coli*

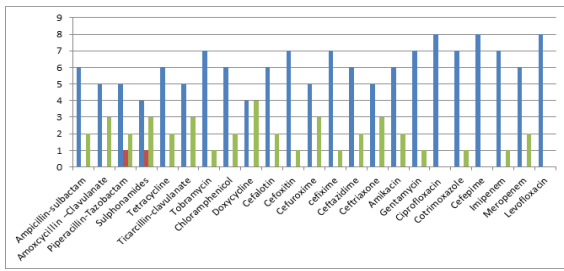


Figure 3: Antibiotic susceptibility pattern of Proteus spp.

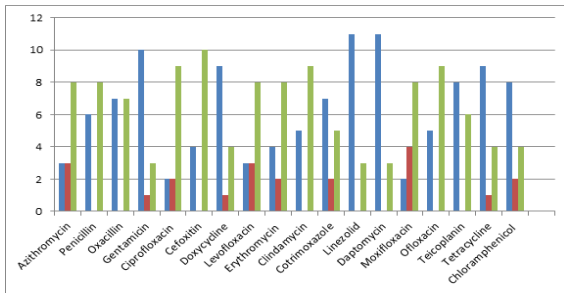


Figure 4: Antibiotic susceptibility pattern of Staphylococcus spp.

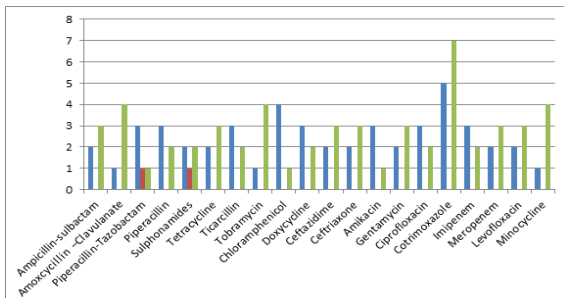


Figure 5: Antibiotic susceptibility pattern of Klebsiella spp.

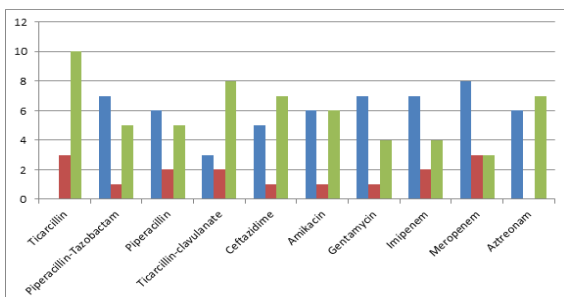


Figure 6: Antibiotic susceptibility pattern of Pseudomonas spp.

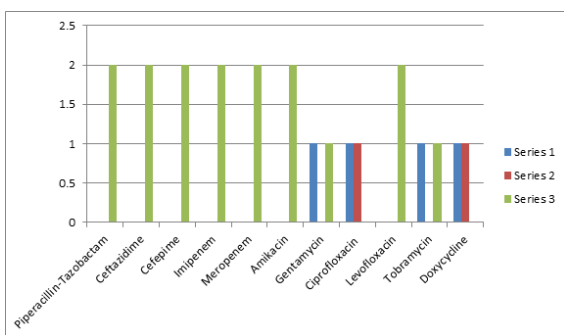


Figure 7: Antibiotic susceptibility pattern of Acinetobacter spp.

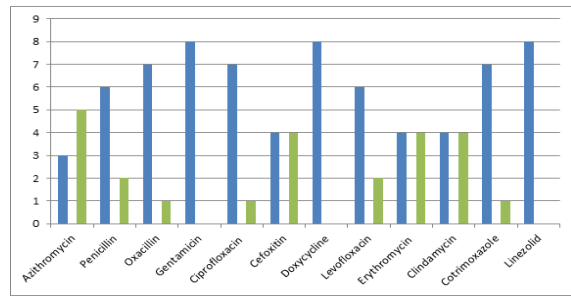


Figure 8: Antibiotic susceptibility pattern of CONS

DISCUSSION

Despite adherence to basic wound care principles, many patients still develop infections that necessitate accurate identification of causative organisms for appropriate management. The spectrum of isolated organisms and their antimicrobial susceptibility patterns often vary between hospitals, highlighting a dynamic trend. The development and spread of antibiotic resistance can be mitigated through the judicious use of antimicrobials, stringent infection control practices, and ongoing surveillance efforts.

In the present study, bacterial growth was observed in 44.7% of cultured samples, which aligns with findings from several previous studies.^[11,12] Consistent with other reports,^[13,14] of the 170 specimens analyzed, 63.5% were pus cultures and 36.5% were wound swabs, indicating that pus samples were the more commonly collected specimens. Among the 76 specimens with positive bacterial growth, 54 (71.1%) yielded gram-negative bacteria, while 22 (28.9%) were gram-positive, suggesting a predominance of gram-negative organisms in this study. However, some studies have reported nearly equal distributions of gram-positive and gram-negative isolates from wound and pus specimens.^[15,16]

In this study, *Escherichia coli* was the most frequently isolated organism (31.5%), followed by *Staphylococcus aureus* (18.4%) and *Pseudomonas* spp. (17.1%). Other isolates included *Klebsiella* spp. (6.5%), *Proteus* spp. (10.5%), coagulase-negative staphylococci (CoNS, 10.5%), and *Acinetobacter* spp. and *Enterococcus* spp., each accounting for 2.6%. These findings indicate that *E. coli* and *S. aureus* were the most prevalent pathogens in this study. The bacterial profile of wound infections is influenced by the hospital environment and the types of surgical procedures performed.

While *Pseudomonas* spp. was the most commonly isolated gram-negative bacterium in other studies, followed by *E. coli*, *Klebsiella* spp., and *Proteus* spp., similar findings were reported in a study conducted in India.^[17] In Bangladesh, the frequency of *Pseudomonas* spp. in wound infections was 28% in 2011 and 26.5% in 2016, both lower than the rate observed in the present study.^[18,19] The higher incidence of *Pseudomonas* in this study may be attributed to a large proportion of wound swab samples being collected from burn units.

Pseudomonas spp. is a ubiquitous and opportunistic pathogen that commonly causes burn wound infections, originating from endogenous gastrointestinal flora or environmental sources.^[20,21] This organism produces various virulence factors that facilitate adhesion, immune evasion, tissue destruction, and bloodstream invasion, making it particularly effective in infecting burn wounds.^[22,23] In contrast, some studies have identified *E. coli* as the predominant gram-negative pathogen. These discrepancies may reflect variations in infection prevalence across hospitals, which handle differing types of infections. In the current study, *Staphylococcus aureus* was the most commonly isolated gram-positive bacterium from both wound swabs and pus samples, consistent with studies conducted in Bangladesh and India.^[24] Approximately 50% of the *S. aureus* isolates were identified as methicillin-resistant *Staphylococcus aureus* (MRSA). The MRSA prevalence in Bangladesh ranges from 32% to 63% in various studies, which aligns with the rate found in this study.^[25] MRSA is a multidrug-resistant bacterium, exhibiting resistance to methicillin, other penicillins, most cephalosporins, and carbapenems. Antibiotic susceptibility data from this study revealed limited effectiveness of several commonly used antibiotics in treating wound infections. Among gram-negative bacilli, the highest resistance was observed against amoxicillin, followed by fluoroquinolones and third-generation cephalosporins, consistent with findings from several studies.^[26,27] Although ciprofloxacin is considered a critical antibiotic, gram-negative organisms in this study demonstrated high levels of resistance to it, which is in line with prior reports.^[28,29] The findings suggest that amikacin may serve as a viable alternative for treating infections caused by gram-negative bacilli in this setting. Carbapenems remained highly effective, showing 66–97% sensitivity against gram-negative organisms, excluding *Acinetobacter* spp., which corroborates results from other studies.^[29] Gram-positive bacteria, particularly *S. aureus*, showed high sensitivity to vancomycin and linezolid. All *S. aureus* isolates were susceptible to vancomycin, a pattern similar to that reported in other studies.^[29]

CONCLUSION

This study concludes that treatment options for resistant bacterial pathogens are notably limited. Therefore, early detection and the judicious use of appropriate antibiotics are critical for managing and preventing the emergence and spread of multidrug-resistant organisms.

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