

Original Research Article

Multidrug resistant gram-negative bacteria in surgical site infection of cancer patients: a cause of concern

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ABSTRACT

Background: A number of variables contribute to the high frequency of surgical site infections (SSI) in cancer patients and the presence of multidrug resistant (MDR) bacteria in SSI's exacerbates the condition. MDR in cancer patients exacerbates SSI problems like extended hospital stays, higher costs and more challenging treatment of these organism, which lowers survival. This study was done to identify antibiotic and microbial resistance in pus samples obtained from post operative SSI cases of cancer patients so that empirical treatment could be started in cancer patients.

Methods: The study was carried out in the department of microbiology, Government Cancer Hospital during the period from January 2022 to December 2022. A total 82 pus samples were collected and processed for culture, identification as per standard recommended procedures and antibiotic susceptibility testing were carried out on isolates as per clinical laboratory standard institute (CLSI) guidelines.

Results: A total of 82 specimens were cultured. *Pseudomonas aeruginosa*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii*, were most commonly encountered. A high level of resistance to various antibiotics was noted among Gram negative bacteria.

Conclusions: The current investigation demonstrated microbiological profile in cancer patients. There exists an unmet need for surveillance of MDR bacteria, as well as for the implementation of effective antimicrobial regimens and antibiotic stewardship programs.

Keywords: Cancer, Gram-negative bacteria, Immunocompromised, Multidrug resistance

INTRODUCTION

Despite the significant progress achieved by medical science in treating cancer, infections continue to pose a significant threat to the health and survival of cancer patients. The immunocompromised state of cancer patients arises from the disease's intrinsic nature and the treatments they undergo, including chemotherapy. Furthermore, factors such as long-term catheterization, mucositis resulting from cytotoxic agents, neutropenia, and stem cell transplantation often increases the risk of infection in these individuals.¹

Surgical site infections (SSI) are a prominent complication associated with surgical treatments and a leading cause of nosocomial infections.²

In managing infections in cancer patients, empirical treatment frequently involves the administration of broad-spectrum or combination antibiotics until culture and susceptibility results become available. The improper and indiscriminate use of antibiotics for both therapeutic and nontherapeutic purposes contribute to the rise of antimicrobial resistance (AMR). Within hospital settings, this phenomenon results in extended hospitalization, heightened levels of morbidity and mortality, and a

growing economic strain on both individuals and nations.³ This holds especially true for members of the Enterobacteriaceae group, including *Escherichia coli* and *Klebsiella spp.*, as well as non-fermenter bacteria such as *Pseudomonas spp.* and *Acinetobacter spp.*⁴

In recent years, the prevalence of multidrug-resistant organisms worldwide has quadrupled. This challenge becomes more intricate in developing nations due to inadequate infection control measures, overcrowded healthcare facilities, and the improper utilization of antimicrobials.⁵ Additionally, the increasing rates of antibiotic resistance in commonly encountered organisms globally exacerbate the susceptibility to bacterial infections.^{6,7}

Understanding the causative agents of infections and their susceptibility to existing drugs is crucial for making informed decisions regarding the selection and utilization of antimicrobial agents. It also plays a significant role in formulating appropriate prescribing guidelines.^{8,9}

Therefore, this study sought to fill the knowledge gap and equip clinicians with the necessary resources to offer safe and efficient empirical therapy. It aimed to achieve this by determining the prevalence of common bacterial isolates and analysing their antimicrobial susceptibility patterns in various clinical samples obtained from patients visiting the cancer hospital.¹⁰

METHODS

The hospital based retrospective study was conducted at the department of microbiology, Government Cancer Hospital, located in Aurangabad, Marathwada.

The study spanned over one-year period from January 2022 to December 2022 and focused on samples obtained from surgical site infections (SSI) occurring in postoperative cancer patients. Pus samples were collected in accordance with the hospital's sample collection protocol from various clinical areas. Clinical data were extracted from requisition forms and patient units and wards. Standard microbiology laboratory procedures were followed for sample processing, with isolates identified based on colonial morphology and Gram staining. Antimicrobial sensitivity testing was conducted according to the clinical laboratory standard institute (CLSI) criteria. The microbiological spectrum and antibiotic sensitivity patterns of bacterial isolates were analysed using VITEK® 2 test cards, including GN ID cards for Gram-negative bacterial identification and GP ID cards for Gram-positive bacterial identification.

RESULTS

Over the course of one year, a total of eight two (82) samples were received and processed from various departments within the hospital. Out Of these, 72 organisms were isolated.

Among the 72 isolated organisms, 58 were gram-negative, while the remaining were gram-positive. The most prevalent gram-negative organism isolated was *Pseudomonas aeruginosa*, followed by *Escherichia coli* and *Klebsiella pneumoniae*. Additionally, *Acinetobacter baumannii* was also identified among the isolates as shown in Table 1.

Table 1: Most prevalent gram-negative organism isolated from pus sample.

Organism	No. of organisms isolated
<i>Pseudomonas aeruginosa</i>	28
<i>Escherichia coli</i>	16
<i>Klebsiella pneumoniae</i>	8
<i>Acinetobacter baumannii</i>	6

Table 2: Number of MDR strains.

Organism	No. of MDR strains
<i>Pseudomonas aeruginosa</i>	18 (64%)
<i>Escherichia coli</i>	14 (87.5%)
<i>Klebsiella pneumoniae</i>	5 (62.5%)
<i>Acinetobacter baumannii</i>	6 (100%)

Gram-negative bacteria (GNB) were the majority of the organisms that caused surgical site infections (SSI) in our analysis. As shown in Table 2, 43 (74%) of the isolates had multidrug resistance.

Furthermore, 33 (55%) isolates showed carbapenem resistance, while 65% of the organisms showed resistance to beta-lactam combination drugs. Notably, our investigation showed that colistin and polymyxin were the most effective antibiotics.

DISCUSSION

The study aimed to assess emerging bacterial trends and their susceptibility patterns, with the goal of understanding prevalent resistance patterns and evaluating the effectiveness of prescribed drugs in treating infections.¹⁰

In our research, the primary group of organisms responsible for surgical site infections (SSI) were gram-negative bacteria, consistent with findings shown by deka et al and Bhat et al.^{1,3} The lack of patient awareness regarding personal hygiene, coupled with a high environmental load of gram-negative bacteria, and inadequate infection control practices- particularly in post-surgical wards- might contribute significantly to the development of SSIs. Notably, *Pseudomonas aeruginosa* emerged as the primary organism causing surgical site infections, similar finding was noted from the study conducted in India by Sapna et al.⁵

Our study revealed a notably high resistance percentage among organisms to beta-lactam antibiotics and the

combination of beta-lactam/beta-lactamase inhibitors. Comparable high rates of resistance to these drugs were observed by Bhat et al and Kotgire et al.^{3,14} *Acinetobacter* spp. exhibited elevated resistance to aminoglycosides and carbapenems in our study as shown in Figure 4, mirroring findings from research conducted by Bhat et al and Garg et al.^{3,4}

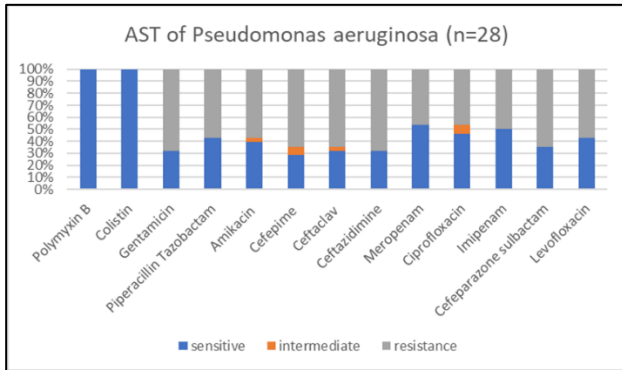


Figure 1: Antibiotic susceptibility pattern of *Pseudomonas aeruginosa*.

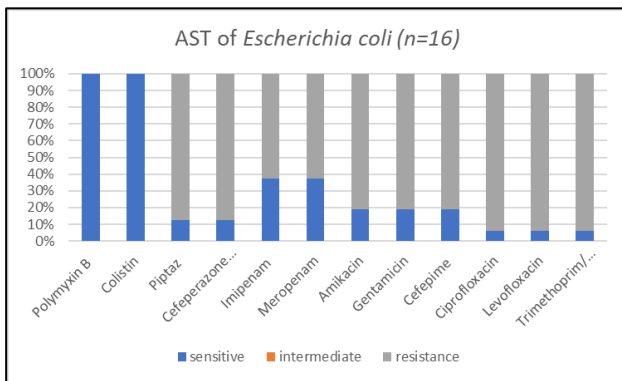


Figure 2: Antibiotic susceptibility pattern of *Escherichia coli*.

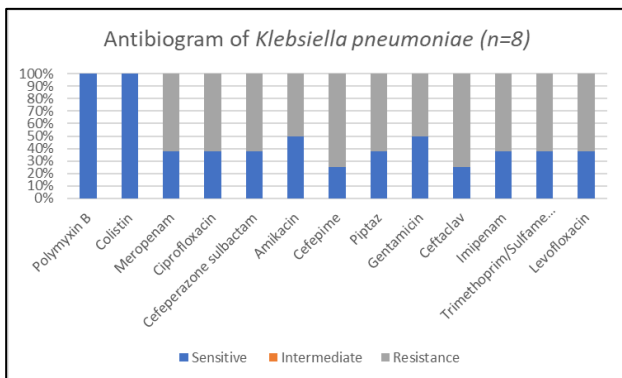


Figure 3: Antibiotic susceptibility pattern of *Klebsiella pneumoniae*.

In our study, resistance to carbapenems was notably prevalent among non-fermenters such as *Acinetobacter* (68%) as shown in Figure 4 and *Pseudomonas* (50%) as

shown in Figure 1, followed by members of the Enterobacteriaceae family like *Escherichia coli* (62%) as shown in Figure 2 and *Klebsiella* (62%) as shown in Figure 3. Additionally, *Acinetobacter* exhibited a resistance rate of 22%. It's noteworthy that the resistance to carbapenems at our institution exceeded that reported by Bhat et al and Kotgire et al.^{3,14}

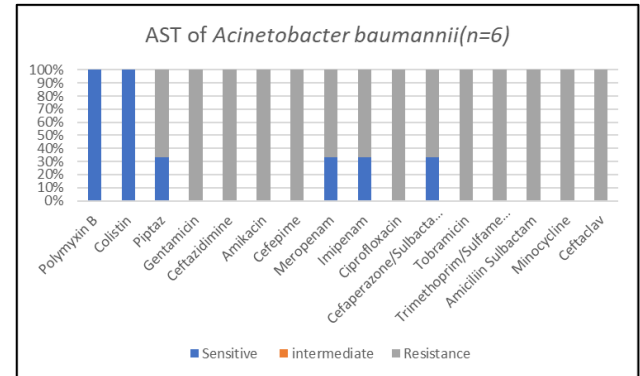


Figure 4: Antibiotic susceptibility pattern of *Acinetobacter baumannii*.

In our study, we observed a significant prevalence of multidrug resistance (MDR), a concerning trend noted by other researchers as well.⁶ This high incidence of resistant organisms underscores the necessity of developing antibiotic policies tailored to local antibiotic susceptibility patterns. Such policies can help mitigate the arbitrary use of antibiotics and minimize the development of resistance.⁴

CONCLUSION

In oncological patients, microbial patterns have shifted towards multidrug resistance, posing a significant challenge. Infections caused by multidrug-resistant (MDR) bacteria can substantially impact patient outcomes. There exists an unmet need for surveillance of MDR bacteria, as well as for the implementation of effective antimicrobial regimens and antibiotic stewardship programs. Furthermore, wide-scale adoption of infection control measures within oncology departments is imperative to address this issue effectively.

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Conflict of interest: None declared

Ethical approval: The study was approved by the Institutional Ethics Committee

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