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# SPECTRUM OF BACTERIAL ISOLATES FROM PUS SAMPLES AND THEIR ANTIMICROBIAL SUSCEPTIBILITY PATTERNS IN A TERTIARY CARE HOSPITAL OF NORTH BIHAR

**Medical Microbiology**

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## ABSTRACT

Pyogenic infections are characterized by pus formation resulting from localized inflammatory responses and active microbial proliferation. Wound infections are frequently polymicrobial and may involve a broad spectrum of microorganisms. This study evaluated the bacterial profile of pus samples and their antimicrobial susceptibility patterns. Of the 107 samples analyzed, 44 (41.1%) were culture-positive, while 63 (58.9%) showed no growth; mixed bacterial growth was observed in two cases. Among the isolates, 20 (43.5%) were Gram-positive and 26 (56.5%) were Gram-negative organisms. These findings underscore the substantial burden of wound infections and highlight the importance of routine antimicrobial susceptibility testing to guide the development of effective local antibiotic policies.

## KEYWORDS

Pyogenic infections, Pus samples, Bacterial isolates, Antimicrobial susceptibility pattern

## INTRODUCTION

Pyogenic infections are defined as infections characterised by the formation of pus due to localised inflammatory responses and the active multiplication of microorganisms. Pus formation is a hallmark feature of such infections [1]. Wound infections commonly arise following disruption of the skin or mucosal barriers, which may occur as a consequence of surgical procedures, traumatic injuries or bites from animals or humans[2].

These infections may be either exogenous or endogenous in origin. Endogenous wound infections and abscesses are frequently associated with conditions such as appendicitis, cholecystitis, cellulitis dental infections, osteomyelitis, septic arthritis and empyema [3]

Wound infections are typically polymicrobial in nature and may harbor a wide range of microorganisms, including bacteria, viruses, fungi and parasites. These pathogens can exist as aerobic, anaerobic or facultative organisms [4] . Both Gram positive and Gram negative bacteria are commonly implicated in wound infections. Amng the Gram positive organisms, coagulase positive *Staphylococcus aureus*, *Enterococcus fecalis* are frequently isolated, while Gram negative pathogens such as *Escherichia coli*, Klebsiella spp, Pseudomonas aeruginosa, Proteus mirabilis and Acinetobacter spp are also widely reported [5]. The spectrum of microorganisms responsible for wound infections varies not only between different countries but also among hospitals within the same country, reflecting differences in patient populations, infection control practices and antibiotic usage pattern[6] . Complications arising from wound infections are frequently linked to suboptimal hospital practices during surgical and other invasive medical procedures. Such infections constitute one of the most common healthcare-associated infections and contribute substantially to prolonged hospital stays, increased healthcare costs, and elevated rates of morbidity and mortality. This burden is particularly pronounced in developing countries, where limitations in resources, infection control measures, and surveillance systems further exacerbate patient outcomes[7]. The irritational and prolonged use of antibiotics has resulted in the emergence and spread of resistant organisms, leading to increased treatment failures, morbidity and mortality [5]. Appropriate antimicrobial therapy relies on accurate pathogen identification, understanding of disease pathophysiology, and consideration of the drug's pharmacokinetic and pharmacodynamic properties. The rising burden of antimicrobial resistance further complicates the development of effective treatment protocols.

Therefore, precise identification of infecting organisms and determination of their antimicrobial susceptibility patterns are essential for guiding targeted therapy and limiting dissemination of resistant strains[8].

## MATERIALS & METHODS

This retrospective observational study was conducted in the Department of Microbiology at Shree Narayan Medical Institute & Hospital, Saharsa (Bihar), over a one-year period from April 2024 to March 2025. A total of 107 pus samples were collected aseptically from patients attending both inpatient (IPD) and outpatient (OPD) services across various clinical departments. All samples were Gram-stained and cultured on blood agar and MacConkey agar, followed by incubation at 37 °C for 24–48 hours. The organisms were identified based on colony morphology, hemolysis patterns, pigment production, Gram's staining and various biochemical tests. Antimicrobial susceptibility testing was performed according to Clinical and Laboratory Standards Institute (CLSI).

## RESULTS

In the present study, a total of 107 samples were collected, of which 44 (41.1%) were culture positive, while the remaining 63 (58.9%) were sterile. Among the culture positive 44 isolates, 2 yielded the mixed growth. Of the total organisms isolated, 20 (43.5%) were Gram positive, 26 (56.5%) were Gram negative organisms.

Among the Gram positive isolates, *Staphylococcus aureus* was the most frequently identified organism (n=15) followed by *Enterococcus spp* (n= 3). Coagulase negative staphylococci (CoNS) and Candida species were detected in one isolate each as shown in table 1.

With respect to Gram negative organisms, *Escherichia coli* is the predominant isolate (n=14), followed by *klebsiella pneumonae* (n=7), pseudomonas species (n=4) and Citrobacter species (n= 1).

Antimicrobial susceptibility testing revealed that among Gram negative organisms, *Escherichia coli* demonstrated the highest sensitivity to amikacin, followed by Piperacillin tazobactam, gentamycin and ceftriaxone.

Gram positive organisms exhibited the highest sensitivity to Linezolide (95%), followed by vancomycin (84%), Clindamycin (79%) and Cotrimoxazole (68%).

Conversely, the lowest sensitivity was observed with Erythromycin (16%), followed by ceftriaxone (26%) and ampicillin (32%).

**Table 1: Organisms Isolated From Pus Cultures**

| Organisms | Growth n = 46 | Percentage (%) |
|---|---|---|
| *Staph aureus* | 15 | 32.6 |
| Enterococcus | 03 | 6.52 |
| CoNS | 01 | 2.17 |
| *Escherichia coli* | 14 | 30.43 |
| Pseudomonas spp | 04 | 8.7 |
| *Klebsiella pneumonae* | 07 | 15.22 |
| Citrobacter spp | 01 | 2.17 |
| Candida spp | 01 | 2.17 |

**Table 2 Antibiotic Susceptibility Pattern Of Gran Negative Isolates**

| Antimicrobials | Sensitive n (%) | Resistance n (%) |
|---|---|---|
| Ampicillin | 6 (23) | 20 (77) |
| Ceftriaxone | 13 (50) | 13 (50) |
| Ceftazidime | 4 (15) | 22 (85) |
| Amikacin | 15 (58) | 11 (42) |
| Gentamicin | 12 (46) | 14 (54) |
| Ciprofloxacin | 7 (27) | 19 (73) |
| Imepenem | 9 (35) | 17 (65) |
| Pipracillin -Tazobactam | 14 (54) | 12 (46) |
| Amocyclav | 7 (27) | 19 (73) |

**Table 3 Antibiotic Susceptibility Pattern Of Gram Positive Isolates**

| Antimicrobials | Sensitive (%) | Resistance (%) |
|---|---|---|
| Ampicillin | 6 (32) | 13 (68) |
| Gentamycin | 11 (58) | 8 (42) |
| Erythromycin | 3 (16) | 16 (84) |
| Clindamycin | 15 (79) | 4 (21) |
| Linezolide | 18(95) | 1 (5) |
| Vancomycin | 16 (84) | 3(16) |
| Cotrimoxazole | 13 (68) | 6 (32) |
| Ceftriaxone | 5 (26) | 14 (74) |
| Amoxyclav | 10 (53) | 9 (47) |

## DISCUSSIONS

The present study evaluated the bacteriological profile of pus samples received in the Department of Microbiology. A high rate of culture positivity was observed with, *Staphylococcus aureus* emerging as the most frequently isolated organism, followed by *Escherichia coli.*

The present study demonstrated a predominance of Gram negative bacterial isolates (56.5%), which is in agreement with the observations previously reported by Shrestha K et al[9]. The predominance of *Staphylococcus aureus* in pyogenic infections observed in this study is consistent with the findings of Wadekar et al. and Roopashree et al.[1,4], both of whom reported *S. aureus* as the leading cause of pyogenic infections. This predominance may be attributed to its ability to colonize the skin and produce multiple virulence factors that facilitate tissue invasion and abscess formation.

The predominance of *Escherichia coli* among Gram negative isolates (30.43%) observed in the present study corroborates with the findings of Sudhaharan S et al, who also reported *Escherichia coli* as the leading Gram - negative pathogen, with a prevalence of 38.6% [10] .The high prevalence of E*scherichi*a *coli* may be attributed to its wide distribution in the human gastrointestinal tract, its ability to acquire virulence factors, and its frequent association with both community acquired and hospital acquired infections. These characteristics contribute to its sustained clinical relevance. The isolation of other Gram negative organisms as shown in table 1 in the present study further reflects the diverse etiological spectrum of Gram negative infections. In our study, Gram positive isolates demonstrated the highest sensitivity to linezolide (95%), followed by vancomycin (84%), clindamycin (79%), and cotrimoxazole (68%). These findings are comparable to those reported by Vijetha S, et al [11], who also reported linezolide and vancomycin as most effective antimicrobials followed by clindamycin, indicating the continued effectiveness of these antibiotics against Gram – positive pathogens. The Gram positive isolates recovered from pus samples exhibited minimal susceptibility to erythromycin and ampicillin as shown in Table 3. This reduced sensitivity pattern is consistent with the observations reported by Vijetha S, et al [11], suggesting a comparable resistance trend among Gram positive pathogens in similar clinical settings.

Among the Gram-negative isolates, the highest sensitivity was observed to amikacin (58%), followed by piperacillin–tazobactam and ceftriaxone (Table 2). This finding is consistent with the study by Gomatheswari S. et al[12], who also reported amikacin as the most effective agent against Gram-negative isolates from pus samples, highlighting the continued efficacy of aminoglycosides in such infections. In contrast, ceftazidime and ampicillin showed the lowest sensitivity among Gram-negative isolates, a pattern that aligns with observations from previous studies.

## CONCLUSIONS

The present study highlights the significant burden of wound infections and emphasise the importance of determining the antibiotic susceptibility patterns to guide the formulation of effective local antibiotic policies. A clear understanding of the bacteriological profile of wound infection is essential for clinicians, as these infections are a significant cause of mortality and morbidity. Looking ahead, optimal management of wound infections will depend on a comprehensive, multifaceted strategy that combines ongoing microbiological research and advanced diagnostic technologies.

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