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Original Research Article

Clinical bacterial isolates and antibiotic susceptibility patterns in surgical site infections among gyneoncology patients at a government cancer hospital

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ABSTRACT

Background: Surgical site infections (SSIs) are a significant cause of morbidity in gyne-oncology patients due to immunosuppression, complex surgeries, and cancer-related treatments. These infections are often polymicrobial, involving both gram-positive and gram-negative organisms with biofilm formation contributing to treatment resistance. SSIs prolong hospitalization, delay cancer therapy, and increase healthcare costs. Understanding the bacterial profile and antibiotic susceptibility pattern of SSIs in gyne-oncology patients is essential to guide effective antimicrobial therapy and improve surgical and oncologic outcomes.

Methods: The study was carried out in the department of microbiology, Government Cancer Hospital during the period from January 2025 to December 2025. A total 100 samples from surgical sites from gyne-oncology 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 100 specimens were cultured, of which 53 showed bacterial growth. *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Staphylococcus* species were the most commonly isolated organisms. A high level of resistance to multiple antibiotics was observed among both Gram-negative and Gram-positive bacteria.

Conclusions: The present study highlighted the microbiological pattern of isolates in gyne-oncology patients. There is a clear need for ongoing monitoring of multidrug-resistant organisms (MDROs), along with the development of appropriate antimicrobial treatment strategies and the strengthening of antibiotic stewardship initiatives.

Keywords: Gram-negative bacteria, Gram positive bacteria, Gyne-oncology, Immunocompromised, Multidrug resistance

INTRODUCTION

Surgical site infections (SSIs) are among the most common and serious complications following cancer surgeries. Women undergoing cancer-related procedures are at a higher risk of developing SSIs because of multiple factors, including weakened immunity, poor nutritional status, extensive surgical procedures, and the need for chemotherapy or radiotherapy.[1]

SSIs are defined by the Centers for Disease Control and Prevention (CDC) as infections occurring within 30 days of an operation, or within one year if an implant is placed and involving the incision, deep soft tissues or organ space at the surgical site.[2,3]

Cancer patients often have longer hospital stays, frequent catheter use, and undergo complex pelvic surgeries that increase exposure to infection-causing bacteria.[4]

The microbiological pattern of SSIs in gyne-oncology patient population is complex and often polymicrobial. *Staphylococcus aureus* and coagulase-negative *staphylococci* remain predominant pathogens in superficial incisional infections due to their capacity for skin colonization and biofilm formation.[5] Gram-negative bacilli such as *Escherichia coli*, *Klebsiella pneumoniae,* and *Pseudomonas aeruginosa* frequently play a larger role in deep incisional and organ-space SSIs following gynecologic cancer surgery.[6]

SSIs develop through several mechanistic pathways: contamination during incision, perioperative translocation of endogenous flora, hematogenous seeding, and postoperative wound colonization. Biofilm formation plays an especially important role; *staphylococci* and some gram-negative bacilli readily form biofilms on sutures, drains, and necrotic tissue, rendering infections more resistant to host immunity and antimicrobial therapy.[5,7]

Coexisting medical comorbidities such as diabetes mellitus, hypertension, obesity, anemia and poor functional status further increase susceptibility to SSI.[8]

In addition, conditions such as neutropenia, tissue damage from cancer treatments and long operative times further raise the risk of postoperative infections.[9]

SSIs in gyne-oncology patients not only delay recovery but also increase treatment costs, antibiotic use, and overall morbidity. Understanding the types of bacteria involved and their antibiotic susceptibility patterns is essential for guiding appropriate treatment and reducing the growing problem of antimicrobial resistance.[10] Therefore, studying bacterial isolates and antibiotic sensitivity patterns in SSI among gyne-oncology patients is important for improving patient outcomes and strengthening infection control practices in cancer hospitals.

METHODS

The present study was a prospective study carried out at the department of microbiology, Government Cancer hospital, Chhatrapati Sambhajinagar.

We conducted a one-year study of all isolates obtained from surgical site samples of patients in the gyne-oncology units from January 2025 to December 2025. All relevant samples were collected according to the hospital's sample collection protocol from the department of gyne-oncology, including pus, wound swabs, and drain fluid specimens. The study was approved by the institutional ethics committee.

Inclusion criteria included all gyne-oncology patients who underwent surgery and were clinically suspected of having a surgical site infection (SSI). Exclusion criteria comprised surgeries performed on cancer patients other than the gyne-oncology patients.eg. radical mastectomy, head-neck surgeries.

The clinical data were obtained from the requisition forms and from the respective units and wards of the patient. All samples were processed as per standard microbiology laboratory operating procedures.[11,12] The isolates were identified by their colonial morphology, Gram-staining, and different biochemical reactions using standard techniques.[11,12] Criteria for antimicrobial sensitivity testing were carried out as per Clinical Laboratory Standard Institute (CLSI).[13]

Antimicrobial sensitivity testing was done on Muller Hinton Agar (MHA) by Kirby-Bauer's disc diffusion method. Commercially available discs (HiMedia) were used. Zones of inhibition were measured the next day and were correlated with CLSI interpretive breakpoints to characterize them as sensitive, intermediate, and resistant. For drugs for which CLSI breakpoints are not available, interpretative breakpoints were provided by the manufacturer. *S. aureus* ATCC 25923, *E. coli* ATCC 25922, and *Pseudomonas aeruginosa* ATCC 27853 were used for quality control.

For Gram-positive organisms, the antibiotics to be tested and reported were chosen from the following (depending on the organism isolated): clindamycin (2 µg), cefoxitin (30 µg), vancomycin (30 µg/minimum inhibitory concentration), linezolid (30 µg), and cotrimoxazole (1.25/23.75 µg), teicoplanin (30 µg).

For Gram-negative, the antibiotics for respective organisms were chosen from the following: ciprofloxacin (5 µg), levofloxacin (5 µg), norfloxacin (5 µg), gentamicin (10 µg), amikacin (30 µg), cefpodoxime (30 µg), cefotaxime (30 µg), ceftazidime (30 µg), cefepime (30 µg), piperacillin-tazobactum (100/10 mcg), imipenem (10 µg), and colistin. MRSA was tested using MHA with cefoxitin disc (30 mcg) by Kirby-Bauer disc diffusion methods as per CLSI guidelines.[13] Colistin sensitivity was tested by Microbroth Dilution.

RESULTS

During the period January to December 2025, total 100 samples were received and processed from gyne-oncology department of the cancer hospital. Table 1 shows the numbers and percentage of various specimens received. Fifty three 53% (53/100) organisms were isolated and 47% (47/100) were sterile.

Table 1: Number and type of clinical samples received (n=100).

Sample	No. of samples (%)
Wound swab	52
Pus	29
Drain fluid	19

Table 2: Number of organisms isolated from various clinical samples (n=53).

Clinical sample	No of organisms isolated (%)
Wound swab	54.71 (29/53)
Pus	30.19 (16/53)
Drain fluid	15.09 (8/53)

A total number of organisms isolated from various clinical samples are shown in Table 2, out of which, 54.71% (29/53) wound swab followed by 30.19% (16/53) were pus and 15.09% (8/53) drain fluid.

Table 3: Gram-negative isolates (n=43).

Gram-negative isolates	Total numbers (%)
Escherichia coli	32.55 (14/43)
Klebsiella pneumoniae	20.93 (9/43)
Pseudomonas aeruginosa	16.27 (7/43)
Enterobacter spp.	11.62 (5/43)
Acinetobacter spp.	9.30 (4/43)
Gram-negative nonfermenter	9.30 (4/43)

81.13% (43/53) were Gram-negative isolates and 18.86% (10/53) were Gram-positive isolates. Most common bacteria isolated were *E. coli* 32.55% (14/43) followed by *Klebsiella pneumoniae* 20.93% (9/43), *P. aeruginosa* 16.27% (7/43), *Enterobacter spp.* 11.62% (5/43), *Acinetobacter spp*. and gram negative non fermenter each 9.30% (4/43) (Table 3).

Table 4: Gram-positive isolates (n=10).

Gram-positive isolates	Total numbers (%)
Staphylococcus spp.	60 (6/10)
Streptococci spp.	20 (2/10)
Enterococci spp.	10 (1/10)
Diphtheroids	10 (1/10)

Among the Gram-positives, the most prevalent organisms isolated were *S. aureus* 60% (6/10) followed by *Streptococcus* 20% (2/10), *Enterococcus* and *Diphtheroids* each 10% (1/10) (Table 4).

Table 5: Age wise distribution of gyne-oncology SSI (n=100).

Age of patient in years	No of patients of SSI
0-20	01
21-40	15
41-60	35
61-80	49

Table 5 shows the age-wise distribution of surgical site infections among gyne-oncology patients. Out of the total 100 patients with SSI, 1% (1/100) was in the 0-20 years age group. 15% (15/100) were between 21-40 years of age. 35% (35/100) belonged to the 41-60 years age group, while the majority, 49% (49/100) were in the 61-80 years age group. Most of these Female (gender) patients were Married, belonged to rural areas. majority were below the poverty line, had low literacy levels, and were housewives.

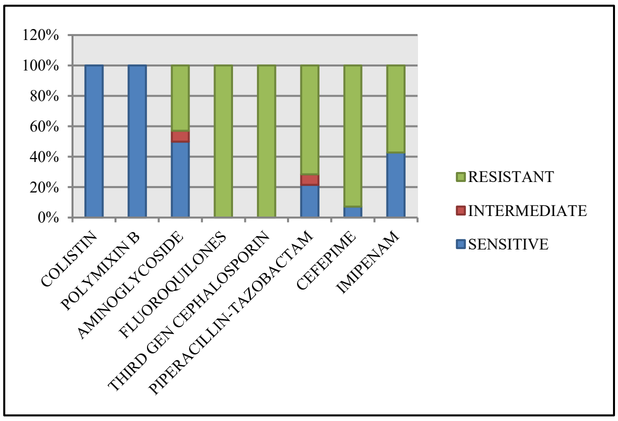

Figure 1: Antibiotic susceptibility pattern of *Escherichia coli.*

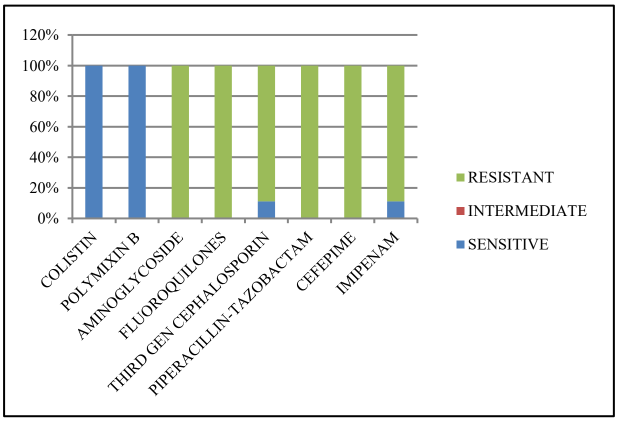

Figure 2: Antibiotic susceptibility pattern of *Klebsiella pneumoniae.*

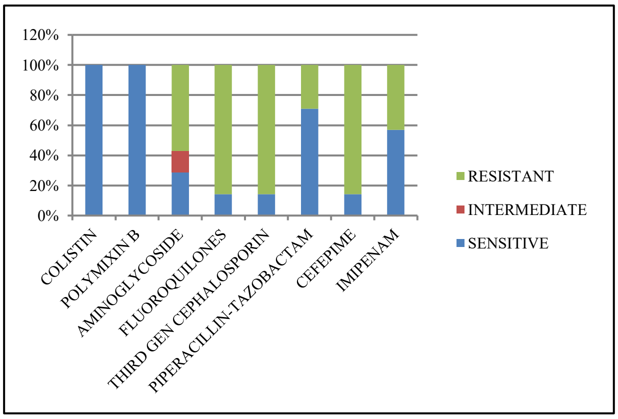

Figure 3: Antibiotic susceptibility pattern of *Pseudomonas aeruginosa.*

Gram negative bacteria were the majority of the organisms causing surgical site infection (SSI). Our study showed a very high resistance among the Gram-negative bacteria

(GNB) against fluoroquinolones and third gen cephalosporins (Figures 1-3). *Staphylococcus spp.* were sensitive to vancomycin, teicoplanin and linezolid and all strains were resistant to fluoroquinolones, clindamycin and cotrimoxazole (Figure 4). All strains of E*nterococcus spp.* and *streptococcus spp.* were sensitive to vancomycin, teicoplanin, linezolid.

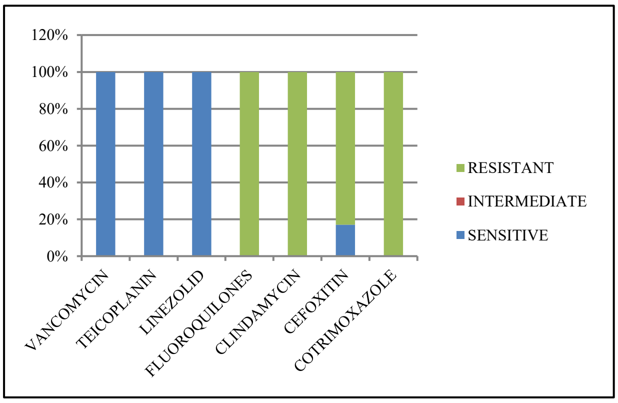

Figure 4: Antibiotic susceptibility pattern of *Staphylococcus spp*.

DISCUSSION

The study aimed to assess antibiotic sensitivity patterns in SSI among gyne-oncology patients with the goal of understanding prevalent resistance patterns and evaluating the effectiveness of prescribed drugs in treating infections.[14]

In our study, 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.[15,16] 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 gyne-onco wards might contribute significantly to the development of SSIs. Notably, *E. coli* followed by *Klebsiella pneumoniae* emerged as the primary organism causing surgical site infections, similar finding was noted from the study conducted in India by Nazneen *et al* and Kulkarni et al.[14,17]

Our study revealed a notably high resistance percentage among organisms to Fluoroquinolones and beta-lactam antibiotics. Comparable high rates of resistance to these drugs were observed by Bhat et al and Kotgire et al.[16,18] *E. coli* exhibited high resistance to fluoroquinolones, third gen cephalosporins and piperacillin-tazobactam in our study as shown in Figure 1, mirroring findings from research conducted by Bhat et al and Garg et al.[16,19]

In our study, resistance to fluoroquinolones and third gen cephalosporin was notably prevalent among *Escherichia coli* (100%) as shown in Figure 1. Non-fermenters Gram negative bacteria and *Acinetobacter spp.* (100%) and *Klebsiella pneumoniae* (94.5%) as shown in Figure 2. *Pseudomonas aeruginosa* (86%) as shown in Figure 3. Additionally, *Acinetobacter spp.* exhibited a resistance rate of 50% in our study which is similar in the studies by Bhat et al and Kotgire et al.[16,18] *Staphylococcus spp.* exhibited resistance to fluoroquinolones, clindamycin and cotrimoxazole as shown in Figure 4 similar to Gupta et al.[21]

CONCLUSION

The present study reveals the microbiological pattern of gyne-oncology patients attending Government Cancer Hospital, Chhatrapati Sambhajinagar. Regular surveillance will aid in implementing more effective therapeutic strategies to reduce morbidity and mortality among patients in cancer treatment facilities. Overall, Gram-negative bacilli showed high resistance to commonly used antibiotics but demonstrated good susceptibility to colistin and polymyxin B. Gram-positive organisms showed susceptibility to linezolid, vancomycin, and teicoplanin; however, the incidence of methicillin-resistant *Staphylococcus aureus* (MRSA) is increasing in our setting.

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

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