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Prevalence and Antimicrobial Resistance Patterns of Multidrug-Resistant Bacterial Pathogens Isolated from Cancer Patients

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ABSTRACT

Background: Antimicrobial resistance has emerged as a major global health concern, particularly among immunocompromised populations such as cancer patients. Frequent hospitalization, invasive procedures, prolonged antibiotic exposure, and immunosuppressive therapies predispose cancer patients to infections caused by multidrug-resistant (MDR) organisms. These infections are associated with increased morbidity, mortality, and limited therapeutic options, highlighting the need for continuous surveillance of antimicrobial resistance patterns in oncology settings.

Objectives: To isolate and identify Gram-positive and Gram-negative bacterial pathogens from clinical samples obtained from cancer patients and to determine their antimicrobial susceptibility patterns with special emphasis on multidrug-resistant organisms.

Methods: A prospective observational study was conducted from January to March 2014. A total of 51 clinical samples, including pus, urine, blood, body fluids, wound swabs, sputum, tracheal secretions, stool, and central line tips, were processed using standard microbiological techniques. Bacterial identification was performed based on culture characteristics, Gram staining, and biochemical tests. Antimicrobial susceptibility testing was carried out using the modified Kirby-Bauer disc diffusion method according to CLSI guidelines. Multidrug resistance was defined as resistance to three or more classes of antibiotics.

Results: Out of 51 samples, 27 (52.9%) yielded bacterial growth. Gram-negative organisms slightly predominated (51.9%). *Escherichia coli* (29.6%) was the most frequently isolated pathogen, followed by *Staphylococcus aureus* (25.9%) and *Streptococci* spp. (22.2%). Overall, 55.6% of isolates were multidrug resistant. The highest MDR rate was observed among *E. coli* (87.5%) and *Pseudomonas aeruginosa* (60.0%). Most isolates remained susceptible to carbapenems, colistin, linezolid, and rifampicin.

Conclusion: The study demonstrates a high prevalence of multidrug-resistant bacterial pathogens among cancer patients, emphasizing the urgent need for rational antibiotic use, continuous resistance surveillance, and effective antimicrobial stewardship programs in oncology care settings.

Keywords: Multidrug-resistant bacteria, Cancer patients, Antimicrobial resistance, Gram-positive and Gram-negative pathogens, Antibiotic susceptibility

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INTRODUCTION

Antimicrobial resistance (AMR) has emerged as a major global health concern, threatening the effective prevention and treatment of bacterial infections. The resistance of pathogenic microorganisms to commonly used antibiotics has increased at an alarming rate, resulting in limited therapeutic options, prolonged hospital stays, increased healthcare costs, and higher mortality rates [1,2]. The widespread misuse and overuse of antibiotics in human medicine, veterinary practice, and agriculture have been identified as the primary drivers of this phenomenon [3]. In recent decades, the lack of development of new antibiotic classes has further intensified the crisis, making the control of resistant infections increasingly difficult [4].

Multidrug-resistant (MDR) organisms represent a particularly serious subset of resistant pathogens. These organisms are defined as bacteria resistant to three or more classes of antimicrobial agents and are often associated with hospital-acquired infections [5]. Clinically significant MDR pathogens include *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus* (VRE), and other Gram-positive and Gram-negative bacteria [6]. The ability of these organisms to acquire and disseminate resistance determinants through horizontal gene transfer mechanisms such as conjugation, transformation, and transduction contributes significantly to their rapid spread within healthcare settings [7].

Cancer patients are among the most vulnerable populations for infections caused by MDR organisms. Immunosuppression resulting from malignancy, chemotherapy, radiotherapy, prolonged hospitalization, invasive procedures, and frequent exposure to broad-spectrum antibiotics markedly increases the risk of acquiring infections [8]. Infections in cancer patients are often severe and may lead to poor clinical outcomes, particularly when caused by MDR Gram-negative organisms such as *E. coli* and *P. aeruginosa*, which are commonly associated with bloodstream infections, urinary tract infections, pneumonia, and wound infections.

Resistance mechanisms employed by MDR bacteria include enzymatic degradation or modification of antibiotics, alteration of antimicrobial targets, reduced permeability of the bacterial cell membrane, and active efflux of drugs from the cell [7]. Among these, the production of extended-spectrum β-lactamases (ESBLs) and carbapenem-hydrolyzing enzymes has become a major concern, especially in Gram-negative bacteria, as these mechanisms confer resistance to multiple β-lactam antibiotics and often coexist with resistance to other antimicrobial classes [9]. The presence of such organisms severely limits treatment options and necessitates the use of last-resort drugs such as carbapenems and colistin.

In developing countries like India, the burden of antimicrobial resistance is further aggravated by unregulated antibiotic use, poor infection control practices, inadequate sanitation, and limited surveillance systems [5]. Regular monitoring of antimicrobial susceptibility patterns, particularly in high-risk groups such as cancer patients, is essential for guiding empirical therapy and implementing effective antimicrobial stewardship programs.

In this context, the present study was undertaken to isolate and identify Gram-positive and Gram-negative bacterial pathogens from various clinical samples obtained from cancer patients and to determine their antimicrobial susceptibility patterns, with special emphasis on the detection of multidrug-resistant organisms.

MATERIALS AND METHODS

Study Design and Study Period: This was a prospective, laboratory-based observational study conducted over a period of three months, from January 2014 to March 2014, at the bacteriology laboratory associated with a tertiary care cancer hospital in Surat, India. The study was designed to isolate, identify, and determine the antimicrobial susceptibility patterns of bacterial pathogens isolated from cancer patients.

Sample Collection: A total of 51 clinical samples were collected from hospitalized cancer patients during the study period. The samples included pus, urine, blood, body

fluids, sputum, wound swabs, tracheal secretions, stool samples, and central line tips. All samples were collected following standard aseptic procedures and universal biosafety precautions to minimize contamination and ensure patient safety.

Sterile, wide-mouthed, screw-capped containers were used for the collection of urine, sputum, and stool samples. Pus and body fluid samples were obtained by needle aspiration under the supervision of trained medical personnel. Swab samples were collected using sterile cotton swabs. Blood samples were collected using standard venipuncture techniques. All samples were transported promptly to the microbiology laboratory and processed within 1-2 hours of collection. Samples that could not be processed immediately were stored under appropriate conditions and analyzed within a maximum of 18 hours [10].

Isolation and Identification of Microorganisms: Each clinical sample was subjected to preliminary examination for physical characteristics, followed by Gram staining for morphological assessment and preliminary classification into Gram-positive or Gram-negative organisms. Samples were inoculated onto appropriate culture media, including Blood agar, MacConkey agar, and Eosin Methylene Blue (EMB) agar, and incubated aerobically at 35-37°C for 18-24 hours.

Bacterial isolates were identified based on colony morphology, hemolytic patterns on Blood agar, lactose fermentation on MacConkey and EMB agar, pigment production on specialized media (such as King's medium for *Pseudomonas aeruginosa*), and standard biochemical tests including Triple Sugar Iron (TSI) agar, citrate utilization, and mannitol fermentation tests, as applicable.

Preparation of Inoculum: For antimicrobial susceptibility testing, bacterial inocula were prepared from freshly grown colonies. The turbidity of the bacterial suspension was adjusted to match the 0.5 McFarland standard, which corresponds to approximately 1.5×10^8 CFU/mL. This standardization ensured uniform and reproducible results during susceptibility testing [11].

Antimicrobial Susceptibility Testing: Antimicrobial susceptibility testing was performed using the modified Kirby-Bauer disc diffusion method. A sterile swab was dipped into the standardized bacterial suspension and evenly spread over the surface of Mueller-Hinton agar plates. Antibiotic discs appropriate for Gram-positive and Gram-negative organisms were applied using a disc dispenser.

The inoculated plates were incubated aerobically at 35-37°C for 18-24 hours. After incubation, the diameter of zones of inhibition was measured in millimeters and interpreted as sensitive, intermediate, or resistant according to the Clinical and Laboratory Standards Institute (CLSI) guidelines [10].

Definition of Multidrug Resistance: Bacterial isolates showing resistance to three or more different classes of antimicrobial agents were classified as multidrug-resistant (MDR) organisms.

Results

A total of 51 clinical samples collected from cancer patients were processed during the study period. These samples included pus, urine, blood, body fluids, wound swabs, sputum, tracheal secretions, stool samples, and central line tips. Of the total samples analyzed, 27 (52.9%) yielded bacterial growth, while 24 (47.1%) showed no growth on culture.

Distribution of Clinical Samples: Among the 51 samples, pus specimens constituted the highest proportion with 17 samples (33.3%), followed by body fluid samples (13; 25.5%) and urine samples (7; 13.7%). Blood samples accounted for 5 samples (9.8%), while wound swabs (3; 5.9%), sputum (2; 3.9%), tracheal secretions (2; 3.9%), stool (1; 2.0%), and central line tips (1; 2.0%) represented smaller proportions (Table 1).

Gender-wise Distribution of Samples: Out of the total samples, 32 (62.7%) were obtained from male patients and 19 (37.3%) from female patients. Male patients contributed a higher proportion of samples across most specimen types. Stool samples were collected exclusively from female patients, whereas sputum, tracheal secretions, and central line tips were collected only from male patients (Table 2).

Table 1: Distribution of clinical samples collected from cancer patients

Sample Type	Number of Samples (%)
Pus	17 (33.3)
Body fluids	13 (25.5)
Urine	7 (13.7)
Blood	5 (9.8)
Wound swab	3 (5.9)
Sputum	2 (3.9)
Tracheal secretion	2 (3.9)
Stool	1 (2)
Central line tip	1 (2)
Total	51 (100)

Table 2: Gender-wise distribution of samples with percentages

Sample Type	Male n (%)	Female n (%)	Total n (%)
Pus	11 (64.7)	6 (35.3)	17 (33.3)
Urine	4 (57.1)	3 (42.9)	7 (13.7)
Blood	3 (60.0)	2 (40.0)	5 (9.8)
Body fluids	7 (53.8)	6 (46.2)	13 (25.5)
Wound swab	2 (66.7)	1 (33.3)	3 (5.9)
Sputum	2 (100)	0 (0)	2 (3.9)
Tracheal secretion	2 (100)	0 (0)	2 (3.9)
Stool	0 (0)	1 (100)	1 (2.0)
Central line tip	1 (100)	0 (0)	1 (2.0)
Total	32 (62.7)	19 (37.3)	51 (100)

Bacterial Isolation and Gram Reaction: Of the 51 samples processed, bacterial growth was detected in 27 samples (52.9%). Gram-negative bacteria accounted for 14 isolates (27.5% of total samples; 51.9% of isolates), while Gram-positive bacteria accounted for 13 isolates (25.5% of total samples; 48.1% of isolates). No bacterial growth was observed in 24 samples (47.1%).

Gram-positive organisms were predominantly isolated from pus samples, whereas Gram-negative organisms were most frequently isolated from urine samples. Blood and central line tip samples showed no bacterial growth (Table 3).

Table 3: Distribution of bacterial isolates based on Gram reaction with percentages

Sample Type	Gram-positive n (%)	Gram-negative n (%)	No Growth n (%)	Total n (%)
Pus	8 (47.1)	3 (17.6)	6 (35.3)	17 (33.3)
Urine	1 (14.3)	5 (71.4)	1 (14.3)	7 (13.7)
Blood	0 (0)	0 (0)	5 (100)	5 (9.8)
Body fluids	2 (15.4)	1 (7.7)	10 (76.9)	13 (25.5)
Wound swab	1 (33.3)	2 (66.7)	0 (0)	3 (5.9)
Sputum	1 (50.0)	1 (50.0)	0 (0)	2 (3.9)
Stool	0 (0)	1 (100)	0 (0)	1 (2.0)
Tracheal secretion	0 (0)	1 (50.0)	1 (50.0)	2 (3.9)
Central line tip	0 (0)	0 (0)	1 (100)	1 (2.0)
Total	13 (25.5)	14 (27.5)	24 (47.1)	51 (100)

Table 4: Distribution of bacterial species isolated (n = 27)

Organism	Number of Isolates (%)
Escherichia coli	8 (29.6)
Staphylococcus aureus	7 (25.9)
Streptococci spp.	6 (22.2)
Pseudomonas aeruginosa	5 (18.5)
Klebsiella pneumoniae	1 (3.7)
Total	27 (100)

Spectrum of Bacterial Isolates: A total of 27 bacterial isolates were identified from culture-positive samples. *Escherichia coli* was the most frequently isolated organism, accounting for 8 isolates (29.6%), followed by *Staphylococcus aureus* with 7 isolates (25.9%). *Streptococci* spp. constituted 6 isolates (22.2%), while *Pseudomonas aeruginosa* accounted for 5 isolates (18.5%). Only one isolate of *Klebsiella pneumoniae* (3.7%) was identified (Table 4).

Table 5: Prevalence of multidrug-resistant (MDR) isolates

Organism	Total Isolates	MDR Isolates n (%)
Escherichia coli	8	7 (87.5)
Pseudomonas aeruginosa	5	3 (60.0)
Staphylococcus aureus	7	3 (42.9)
Streptococci spp.	6	2 (33.3)
Klebsiella pneumoniae	1	0 (0)
Total	27	15 (55.6)

Prevalence of Multidrug-Resistant Isolates: Out of the 27 bacterial isolates, 15 (55.6%) were classified as multidrug resistant. The highest proportion of MDR was observed among *Escherichia coli* isolates, with 7 out of 8 isolates (87.5%) exhibiting multidrug resistance. Among *Pseudomonas aeruginosa*, 3 out of 5 isolates (60.0%) were MDR. MDR was detected in 3 out of 7 *Staphylococcus aureus* isolates (42.9%) and in 2 out of 6 *Streptococci* spp. isolates (33.3%). The single *Klebsiella pneumoniae* isolate was susceptible to all tested antibiotic classes (Table 5).

DISCUSSION

The present study highlights the significant burden of multidrug-resistant (MDR) bacterial infections among cancer patients. More than half of the clinical samples yielded bacterial growth, and a substantial proportion of the isolates demonstrated resistance to multiple classes of antimicrobial agents. These findings reinforce the growing concern that antimicrobial resistance has become a critical threat in immunocompromised populations, particularly among patients undergoing cancer treatment.

In this study, Gram-negative organisms constituted a slightly higher proportion of isolates compared to Gram-positive organisms. This observation is consistent with earlier reports indicating that Gram-negative bacteria are the predominant cause of healthcare-associated infections, especially in hospitalized and critically ill patients [5,12]. Among Gram-negative isolates, *Escherichia coli* was the most frequently isolated pathogen, followed by *Pseudomonas aeruginosa*. These organisms are well recognized as major contributors to urinary tract infections, bloodstream infections, and wound infections in hospital environments [6,13].

A striking finding of this study was the high prevalence of multidrug resistance among *E. coli* isolates, with 87.5% classified as MDR. Resistance to penicillins and cephalosporins was widespread, which may be attributed to the extensive and often empirical use of these antibiotics in hospital settings. The production of extended-spectrum β-lactamases (ESBLs) is a well-documented mechanism underlying such resistance and has been increasingly reported in *E. coli* and *Klebsiella* species [9,14]. The predominance of ESBL-mediated resistance significantly limits treatment options and often necessitates the use of carbapenems as last-resort drugs.

Pseudomonas aeruginosa also exhibited a high level of multidrug resistance, with 60% of isolates classified as MDR. This organism is inherently resistant to many antibiotics and can rapidly acquire additional resistance through multiple mechanisms, including efflux pumps, reduced membrane permeability, and β-lactamase production [7,15]. The observed susceptibility of *P. aeruginosa* isolates to colistin and carbapenems aligns with existing evidence that these agents remain among the few effective therapeutic options for severe MDR infections [13]. However, the reliance on such last-line antibiotics raises serious concerns regarding the potential emergence of pan-drug resistance.

Among Gram-positive organisms, *Staphylococcus aureus* and *Streptococci* spp. were commonly isolated. Nearly 43% of *S. aureus* isolates were identified as MDR, reflecting the persistent problem of methicillin-resistant *Staphylococcus aureus* (MRSA) in

healthcare settings. MRSA infections are particularly problematic in cancer patients due to limited treatment options and the risk of invasive disease [16,17]. In the present study, *S. aureus* isolates showed high susceptibility to linezolid, rifampicin, quinolones, and carbapenems, suggesting that these agents remain effective choices for the management of resistant Gram-positive infections.

The proportion of MDR isolates among *Streptococci* spp. was comparatively lower; however, resistance to multiple antibiotic classes was still observed in a subset of isolates. This finding underscores the importance of continuous surveillance, as resistance patterns among traditionally susceptible organisms are gradually evolving [17]. The overall susceptibility of Gram-positive isolates to glycopeptides and oxazolidinones observed in this study is encouraging but should not lead to complacency, given reports of increasing minimum inhibitory concentrations for vancomycin in staphylococcal infections [6].

The high prevalence of MDR organisms observed in this study can be attributed to several factors common in oncology settings, including prolonged hospital stays, repeated invasive procedures, immunosuppression, and frequent exposure to broad-spectrum antibiotics [10,11]. In developing countries like India, additional challenges such as unregulated antibiotic use, inadequate infection control practices, and limited antimicrobial stewardship programs further exacerbate the problem [5,18].

This study emphasizes the critical need for rational antibiotic prescribing practices and the implementation of effective antimicrobial stewardship programs. Routine monitoring of antimicrobial susceptibility patterns is essential to guide empirical therapy and reduce unnecessary exposure to broad-spectrum antibiotics. Early identification of MDR organisms, coupled with strict infection control measures, can significantly reduce transmission within hospital settings.

Limitations of the Study

Despite providing valuable insights into the prevalence and antimicrobial resistance patterns of bacterial pathogens among cancer patients, the present study has certain limitations. First, the sample size was relatively small and the study was conducted over a short duration of three months, which may limit the generalizability of the findings. Second, the study was carried out at a single laboratory, and resistance patterns may vary across different institutions and geographical regions. Third, molecular characterization of resistance mechanisms, such as confirmation of ESBL or carbapenemase production, was not performed due to resource constraints. Finally, clinical outcomes of infected patients were not evaluated, which could have provided additional insight into the impact of multidrug-resistant infections on patient prognosis. These limitations should be considered when interpreting the results, and larger multicentric studies with molecular analysis are recommended for future research.

Conclusion

The present study demonstrates a high prevalence of multidrug-resistant bacterial pathogens among cancer patients, emphasizing the growing challenge of antimicrobial resistance in oncology care settings. Gram-negative organisms, particularly *Escherichia coli* and *Pseudomonas aeruginosa*, were the predominant pathogens and exhibited high levels of resistance to commonly used antibiotics such as penicillins and cephalosporins. A considerable proportion of Gram-positive organisms, including *Staphylococcus aureus* and *Streptococci* spp., also showed multidrug resistance.

The retained susceptibility of most isolates to carbapenems, colistin, linezolid, and rifampicin highlights their importance as effective therapeutic options; however, reliance on these last-resort drugs underscores the urgent need for judicious antibiotic use. Continuous surveillance of antimicrobial resistance patterns, strict infection control practices, and implementation of robust antimicrobial stewardship programs are essential to limit the further emergence and spread of multidrug-resistant organisms. Early detection and appropriate management of infections in cancer patients can significantly improve clinical outcomes and reduce the burden of antimicrobial resistance.

Authors contribution: PD was involved in the study design, data collection, interpretation of the study. **KC** was involved in manuscript writing.

REFERENCES

1. Alekshun MN, Levy SB. Molecular mechanisms of antibacterial multidrug resistance. Cell. 2007;128(6):1037-1050. DOI: https://doi.org/10.1016/j.cell.2007.03.004 PMid:17382878
2. Alfonso JA. Resistance to antibiotics: are we in the post-antibiotic era? Arch Med Res. 2005;36(6):697-705. DOI: https://doi.org/10.1016/j.arcmed.2005.06.009 PMid:16216651
3. Fox JL. The business of developing antibacterials. Nat Biotechnol. 2006;24(12):1521-1528. DOI: https://doi.org/10.1038/nbt1206-1521 PMid:17160056
4. Barrett JF. Can biotech deliver new antibiotics? Curr Opin Microbiol. 2005;8(5):498-503. DOI: https://doi.org/10.1016/j.mib.2005.08.007 PMid:16125445
5. Gould IM. Antibiotic stewardship: the past, the present and the future. J Antimicrob Chemother. 2009;63(3):447-448.
6. Kluytmans J, van Belkum A, Verbrugh H. Nasal carriage of Staphylococcus aureus: epidemiology, underlying mechanisms, and associated risks. Clin Microbiol Rev. 1997;10(3):505-520. DOI: https://doi.org/10.1128/CMR.10.3.505 PMid:9227864 PMCid:PMC172932
7. Heymann DL, editor. Control of communicable diseases manual. 19th ed. Washington (DC): American Public Health Association; 2008.
8. Hartstein AI, Rashad AL, Liebler JM, Actis LA, Freeman J, Rourke JW, et al. Multiple intensive care unit outbreak of Acinetobacter baumannii resistant to ampicillin-sulbactam and aminoglycosides. Infect Control Hosp Epidemiol. 2004;25(6):557-560.
9. Chenoweth CE. Enterococcus species. In: Mayhall CG, editor. Hospital epidemiology and infection control. 3rd ed. Philadelphia: Lippincott Williams & Wilkins; 2004. p. 530-537.
10. Raghunath D. Emerging antibiotic resistance in bacteria with special reference to India. J Biosci. 2011;36(3):447-454.
11. Falagas ME, Koletsi PK, Bliziotis IA. The diversity of definitions of multidrug-resistant (MDR) and pandrug-resistant (PDR) Acinetobacter baumannii and Pseudomonas aeruginosa. J Med Microbiol. 2006;55(Pt 12):1619-1629. DOI: https://doi.org/10.1099/jmm.0.46747-0 PMid:17108263
12. Wattal C, Oberoi JK, Goel N, Raveendran R, Datta S, Prasad KJ. Multidrug resistant gram-negative bacilli in intensive care units: changing trends. Indian J Med Res. 2010;132:599-606.
13. Paterson DL, Doi Y. A step closer to extreme drug resistance (XDR) in gram-negative bacilli. Clin Infect Dis. 2007;45(9):1179-1181. DOI: https://doi.org/10.1086/522287 PMid:17918079
14. Bradford PA. Extended-spectrum β-lactamases in the 21st century: characterization, epidemiology, and detection of this important resistance threat. Clin Microbiol Rev. 2001;14(4):933-951. DOI: https://doi.org/10.1128/CMR.14.4.933-951.2001 PMid:11585791 PMCid:PMC89009
15. Bonomo RA, Szabo D. Mechanisms of multidrug resistance in Acinetobacter species and Pseudomonas aeruginosa. Clin Infect Dis. 2006;43(Suppl 2):S49-S56. DOI: https://doi.org/10.1086/504477 PMid:16894515
16. Frost LS, Leplae R, Summers AO, Toussaint A. Mobile genetic elements: the agents of open source evolution. Nat Rev Microbiol. 2005;3(9):722-732. DOI: https://doi.org/10.1038/nrmicro1235 PMid:16138100
17. Tiwari HK, Sen MR. Emergence of vancomycin resistant Staphylococcus aureus (VRSA) from a tertiary care hospital from northern part of India. BMC Infect Dis. 2006;6:156. DOI: https://doi.org/10.1186/1471-2334-6-156 PMid:17067393 PMCid:PMC1634751
18. Davies J. Origins and evolution of antibiotic resistance. Microbiologia. 1996;12(1):9-16.
19. Drlica K, Malik M, Kerns RJ, Zhao X. Quinolone-mediated bacterial death. Antimicrob Agents Chemother. 2008;52(2):385-392. DOI: https://doi.org/10.1128/AAC.01617-06 PMid:17724149 PMCid:PMC2224783