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Microbiology Section

Bacteriological Profile and Antimicrobial Resistance Patterns of Skin and Soft-tissue Infections: A Five-year Retrospective Study

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ABSTRACT

Introduction: Skin and Soft-Tissue Infections (SSTIs) constitute a major burden of infectious diseases and are among the most common conditions encountered in clinical practice. The emergence and rapid spread of antimicrobial resistance among pathogens causing SSTIs have significantly limited therapeutic options, increasing morbidity, prolonging hospital stays, and raising healthcare costs. Periodic surveillance of the bacteriological profile and antimicrobial susceptibility patterns of pus isolates is essential to guide empirical therapy and strengthen antimicrobial stewardship in tertiary care settings.

Aim: To determine the bacteriological profile and antimicrobial resistance patterns of pathogens isolated from SSTI.

Materials and Methods: This retrospective observational study was conducted in the Department of Microbiology, BJ Government Medical College and Sassoon General Hospital, Pune, Maharashtra, India, from January 2020 to December 2024. Laboratory records of pus samples received were reviewed. Data extraction, compilation and analysis were performed between October 2025 and January 2026. Bacterial isolates were identified using standard microbiological techniques, and antimicrobial susceptibility was assessed by standardised antimicrobial susceptibility testing methods. The bacteriological profile, antimicrobial resistance patterns, and prevalence of Multidrug-Resistant (MDR), Extensively Drug-Resistant (XDR), Carbapenem-Resistant *Enterobacterales* (CRE), Methicillin-Resistant *Staphylococcus aureus* (MRSA), and Extended-Spectrum β-Lactamase (ESBL)-producing isolates were assessed. Data were analysed using descriptive statistics and the Chi-square test for trend where applicable. A p-value<0.05 was considered statistically significant.

Results: A total of 18,391 pus samples were received and wound swabs processed; 10,264 (55.8%) showed significant bacterial growth. Gram Negative Bacilli (GNB) predominated, accounting for 8,039 (78.3%) isolates, while Gram positive Cocci (GPC) constituted 2,225 (21.7%). *Escherichia coli* 2638 (25.7%) was the most common Gram negative isolate, followed by *Klebsiella pneumoniae* 2361 (23.0%) and *Pseudomonas aeruginosa* 1540 (15%). Among GPC, *Staphylococcus aureus* was predominant 1755 (17.1%). A high burden of antimicrobial resistance was observed, with 7,027 (68.4%) isolates classified as MDR and 5,071 (49.4%) as XDR. Extended-spectrum beta-lactamase production was noted in 4,697 (58.4%) of Gram negative isolates, and carbapenem resistance was observed in 3,085 (38.4%). Among *S. aureus* isolates, 1,038 (59.1%) were MRSA.

Conclusion: The study demonstrated a predominance of gram negative pathogens and a high prevalence of MDR among bacteria causing SSTI. High burdens of MDR, XDR, ESBL-producing, and carbapenem-resistant organisms were observed, with statistically significant increasing trends identified for selected organisms and resistance phenotypes.

Keywords: Carbapenem resistance, Drug resistance, Extended-spectrum beta-lactamases, Methicillin-resistant *Staphylococcus aureus*

INTRODUCTION

The SSTIs encompass a wide range of infections affecting the epidermis, dermis, subcutaneous tissue, fascia, or muscle. Disruption of the skin barrier due to trauma, surgery, burns, or systemic illness facilitates microbial invasion and infection. Pyogenic infections, characterised by suppurative inflammation and pus formation composed of necrotic debris, leukocytes, and microorganisms, are an important cause of sepsis [1].

The bacterial aetiology of SSTIs is diverse and may be monomicrobial or polymicrobial, involving both GPC and GNB. Although *Staphylococcus aureus* has traditionally been regarded as the predominant pathogen, recent studies from tertiary care centres indicate an increasing predominance of GNB -such as *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter* species- particularly in complicated and hospital-acquired wound infections [2]. The emergence and spread of antibiotic-resistant strains pose a major challenge in management, significantly limiting therapeutic options and contributing to increased morbidity, mortality, and healthcare costs worldwide [3].

According to the Global Burden of Disease Study, 4.71 million deaths were associated with bacterial AMR in 2021, including 1.14 million directly attributable deaths. By 2050, AMR deaths are projected to reach 1.91 million attributable and 8.22 million associated globally. Overall deaths are expected to increase by 69.6% (2022-2050), while Disability-Adjusted Life Years (DALYs) will rise modestly by 9.4% to 46.5 million [4]. India accounts for a significant share of the global AMR burden due to widespread antibiotic misuse and overuse. AMR in India is escalating, particularly resistance to extended-spectrum cephalosporins and carbapenems. Emerging colistin resistance, NDM prevalence, and novel resistance mechanisms are further limiting therapeutic options. Additionally, rates of MRSA and Vancomycin-Resistant Enterococcus (VRE), especially *E. faecium*, continue to rise [5].

In 2015, the World Health Organisation (WHO) endorsed the Global Action Plan on AMR (GAP-AMR) to preserve antimicrobial effectiveness through rational use, surveillance, and research across human, animal, and agricultural sectors [6]. WHO further recommends that ≥70% of human antibiotic consumption come from the Access, Watch and Reserve (AWaRe) Access group and urges countries to strengthen Antimicrobial Use (AMU) reporting to the Global Antimicrobial Resistance and Use Surveillance System (GLASS) by 2030 [7].

In India, the Indian Council of Medical Research (ICMR) released Antimicrobial Stewardship Program guidelines in 2018 to support hospital Antimicrobial Stewardship (AMS) implementation. Earlier, in 2017, the Ministry of Health and Family Welfare launched the National Action Plan (NAP) on AMR (2017-2021) using a One Health approach, followed by NAP-AMR (2025-2029) to address implementation gaps [8].

The bacteriological profile and antimicrobial susceptibility patterns of SSTI pathogens vary considerably across geographical regions and healthcare settings. Therefore, periodic local surveillance is essential to monitor changing epidemiological trends, detect emerging resistance phenotypes, and formulate evidence-based empirical treatment guidelines. However, long-term Institution-specific data on SSTI pathogens and their resistance patterns remain limited in many tertiary care hospitals [9]. The present study aimed to evaluate the bacteriological profile of SSTI and determine the antimicrobial susceptibility patterns of bacterial isolates recovered from pus samples over five years in a tertiary care hospital.

MATERIALS AND METHODS

This retrospective observational study was conducted in the Department of Microbiology, BJ Government Medical College and Sassoon General Hospital, Pune, Maharashtra, India, from January 2020 to December 2024. Laboratory records of pus samples received were retrospectively reviewed. Data extraction, compilation and analysis were performed between October 2025 and January 2026 following approval from the Institutional Ethics Committee (BJGMC/IEC/Pharmac/ND-0925310-310, September 2025). Since the study involved retrospective analysis of anonymised laboratory records generated as part of routine patient care, the requirement for individual informed consent was waived by the Ethics Committee.

Sample size: This was a time-bound retrospective study. All eligible pus specimens received during the study period were included. A total of 18,391 pus samples were received from patients with clinically suspected SSTI attending Outpatient Departments (OPD), inpatient wards and Intensive Care Units (ICU).

Inclusion criteria: All pus aspirates and wound swabs received in the Department of Microbiology from patients with clinically suspected SSTI during the study period were included, and samples were processed according to standard microbiological laboratory protocols. Only aerobic bacterial isolates were included in the analysis.

Exclusion criteria: Specimens that were improperly collected, leaked, or inadequately labelled were excluded from the analysis. Duplicate isolates were also excluded, with only the first isolate of the same organism per patient per calendar year included, in accordance with Clinical and Laboratory Standards Institute (CLSI) M39 guidelines [10].

Specimens yielding mixed growth of more than two bacterial species were considered likely to represent colonisation or contamination and were excluded from susceptibility trend analysis. Additionally, anaerobic and fungal isolates were excluded.

Study Procedure

Sample collection and transport: Pus aspirates were routinely collected in sterile leak-proof containers, while wound swabs were collected using two sterile cotton swabs, one for gram staining and the other for culture and antimicrobial susceptibility testing. Specimens were transported immediately to the Microbiology laboratory at ambient temperature without transport medium and processed within two hours of receipt whenever possible as part of routine laboratory practice.

Microbiological processing and identification: As part of routine diagnostic laboratory procedures, all specimens were inoculated onto Nutrient Agar, 5% Sheep Blood Agar and MacConkey Agar and incubated aerobically at 37°C. Plates showing no growth after 24 hours were reincubated for an additional 24 hours before being reported as culture-negative.

Direct gram-stained smears were examined for pus cells and microorganisms. Bacterial identification was performed manually using standard microbiological methods based on colony morphology, gram staining characteristics, motility testing and conventional biochemical reactions.

For GNB, identification included combinations of indole, citrate utilisation, urease, triple sugar iron agar reaction, oxidase test, motility and lysine decarboxylase tests. For GPC, catalase, coagulase, bile esculin hydrolysis and Pyrrolidonyl Arylamidase (PYR) tests were used as appropriate. Identification procedures followed standard microbiological protocols and CLSI (2022) recommendations applicable during the study period [10].

Antimicrobial susceptibility testing: Antimicrobial susceptibility testing was routinely performed using the Kirby-Bauer disc diffusion method on Mueller-Hinton agar according to CLSI M100 guidelines (2026) [11]. Inoculum density was standardised to 0.5 McFarland turbidity, and plates were incubated aerobically at 35±2°C for 16-18 hours before interpretation.

The antibiotic panel tested for gram negative isolates included ampicillin, amoxicillin-clavulanate, piperacillin-tazobactam, cefuroxime, ceftazidime, ceftriaxone, cefotaxime, cefepime, aztreonam, imipenem, meropenem, amikacin, gentamicin, ciprofloxacin, cotrimoxazole, doxycycline, minocycline, tetracycline and colistin.

The antibiotic panel tested for gram positive isolates included penicillin, cefoxitin, gentamicin, ciprofloxacin, cotrimoxazole, clindamycin, erythromycin, doxycycline, tetracycline, vancomycin, teicoplanin and linezolid.

All antibiotic discs were procured from HiMedia Laboratories, Mumbai, India and used according to the manufacturer's instructions.

Detection of Methicillin-Resistant *Staphylococcus Aureus* (MRSA): Methicillin resistance among *Staphylococcus aureus* isolates was determined using the cefoxitin (30 µg) disc diffusion method on Mueller-Hinton agar according to CLSI M100 guidelines, 36th edition (2026) [11]. *Staphylococcus aureus* ATCC 25923 was used as the quality control strain.

Detection of vancomycin resistance: Vancomycin resistance screening was performed using vancomycin screen agar containing 6 µg/mL vancomycin. Plates were incubated at 35°C for 24 hours and interpreted according to CLSI M100 guidelines, 36th edition (2026) [11]. *Staphylococcus aureus* ATCC 29213 was used for quality control.

Colistin susceptibility testing: Colistin susceptibility among Gram negative isolates was determined using broth microdilution according to CLSI M100 guidelines, 36th edition (2026) [11]. An MIC ≥4 µg/mL was considered resistant. *Escherichia coli* ATCC 25922 was used for quality control.

Detection of Extended-Spectrum β-Lactamase (ESBL): The ESBL production was detected by the combined disc method using ceftazidime (30 µg) and cefotaxime (30 µg) alone and in combination with clavulanic acid (10 µg) on Mueller–Hinton agar.

Plates were incubated at 35±2°C for 16-18 hours. An increase of ≥5 mm in inhibition zone diameter in the presence of clavulanate was interpreted as ESBL production. *Klebsiella pneumoniae* ATCC 700603 served as the quality control strain.

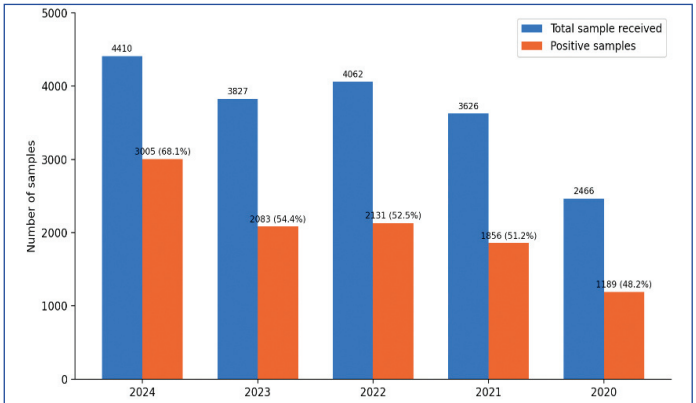
The CRE were defined according to Centres for Disease Control and Prevention (CDC) criteria [12] as *Enterobacterales* exhibiting resistance to at least one carbapenem agent, including ertapenem, doripenem, imipenem, or meropenem. MDR and XDR were defined according to the international expert proposal by Magiorakos AP et al., with MDR defined as non susceptibility to at least one agent in three or more antimicrobial categories, and XDR defined as non susceptibility to at least one agent in all but two or fewer antimicrobial categories [13].

STATISTICAL ANALYSIS

Data were compiled using WHO NET version 5.6 and analysed using Microsoft Excel 2021 and IBM Statistical Package for Social Sciences (SPSS) Statistics version 26.0. Categorical variables were expressed as frequencies and percentages. Year-wise trends in antimicrobial resistance were assessed using the Chi-square test for trend (Cochran-Armitage trend test where applicable). A p-value <0.05 was considered statistically significant.

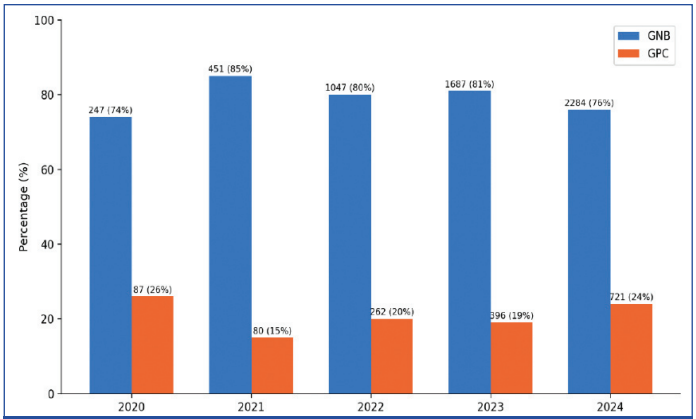
RESULTS

A total of 18,391 pus samples were received in the Department of Microbiology. Of these, 10,264 (55.8%) yielded significant bacterial growth, whereas 8,127 (44.2%) showed no growth. The year-wise distribution of pus samples received and culture positivity rates is presented in [Table/Fig-1].



[Table/Fig-1]: Year-wise total samples received and culture-positive samples (2020-2024).

The annual distribution of GNB and GPC isolated from culture-positive specimens is shown in [Table/Fig-2].

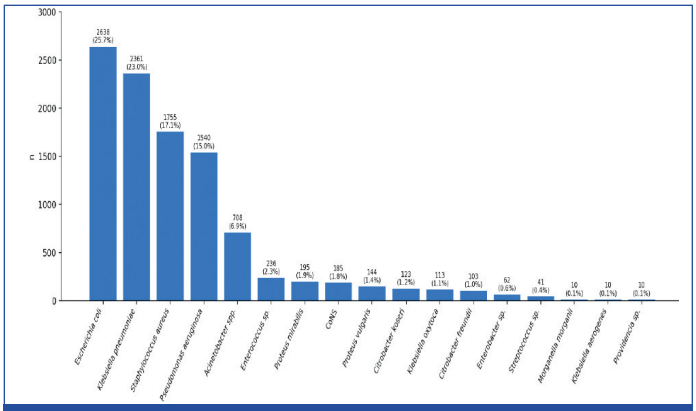


[Table/Fig-2]: Year-wise distribution of Gram negative Bacilli (GNB) and Gram-Positive Cocci (GPC) isolated from pus samples (2020-2024).

Among the culture-positive cases, male patients predominated, with a male-to-female ratio of 2.1:1. The highest incidence of infections was observed in the 31-45 years age group, 4311 (42%), followed by individuals aged >45 years, 3182 (31%), 15-30 years, 2297 (22%), and 0-14 years, 474 (5%).

Based on the source of sample collection, the majority of specimens were obtained from inpatients 8594 (84%), followed by OPD patients 1193 (11%), and ICU patients 477 (5%). On microbiological analysis, GNB constituted the predominant isolates, accounting for 8,039 (78.3%), while GPC comprised 2,225 (21.7%) of the total isolates.

Among GPC, coagulase-positive *Staphylococcus aureus* was the most common isolate, accounting for 1,755 isolates (17.1%), followed by *Enterococcus* spp. (236; 2.3%) and Coagulase-Negative *Staphylococci* (CoNS) (185; 1.8%). Among GNB, *Escherichia coli* (2,638; 25.7%) was the predominant organism, followed by *Klebsiella pneumoniae* (2,361; 23.0%). Among non fermenting GNB, *Pseudomonas aeruginosa* (1,540; 15%) was the most frequently isolated organism, followed by *Acinetobacter baumannii* complex (708; 6.9%). Rare pathogens such as *Burkholderia pseudomallei* (n=1) and *Serratia marcescens* (n=1) were also isolated [Table/Fig-3].



[Table/Fig-3]: Distribution of bacterial isolates from pus samples and wound swabs.

Out of the total 10,264 bacterial isolates, 7,027 (68.4%) were classified as MDR and 5,071 (49.4%) were categorised as XDR. Among GPC, 1,305 isolates (12.7%) were MDR and 783 (7.6%) were XDR, whereas among GNB, 5,722 isolates (55.7%) were MDR and 4,288 (41.8%) were XDR. ESBL production was identified in 4,697 isolates (58.4%) of GNB, while CRE accounted for 3,085 isolates (38.4%) [Table/Fig-4].

Among *E. coli*, resistance to ampicillin remained extremely high (91.1-96.9%), with similarly elevated resistance to third-generation cephalosporins such as ceftriaxone (86.7-91.1%) and cefotaxime (74.4-88.2%). Ciprofloxacin resistance persisted at high levels (69.2-80.9%). Notably, carbapenem resistance increased over time, with imipenem rising from 17.0% (2020) to 44.8% (2024) and meropenem reaching 35.9% in 2024 [Table/Fig-5].

In *Klebsiella* spp., resistance to cephalosporins remained high (≥82%), and ciprofloxacin resistance ranged from 62.5% to 84.7%. Carbapenem resistance was considerable and showed an upward trend, with imipenem and meropenem resistance reaching 65.7% and 60.0%, respectively, in 2024.

For *Proteus vulgaris* and *Proteus mirabilis* (2023-2024), high resistance was observed to cephalosporins (up to 80.6%), ciprofloxacin (66.7-77.6%), and cotrimoxazole (60.5-78.3%). Carbapenem resistance was moderate to high, particularly for imipenem (45.5-63.6%). Overall, the findings reflect sustained high ESBL-associated resistance and rising carbapenem resistance, especially among *Klebsiella* spp.

Among non fermenting GNB, Pseudomonas spp. showed moderate but rising resistance to piperacillin-tazobactam (20.6-37.8%), carbapenems (imipenem 21.9-47.6%; meropenem 19.7-31.1%), and ciprofloxacin (34.3-58.1%), with ceftazidime and cefepime resistance around 40-53%. *Acinetobacter* spp. exhibited resistance to several antimicrobial

Resistance phenotype	Organism	2020 n/N(%)	2021 n/N(%)	2022 n/N(%)	2023 n/N(%)	2024 n/N(%)	χ^2 (trend)	p-value
MDR	E. coli	276/336 (82.0%)	467/534 (87.5%)	489/610 (80.2%)	422/527 (80.1%)	563/631 (89.2%)	2.368	0.124
	Klebsiella spp.	238/274 (87.0%)	554/612 (90.6%)	440/545 (80.8%)	311/377 (82.4%)	486/553 (87.9%)	1.176	0.278
	Pseudomonas spp.	52/129 (40.0%)	108/256 (42.2%)	171/366 (46.7%)	204/337 (60.4%)	280/452 (61.9%)	43.625	<0.001
	Acinetobacter spp.	17/21 (80.0%)	86/116 (74.2%)	111/126 (87.7%)	138/155 (89.3%)	227/290 (78.3%)	0.000	0.992
	S. aureus	219/350 (62.7%)	140/240 (58.5%)	221/357 (61.8%)	197/319 (61.9%)	326/489 (66.6%)	2.424	0.120
XDR	E. coli	170/336 (50.5%)	244/534 (45.6%)	301/610 (49.3%)	288/527 (54.6%)	370/631 (58.6%)	16.493	<0.001
	Klebsiella spp.	153/274 (55.8%)	323/612 (52.8%)	331/545 (60.8%)	258/377 (68.5%)	397/553 (71.8%)	49.588	<0.001
	Pseudomonas spp.	44/129 (34.3%)	83/256 (32.4%)	146/366 (39.9%)	166/337 (49.4%)	244/452 (53.9%)	40.588	<0.001
	Acinetobacter spp.	17/21 (80.0%)	90/116 (77.2%)	99/126 (78.4%)	122/155 (78.6%)	216/290 (74.6%)	0.958	0.328
	S. aureus	140/350 (40.0%)	77/240 (32.0%)	117/357 (32.8%)	116/319 (36.3%)	171/489 (34.9%)	0.730	0.393
CRE	E. coli	112/336 (33.3%)	127/534 (23.75%)	186/610 (30.53%)	260/527 (49.36%)	342/631 (54.24%)	117.400	<0.001
	Klebsiella spp.	121/274 (44.32%)	243/612 (39.64%)	275/545 (50.54%)	246/377 (65.14%)	396/553 (71.57%)	135.193	<0.001
	P. mirabilis	—	—	—	31/56 (56.0%)	35/60 (57.6%)	Not performed	—
	P. vulgaris	—	—	—	23/37 (63.1%)	48/63 (76.6%)	Not performed	—
ESBL	E. coli	255/336 (75.75%)	414/534 (77.5%)	503/610 (82.44%)	451/527 (85.53%)	528/631 (83.6%)	16.031	<0.001
	Klebsiella spp.	215/274 (78.4%)	507/612 (82.9%)	458/545 (84.05%)	313/377 (83.14%)	466/553 (84.2%)	2.663	0.103
	P. mirabilis	—	—	—	37/56 (66.7%)	39/60 (64.4%)	Not performed	—
	P. vulgaris	—	—	—	26/37 (71.0%)	46/63 (73.4%)	Not performed	—
MRSA	S. aureus	196/350 (56.0%)	124/240 (51.6%)	189/357 (52.9%)	196/319 (61.3%)	333/489 (68.0%)	19.586	<0.001

[Table/Fig-4]: Year-wise trend in antimicrobial resistance phenotypes among key pathogens (2020–2024).
n/N(%)=number resistant / total isolates tested that year (percentage). Statistically significant trends (p<0.05) are highlighted. - indicates data not available or trend analysis not performed due to limited sample size.

		E. coli					Klebsiella spp.					Proteus vulgaris		Proteus mirabilis	
		2020 (336)	2021 (534)	2022 (610)	2023 (527)	2024 (631)	2020 (274)	2021 (612)	2022 (545)	2023 (377)	2024 (553)	2023 (37)	2024 (63)	2023 (56)	2024 (60)
Antibiotics		N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)	N (%R)
Penicillins	AMP	326 (96.9%)	511 (95.6%)	556 (91.1%)	490 (93%)	584 (92.5%)	IR	IR	IR	IR	IR	31 (83.3%)	54 (86.4%)	41 (73.3%)	46 (76.5%)
ß-lactam combination	AMC	208 (61.8%)	301 (56.3%)	346 (56.8%)	353 (67%)	396 (62.7%)	190 (69.4%)	421 (68.8%)	321 (58.9%)	272 (72.2%)	434 (78.5%)	22 (60%)	47 (74.1%)	25 (45.5%)	32 (53.1%)
	TZP	140 (41.8%)	252 (47.2%)	235 (38.6%)	243 (46.1%)	321 (50.9%)	154 (56.1%)	320 (52.3%)	281 (51.6%)	241 (63.8%)	364 (65.8%)	8 (21.6%)	23 (36.4%)	15 (26.3%)	14 (23.9%)
Cephalosporins	CXM	296 (88.2%)	461 (86.4%)	534 (87.6%)	460 (87.3%)	553 (87.7%)	232 (84.6%)	504 (82.3%)	475 (87.1%)	332 (88.1%)	462 (83.6%)	26 (71.4%)	47 (75%)	45 (81%)	39 (65.7%)
	CAZ	229 (68.3%)	370 (69.2%)	409 (67%)	378 (71.8%)	439 (69.5%)	186 (67.8%)	447 (73%)	385 (70.7%)	300 (79.7%)	419 (75.7%)	22 (60.6%)	41 (65.4%)	39 (70.3%)	37 (61.2%)
	CRO	296 (88.2%)	468 (87.7%)	556 (91.1%)	457 (86.7%)	548 (86.8%)	226 (82.3%)	520 (84.9%)	452 (83%)	328 (86.9%)	456 (82.4%)	22 (58.3%)	51 (80.6%)	40 (71.4%)	34 (57.1%)
	CTX	267 (79.6%)	397 (74.4%)	478 (78.4%)	465 (88.2%)	549 (87%)	257 (93.8%)	494 (80.7%)	453 (83.1%)	325 (86.1%)	452 (81.7%)	26 (71.4%)	47 (75%)	40 (71.4%)	38 (63%)
	FEP	228 (67.9%)	354 (66.2%)	426 (69.9%)	359 (68.1%)	404 (64.1%)	209 (76.2%)	474 (77.4%)	443 (81.3%)	280 (74.2%)	389 (70.3%)	20 (55.2%)	32 (50%)	33 (59.6%)	26 (42.9%)
Monobactams	ATM	260 (77.5%)	314 (58.8%)	288 (47.2%)	336 (63.7%)	418 (66.2%)	212 (77.3%)	450 (73.6%)	395 (72.4%)	279 (74%)	398 (71.9%)	22 (58.3%)	30 (47.4%)	25 (44.4%)	25 (41.4%)
Carbapenems	IPM	57 (17%)	81 (15.1%)	109 (17.9%)	265 (50.3%)	283 (44.8%)	139 (50.8%)	165 (26.9%)	171 (31.4%)	275 (73%)	363 (65.7%)	24 (63.6%)	39 (61.8%)	33 (58.8%)	27 (45.5%)
	MEM	79 (23.5%)	81 (15.1%)	133 (21.8%)	161 (30.6%)	227 (35.9%)	149 (54.2%)	171 (28%)	232 (42.6%)	217 (57.5%)	332 (60%)	6 (15.8%)	23 (36.2%)	15 (26.8%)	12 (20.4%)
Aminoglycosides	AMK	120 (35.6%)	157 (29.4%)	144 (23.6%)	213 (40.4%)	175 (27.7%)	156 (57%)	241 (39.4%)	256 (46.9%)	251 (66.5%)	306 (55.4%)	17 (46.2%)	37 (58.3%)	28 (50%)	28 (46.7%)
	GEN	139 (41.3%)	218 (40.9%)	184 (30.1%)	183 (34.8%)	251 (39.7%)	167 (60.9%)	323 (52.8%)	322 (59.1%)	222 (58.9%)	336 (60.8%)	14 (38.5%)	37 (58.3%)	20 (36.6%)	25 (42.3%)

Fluoroquinolones	CIP	264 (78.5%)	370 (69.2%)	441 (72.3%)	409 (77.7%)	510 (80.9%)	232 (84.7%)	382 (62.5%)	349 (64%)	286 (75.8%)	442 (79.9%)	25 (66.7%)	49 (77.6%)	34 (61.5%)	42 (70%)
Folate antagonists	SXT	263 (78.3%)	374 (70%)	402 (65.9%)	296 (56.1%)	404 (64.1%)	191 (69.7%)	397 (64.8%)	356 (65.3%)	224 (59.3%)	355 (64.2%)	29 (78.3%)	49 (77.8%)	34 (60.5%)	37 (61.8%)
Lipopeptides	COL	0 (0%)	0 (0%)	1 (0.1%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (0.2%)	0 (0%)	1 (0.1%)	IR	IR	IR	IR
Tetracyclines	DOX	NT	NT	348 (57.1%)	213 (40.4%)	129 (20.5%)	NT	NT	156 (28.6%)	153 (40.7%)	123 (22.2%)	18 (50%)	40 (63.6%)	40 (70.6%)	32 (52.6%)
	MNO	NT	NT	NT	422 (80%)	446 (70.7%)	NT	NT	NT	251 (66.7%)	296 (53.6%)	19 (52.3%)	32 (50%)	31 (54.6%)	34 (57.1%)
	TCY	205 (60.9%)	267 (50%)	328 (53.8%)	340 (64.6%)	368 (58.3%)	127 (46.3%)	304 (49.7%)	314 (57.6%)	193 (51.3%)	223 (40.4%)	NT	NT	NT	NT

[Table/Fig-5]: Year-wise antibiotic resistance profile (%) of major Gram negative bacterial isolates from pus samples (2020-2024).
Abbreviations: AMP: Ampicillin; AMC: Amoxicillin–Clavulanic acid; TZP: Piperacillin–Tazobactam; CXM: Cefuroxime; CAZ: Ceftazidime; CRO: Ceftriaxone; CTX: Cefotaxime; FEP: Cefepime; ATM: Aztreonam; IPM: Imipenem; MEM: Meropenem; AMK: Amikacin; GEN: Gentamicin; CIP: Ciprofloxacin; SXT: Trimethoprim-Sulfamethoxazole; COL: Colistin; DOX: Doxycycline; MNO: Minocycline; TCY: Tetracycline; IR: Intrinsic resistance; NT: Not tested N (%R): number of resistant isolates (percentage resistant).”

classes, including piperacillin-tazobactam (67.7-80.0%), ceftazidime (66.7-87.3%), carbapenems (46.4-76.0%), and ciprofloxacin (60.0-85.6%). Colistin resistance was found to be minimal across all tested organisms, with prevalence rates remaining below 1% [Table/Fig-6].

Out of 1,755 *S. aureus* isolates, 1,038 (59.1%) were identified as cefoxitin-resistant (MRSA), while the remaining isolates were cefoxitin-susceptible (MSSA). *Staphylococcus aureus* showed persistently high penicillin resistance (91.3-93.9%). Cefoxitin resistance (MRSA marker) increased from 56.0% in 2020 to 68.0% in 2024, indicating a rising MRSA trend. Ciprofloxacin resistance fluctuated widely (31.4-76.8%), peaking at 76.8% in 2024, while erythromycin remained consistently high (39.4-62.8%). Clindamycin showed moderate resistance (22.5-39.8%). Gentamicin resistance declined overall to 13.5% in 2024. Cotrimoxazole resistance steadily decreased from 25.7% (2020) to 7.7% (2024). Doxycycline (6.6% in 2024) and tetracycline (8.2% in 2024) maintained low resistance rates. Vancomycin, linezolid, and tigecycline showed 0% resistance throughout the study period [Table/Fig-7].

The CoNS isolates had high resistance to penicillin (94.8%), ciprofloxacin (69.9%), and erythromycin (71.6%), while remaining fully susceptible to vancomycin. *Enterococcus* spp. demonstrated moderate ampicillin resistance (42.1%) and high erythromycin resistance (65.5%). A progressive increase in the total number of *S. aureus* isolates was observed over the study period, with MRSA consistently predominating over MSSA in all years. No isolates of Vancomycin-Intermediate *S. aureus* (VISA), Vancomycin-Resistant *S. aureus* (VRSA), or VRE were detected during the study period [Table/Fig-8].

		Pseudomonas spp.					Acinetobacter spp.				
		2020 (129)	2021 (256)	2022 (366)	2023 (337)	2024 (452)	2020 (21)	2021 (116)	2022 (126)	2023 (155)	2024 (290)
Antibiotics		%R	%R	%R	%R	%R	%R	%R	%R	%R	%R
Penicillins	AMP	IR	IR	IR	IR	IR	IR	IR	IR	IR	IR
ß-lactam combination	AMC	IR	IR	IR	IR	IR	IR	IR	IR	IR	IR
	TZP	27 (20.6%)	72 (28.2%)	81 (22.1%)	97 (28.7%)	171 (37.8%)	17 (80%)	79 (67.9%)	85 (67.7%)	118 (76.2%)	198 (68.3%)
Cephalosporins	CXM	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
	CAZ	64 (50%)	115 (45.1%)	171 (46.8%)	152 (45.2%)	238 (52.7%)	14 (66.7%)	86 (74.1%)	110 (87.3%)	131 (84.5%)	235 (81.1%)
	CRO	IR	IR	IR	IR	IR	18 (86.3%)	98 (84.7%)	101 (80%)	144 (93%)	249 (85.8%)
	CTX	IR	IR	IR	IR	IR	19 (90%)	93 (80%)	110 (87.5%)	135 (87.4%)	258 (89%)
	FEP	59 (45.4%)	114 (44.7%)	150 (41.1%)	161 (47.9%)	179 (39.5%)	16 (76.9%)	92 (79.4%)	104 (82.9%)	140 (90.2%)	189 (65.1%)
Monobactams	ATM	47 (36.4%)	100 (39.1%)	120 (32.8%)	125 (37.1%)	203 (45%)	IR	IR	IR	IR	IR
Carbapenems	IPM	28 (21.9%)	50 (19.7%)	94 (25.8%)	160 (47.6%)	168 (37.1%)	14 (66%)	58 (50%)	96 (76%)	101 (65.1%)	206 (70.9%)
	MEM	26 (20%)	50 (19.7%)	85 (23.2%)	87 (25.9%)	141 (31.1%)	16 (75%)	54 (46.4%)	73 (57.8%)	99 (63.6%)	183 (63.2%)
Aminoglycosides	AMK	46 (35.3%)	72 (28.2%)	167 (45.6%)	139 (41.1%)	154 (34.1%)	15 (72.6%)	62 (53.6%)	96 (76.2%)	120 (77.4%)	183 (63.1%)
	GEN	NT	NT	NT	NT	NT	15 (71.8%)	66 (57.1%)	100 (79.7%)	132 (85%)	218 (75.2%)
Fluoroquinolones	CIP	44 (34.3%)	97 (38%)	157 (42.9%)	182 (53.9%)	263 (58.1%)	13 (60%)	75 (64.3%)	91 (71.9%)	130 (84.1%)	248 (85.6%)
Folate antagonists	SXT	IR	IR	IR	IR	IR	16 (75.1%)	62 (53.6%)	105 (83.6%)	114 (73.5%)	215 (74.1%)
Lipopeptides	COL	NT	NT	NT	NT	NT	0 (0%)	0 (0%)	0 (0%)	0 (0.1%)	0 (0.0%)
Tetracyclines	DOX	NT	NT	NT	NT	NT	NT	NT	NT	NT	NT
	MNO	NT	NT	NT	NT	NT	7 (33.3%)	56 (48.1%)	50 (40%)	88 (56.8%)	71 (24.4%)
	TCY	IR	IR	IR	IR	IR	NT	NT	NT	NT	NT

[Table/Fig-6]: Year-wise antibiotic resistance profile (%) of major non fermenter Gram negative bacterial isolates from pus samples (2020-2024).
AMP: Ampicillin; AMC: Amoxicillin-Clavulanic acid; TZP: Piperacillin-Tazobactam; CXM: Cefuroxime; CAZ: Ceftazidime; CRO: Ceftriaxone; CTX: Cefotaxime; FEP: Cefepime; ATM: Aztreonam; IPM: Imipenem; MEM: Meropenem; AMK: Amikacin; GEN: Gentamicin; CIP: Ciprofloxacin; SXT: Trimethoprim–Sulfamethoxazole; COL: Colistin; DOX: Doxycycline; MNO: Minocycline; TCY: Tetracycline; IR: Intrinsic resistance; NT: Not tested

	Staphylococcus aureus				
Resistance pattern	2020 (350) N (%R)	2021 (240) N (%R)	2022 (357) N (%R)	2023 (319) N (%R)	2024 (489) N (%R)
PEN	320 (91.3%)	220 (91.8%)	332 (92.9%)	298 (93.4%)	459 (93.9%)
FOX	196 (56%)	124 (51.6%)	189 (52.9%)	196 (61.3%)	333 (68%)
GEN	100 (28.6%)	41 (16.9%)	86 (24.1%)	41 (12.9%)	66 (13.5%)
CIP	229 (65.3%)	75 (31.4%)	158 (44.3%)	140 (43.9%)	376 (76.8%)

SXT	90 (25.7%)	47 (19.7%)	54 (15.2%)	20 (6.2%)	38 (7.7%)
CLI	137 (39.1%)	54 (22.5%)	142 (39.8%)	112 (35.2%)	139 (28.5%)
ERY	220 (62.8%)	95 (39.4%)	198 (55.6%)	175 (55%)	282 (57.7%)
DOX	28 (7.9%)	51 (21.1%)	43 (12.1%)	25 (7.7%)	32 (6.6%)
TCY	32 (9.1%)	23 (9.4%)	36 (10.1%)	41 (12.8%)	40 (8.2%)

[Table/Fig-7]: Year-wise percentage resistance pattern of *Staphylococcus aureus* (2020-2024).
Abbreviations: MRSA: Methicillin-resistant *staphylococcus aureus*; MSSA: Methicillin-susceptible *staphylococcus aureus*; FOX: Cefoxitin; PEN: Penicillin; GEN: Gentamicin; CIP: Ciprofloxacin; SXT: Trimethoprim–Sulfamethoxazole; CLI: Clindamycin; ERY: Erythromycin; VAN: Vancomycin; LZ: Linezolid; DOX: Doxycycline; TCY: Tetracycline.

Antibiotic name		S. aureus n=1755 %R	CoNS n=185 %R	Enterococcus n=236 %R
Penicillin G	PEN	1643 (93.6%)	175 (94.8%)	86 (36.4%)
Ampicillin	AMP	NT	NT	99 (42.1%)
Cefoxitin	FOX	1038 (59.1%)	164 (88.8%)	NT
Gentamicin	GEN	311 (17.7%)	61 (32.8%)	83 (35.0%)
Ciprofloxacin	CIP	1035 (59.0%)	129 (69.9%)	114 (48.2%)
Trimethoprim/Sulfamethoxazole	SXT	237 (13.5%)	51 (27.7%)	NT
Clindamycin	CLI	577 (32.9%)	81 (43.8%)	NT
Erythromycin	ERY	978 (55.7%)	132 (71.6%)	155 (65.5%)
Vancomycin	VAN	0 (0.0%)	0 (0.0%)	0 (0.0%)
Teicoplanin	TEC	NT	NT	10 (4.1%)
Doxycycline	DOX	153 (8.7%)	8 (4.3%)	19 (7.9%)
Tetracycline	TCY	186 (10.6%)	25 (13.6%)	105 (44.3%)

[Table/Fig-8]: Percentage resistance pattern of Gram-positive bacteria (2020-2024).
Abbreviations: CoNS: Coagulase negative staphylococci; NT: Not tested; PEN: Penicillin; AMP: Ampicillin; FOX: Cefoxitin; GEN: Gentamicin; CIP: Ciprofloxacin; SXT: Trimethoprim–Sulfamethoxazole; CLI: Clindamycin; ERY: Erythromycin; VAN: Vancomycin; TEC: Teicoplanin; DOX: Doxycycline; TCY: Tetracycline

DISCUSSION

The SSTIs remain a significant cause of morbidity in both community and hospital settings, particularly in tertiary care centres catering to referral patients. The present five-year retrospective study provides a comprehensive overview of the bacteriological profile and antimicrobial resistance patterns among pus isolates and highlights a sustained and increasing burden of MDR organisms.

In the present study, culture positivity was observed in 56% of pus samples, which is comparable to reports from similar tertiary care settings in India. Studies by Trojan R et al., have documented culture positivity rates of 60.1% and 60.5% Manoj K et al., in pus samples, reflecting a similar burden of pyogenic infections in tertiary healthcare facilities [9,14]. In the present study, males had a wound infection rate 2.1 times higher than females. This may be attributed to men's greater likelihood of working outdoors, which increases their risk of injury and exposure to contaminated environments. Sudhaharan S et al., also noted a similar trend, reporting a male-to-female ratio of 2.5:1 for wound infections [15].

The predominance of GNB (78.3%) over GPC in the present study aligns with recent Indian reports, reflecting a shift from the traditionally described Gram-positive dominance in SSTIs toward Gram negative pathogens, particularly in hospital-acquired and complicated wound infections [14]. Among the gram negative isolates, *Escherichia coli* and *Klebsiella pneumoniae* were the most common, followed by *Pseudomonas aeruginosa* and the *Acinetobacter baumannii* complex. Similar distribution patterns have been documented in multicentric Indian studies and national surveillance data, indicating widespread dissemination of these organisms across healthcare settings [9,15,16]. Over the five years (2020-2024), although the spectrum of pathogens remained largely unchanged, a progressive increase in antimicrobial resistance was observed. The notable presence of non fermenting GNB, particularly *Pseudomonas aeruginosa* and *Acinetobacter baumannii* complex, is clinically significant, as these organisms are associated with biofilm formation, prolonged hospitalisation, and limited therapeutic options, as highlighted by Peleg AY et al., [17].

A high prevalence of MDR was observed in the present study, with 68.4% of isolates classified as MDR and nearly half as XDR. Comparable findings have been reported by Ingale HD, who documented MDR rates exceeding 60% among pus isolates from tertiary care hospitals [16]. The higher proportion of MDR and XDR among GNB compared to GPC further underscores the therapeutic challenges posed by these organisms and reflects increasing antimicrobial pressure in hospital settings.

The ESBL production was detected in 58.4% of gram negative isolates in the present study. A comparable study by Sharma S et al., from a tertiary care centre in Western Maharashtra, reported a slightly higher prevalence (67.8%), while Umadevi S et al., documented an ESBL rate of 69%, indicating consistently high ESBL burden across tertiary care settings [18,19]. The high ESBL burden significantly limits the utility of third-generation cephalosporins for empirical therapy and contributes to increased carbapenem use, thereby accelerating the emergence of carbapenem resistance. In the present study, CRE accounted for 38.4% of gram negative isolates, reflecting an alarming rise consistent with trends reported by National Surveillance Data (2022) [20,21].

Among non fermenters, *Acinetobacter baumannii* demonstrated high levels of resistance across multiple antimicrobial classes, corroborating findings reported by National surveillance data, where carbapenem resistance rates exceeding 80% have been observed, particularly in intensive care settings [20,21]. Although comprehensive national data on colistin resistance among nosocomial pathogens in India remain limited, some studies have reported resistance rates as high as 9.98% [22]. However, surveillance data from the Indian Council of Medical Research indicate lower rates (3-6%), while the National Antimicrobial Resistance Surveillance Network reports resistance of <1% in most organisms [20,21]. In the present study, colistin resistance was minimal, with rates below 1%, suggesting preserved susceptibility in this setting.

Among GPC, *Staphylococcus aureus* remained the predominant isolate, with methicillin resistance detected in 59.1% of isolates. Similar results were observed in the study by Singh A et al., [23];

MRSA was 52.2%, and MSSA was 41.2%, and another study reported by Patil P et al., [24] the MRSA was 56.1% and MSSA was 43.9%. The absence of VISA or VRSA and VRE in the present study is encouraging. National surveillance data ICMR reports an MRSA prevalence of 44.5%, while the National Antimicrobial Resistance Surveillance Network (NARS-Net) documents a higher rate of 59%. Vancomycin resistance in Enterococcus faecium (27%) and Enterococcus faecalis (5%) has been reported by ICMR, whereas NARS-Net reports an overall VRE prevalence of 13% [20, 21]. These data highlight a sustained MRSA burden and the growing concern of vancomycin resistance among Enterococci in Indian healthcare settings. These findings underscore the importance of continuous local surveillance, regular antibiogram generation, and strict implementation of antimicrobial stewardship and infection prevention strategies, as advocated by WHO and national expert groups [21].

Limitation(s)

The present study has certain limitations. As a retrospective, single-centre, laboratory-based study, important clinical details such as infection severity, prior antibiotic use, treatment outcomes, and patient comorbidities could not be reliably assessed. Detailed clinical information regarding the specific type of SSTI was not uniformly available; therefore, infection-specific subgroup analysis could not be performed. Being conducted at a tertiary care referral hospital, the study may be subject to referral bias, and the findings may not be directly generalizable to other healthcare settings. The study was limited to aerobic bacterial isolates recovered from pus samples; anaerobic bacteria and fungal pathogens were not evaluated, which may have led to underestimation of the complete microbiological spectrum of SSTIs. Molecular confirmation of resistance mechanisms, including ESBL, carbapenemase, and methicillin resistance, was not performed due to resource constraints.

CONCLUSION(S)

The present five-year retrospective study demonstrates a predominance of GNB and a high burden of antimicrobial resistance in SSTI, likely driven by the ongoing spread of resistance genes. As a tertiary referral centre, prior treatment and exposure to broad-spectrum antibiotics among patients may have contributed to the selection of MDR strains. The year-wise increase in MDR, XDR, ESBL-producing, and CRE isolates reflects the combined impact of antibiotic pressure, prolonged hospitalisation, and referral patterns typical of such settings. The considerable proportion of MRSA further highlights the need for vigilant surveillance. Institution-specific antimicrobial susceptibility data can guide appropriate empirical therapy and strengthen antimicrobial stewardship efforts. Enhanced infection control measures and judicious antibiotic use are essential to curb the emergence and spread of antimicrobial resistance.

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