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Original Article

Microbiology Section

Bacteriological Profile, Characterisation of MDR and XDR Bacteria in Pyogenic Infections among Patients: A Descriptive Retrospective Study from a Tertiary Care Hospital, Ujjain, Madhya Pradesh, India

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ABSTRACT

Introduction: Pyogenic infections are prevalent in India and can manifest in diverse body parts, including the skin and soft-tissues, respiratory tract, and visceral organs. The pathogenesis of pyogenic infections is typically attributed to microorganisms such as *Staphylococcus aureus, Klebsiella pneumoniae, Escherichia coli*, and *Pseudomonas aeruginosa*. The emergence of Multidrug-Resistant (MDR) and Extensively Drug-Resistant (XDR) organisms complicates their management. A comprehensive understanding of aetiology, predisposing factors, and therapeutic modalities of pyogenic infections is essential for effective management.

Aim: To identify MDR and XDR isolates in pus samples and to determine their antimicrobial susceptibility patterns.

Materials and Methods: This hospital-based descriptive retrospective study was conducted in the Microbiology Laboratory at CRGH Hospital and Ruxmaniben Deepchand Gardi Medical College, Ujjain, Madhya Pradesh, India, from March 2024 to April 2025. The study included all pus samples, regardless of age and gender, that yielded growth of pathogenic bacteria. A total of 342 pus samples were received in sterile containers and were immediately processed for microscopic examination and culture on routine Blood Agar and Mac Conkey Agar, following standard guidelines. After identifying bacteria using various biochemical tests, their Antimicrobial Susceptibility Testing (AST) was performed according to established standards. Isolates were classified as MDR or XDR based on standard definitions. For statistical analysis, the Chi-square test was applied to find the association of risk factors and co-morbidities with pyogenic infections, with a p-value <0.05 considered statistically significant.

Results: Among the 342 pus samples, 174 were male (51%) and 168 were female (49%). The majority of samples from males were received from the 51 to 60-year age group (51 samples, 29.4%), followed by the 41 to 50-year age group (42 samples, 24.1%). A total of 164 organisms (48%) were isolated. Co-morbid conditions included diabetes mellitus (62 cases, 18%) and addictive behaviours such as smoking (121 cases, 35%) and alcoholism (108 cases, 32%). The associations of co-morbidities (such as diabetes mellitus, hypertension, their co-existence, trauma, and tuberculosis) and addictive behaviours (such as smoking, alcoholism, and their co-existence) with pyogenic infections were analysed, with a p-value <0.05 considered statistically significant. The predominant Gram-Negative Bacteria (GNB) isolated from the Enterobacterales were *E. coli* (44 isolates, 26.8%), followed by *Klebsiella pneumoniae* (31 isolates, 18.9%). Among the non fermenting GNB, *Pseudomonas aeruginosa* was isolated in 10 cases (6.1%) and *Acinetobacter* spp. in 3 cases (1.8%). The Gram-Positive Cocci (GPC) isolated included *Staphylococcus aureus* (41 cases, 25%). GNB were mainly susceptible to the carbapenem group (Meropenem and Ertapenem), and all *S. aureus* isolates were susceptible to vancomycin, linezolid, and teicoplanin. The prevalence of MDR and XDR among GNB was 37 (40.2%) and 31 (33.6%), respectively. The percentages of MDR and XDR in *E. coli* were 24 (54.5%) and 10 (22.7%), respectively, while in *K. pneumoniae*, both MDR and XDR were found in 11 cases (35.4%). The prevalence of MDR among *S. aureus* was 34 (82.9%), with methicillin-resistant *S. aureus* found in 24 cases (59%).

Conclusion: This study identified diabetes mellitus, smoking, and alcoholism as frequently observed risk factors. Antimicrobial resistance (AMR) is rising significantly in MDR and XDR strains among both GNB and GPC. It is crucial to initiate the development and implementation of effective antimicrobial stewardship programs.

Keywords: Alcoholism, Diabetes mellitus, Extensive drug resistant, Multidrug resistant, Smoking

INTRODUCTION

The term pyogenic infections refers to infections that produce pus. These are characterised by local inflammation, typically resulting from the infiltration and multiplication of pyogenic organisms within the human body through various routes, leading to the accumulation of dead leukocytes and infectious agents [1]. The body's immune system acts against the invading microorganisms, and the accumulation of dead leukocytes results in the formation of a thick whitish or yellow liquid known as pus [2].

Pyogenic infections can occur either endogenously or exogenously, with bacteria, fungi, viruses, or parasites being the main causative agents. Impetigo, cellulitis, furuncles, abscesses, blepharitis, and necrotising fasciitis are examples of skin and soft-tissue infections (SSTIs) [3]. Bone infections include osteomyelitis, septic arthritis, and spondylodiscitis, while ear infections include otitis media, and urinary tract infections include cystitis [1]. Pyogenic granulomas, lesions of the skin and mucous membranes, may appear on the face, mouth, lips, tongue, nose, fingers, and toes. Meningitis and surgical site

infections are also common forms of pyogenic infections. Human SSTIs often occur during or after trauma, burn injuries, or surgical procedures [1,3].

Several factors influence the development of pyogenic infections, including wound condition, microbial load, and host defense mechanisms. Advanced age, diabetes mellitus, malignancies, postsurgical complications, heavy exercise, muscular injuries, infancy (under two years of age), smoking, alcoholism, and chronic conditions such as chronic renal and chronic liver diseases are recognised risk factors that vary depending on the type of infection [4,5]. In developing countries, about 40% of reported cases are classified as suppurative pyogenic infections [6].

The global rise of MDR, XDR, and pan-drug-resistant bacteria has made the management of such infections increasingly difficult [7]. MDR and XDR GNB strains- including *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Acinetobacter baumannii*- and the GPC Methicillin-Resistant *Staphylococcus aureus* (MRSA) have become increasingly associated with pyogenic infections in hospital settings over recent decades [8-10]. Studies from India have reported the prevalence of MDR-GNB ranging from 26% to 34%, with 12.1% being XDR, whereas a study from Pakistan reported a prevalence as high as 64% [11-13]. The rising prevalence of these MDR and XDR organisms poses a serious public health concern. Continuous surveillance of these pathogens is essential for developing appropriate treatment regimens and early therapeutic strategies, as no single antibiotic is effective against all of them.

This study aims to determine the burden, risk factors, Aetiological agents, and antibiogram of MDR and XDR organisms isolated from pus samples at a tertiary care hospital, with the goal of aiding empirical therapy formulation and implementing infection control strategies to prevent MDR.

The research involves isolating and identifying common pyogenic infection-causing pathogens such as *Staphylococcus aureus*, along with emerging drug-resistant strains like *Acinetobacter baumannii* and *Klebsiella pneumoniae*, from patient pus samples to determine their specific AST patterns. Concurrently, patient data are analysed to identify risk factors, including underlying health conditions such as diabetes mellitus and hypertension, as well as lifestyle factors such as smoking and alcoholism.

The ultimate goal is to establish a clinicomicrobiological correlation, linking patient risk factors to the type of bacteria and its resistance profile. This local data is crucial for developing tailored antibiotic stewardship programs and treatment guidelines to effectively combat the growing threat of MDR infections within a specific hospital setting.

The primary and secondary objectives of the study are to analyse the AST patterns of isolates from pyogenic infections and to identify associated risk factors and co-morbid conditions.

MATERIALS AND METHODS

The present study was a hospital-based descriptive retrospective study conducted in the Department of Microbiology at CRGH and Ruxmaniben Deepchand Gardi Medical College, Ujjain, Madhya Pradesh, India, from March 2024 to April 2025. The study commenced after obtaining permission from the Institutional Ethics Committee (IEC), with approval letter number IEC/06/25, dated 18/04/2025. Retrospective data collection was performed by reviewing patients' case files (secondary data) from April 2025 to May 2025, and data analysis was carried out in June 2025.

Inclusion criteria: Data from patients' medical records with confirmed pyogenic infections were included in the study. The selected case files contained culture and susceptibility reports of pus samples showing the growth of pathogenic bacteria.

Exclusion criteria: Case files of patients whose pus culture reports showed commensal or contaminant growth (e.g., unusual colony morphology or growth on negative control plates) and repetitive samples were excluded from the study.

Sample size calculation: The sample size was calculated based on the study by Devi KD et al., assuming a prevalence (p) of 30.9% [14]. The formula used for calculation was: $n=z^{2*} P^{*}(100-P)/ e^{2}$,

Where,

Z = 1.96 (at 95% confidence interval)

P= 30.9% (assumed prevalence)

e= 5% (absolute error)

n= (1.96^2) \times 30.9 \times (100 - 30.9) / 5^2=342

Thus, the calculated sample size was N=342.

Study Procedure

Medical records of patients were reviewed to obtain demographic information, clinical profiles, associated risk factors, and details of pathogen isolates along with their antimicrobial susceptibility patterns for analysis. All pus samples received in sterile containers were subjected to culture on blood agar and MacConkey agar, followed by microscopic examination (Gram staining and Ziehl-Neelsen staining). Plates were incubated aerobically at 37°C for 24 hours. Organisms were identified using standard laboratory procedures [1,15]. AST of bacterial isolates was performed on Mueller-Hinton Agar (MHA) using the modified Kirby-Bauer disk diffusion method as per Clinical and Laboratory Standards Institute (CLSI) guidelines [16]. Reference strains of *Staphylococcus aureus* (ATCC 25923), *Escherichia coli* (ATCC 25922), and *Pseudomonas aeruginosa* (ATCC 27853) were used as quality controls for susceptibility testing in accordance with CLSI standards [16].

All bacterial isolates were classified as MDR or XDR based on standard definitions [7]:

MDR: An isolate not susceptible to at least one agent in three or more antimicrobial classes tested.

XDR: An MDR isolate not susceptible to at least one agent in all but two or fewer antimicrobial classes.

STATISTICAL ANALYSIS

All statistical analyses were performed using Statistical Package for the Social Sciences (SPSS) version 21.0 (SPSS Inc., Chicago, IL, USA) for Microsoft Windows. Data were described in terms of percentages. The Chi-square test was applied to determine the association between risk factors (smoking and alcohol consumption) and co-morbid conditions (such as diabetes mellitus and hypertension) with the type of pyogenic infection. A p-value <0.05 was considered statistically significant.

RESULTS

Of the 342 pus samples received, 164 (48%) showed bacterial growth, with a slight predominance of GNB-92 (56%)- over GPC-72 (44%). Three samples showed mixed growth (included in the total bacterial isolates, n=164). The study found a nearly equal distribution of samples between male (174; 51%) and female (168; 49%) patients. The highest number of male samples were from the 51-60-year age group (51; 29.4%), while female samples were most frequent in the 41-50-year age group (42; 25%). Most samples were received from the Surgery department (102; 30%), followed by Orthopaedics (85; 25%), Obstetrics and Gynaecology (65; 19%), ENT (31; 9%), Pulmonary Medicine (21; 6%), Medicine and Dermatology (14; 4%) each, and Paediatrics (10; 3%). The most common infection source was infected wounds (102; 30%), followed by non healing ulcers (85; 25%), pyothorax (47; 14%), and abscesses (40; 12%). Other infections included surgical site infections (16; 5%), discharging sinuses (16; 5%), Chronic Suppurative Otitis Media (CSOM) and burn wounds (13; 4%) each, and others such as Fournier's gangrene and necrotising fasciitis

Co-morbid conditions	Type of Pyogenic Infections												
	Total (n= 342)	Infected wound 102 (30%)	NHU* 85 (25%)	Pyothorax 47 (14%)	Abscess 40 (12%)	SSI* 16 (5%)	Discharging sinuses 16 (5%)	CSOM* 13 (4%)	Burn wound 13 (4%)	Other* 7 (2%)	Urethritis 3 (1%)	Chi-square value	p-value
DM*	62 (18.1)	17 (16.6)	12 (14.1)	5 (10.6)	10 (25)	5 (31.2)	5 (31.2)	2 (15.3)	2 (15.3)	4 (57.1)	00	20.4492	6.123
DM and HTN	55 (16)	39 (38.2)	5 (5.8)	00	3 (7.5)	00	3 (18.7)	00	2 (15.3)	3 (42.8)	00	35.4506	2.6501
HTN*	15 (4.3)	4 (3.9)	2 (2.3)	00	00	3 (18.7)	2 (12.5)	00	00	2 (28.5)	2 (66.6)	32.3774	1.2718
Trauma	14 (4)	2 (1.9)	2 (2.3)	00	00	00	3 (18.7)	7 (53.8)	00	00	00	4.2616	0.039
M.Tb*	10 (3)	3 (2.9)	2 (2.3)	3 (6.3)	00	00	2 (12.5)	00	00	00	00	17.7187	2.56125
Addiction													
Smoking	121 (35.3)	56 (54.9)	11 (12.9)	29 (61.7)	7 (17.5)	5 (31.2)	3 (18.7)	5 (38)	3 (23)	2 (28.5)	00	60.3	0.00001
Alcohol	108 (32)	44 (43.1)	25 (29.4)	15 (31.9)	9 (22.5)	3 (18.7)	5 (31.2)	00	2 (15.3)	3 (42.8)	2 (66.6)	18.94	0.00011
Smoking and Alcohol	87 (25.4)	45 (44.1)	19 (22.3)	9 (19.1)	3 (7.5)	2 (12.5)	2 (12.5)	00	3 (23)	3 (42.8)	1 (33.3)	9.8333	0.0017

[Table/Fig-1]: Association of co-morbid conditions and addictions with type of pyogenic infection %(n=342)*.
p-value <0.05 is considered statistically highly significant.(Chi square test applies to calculate p-value)
NHU*: Non-healing ulcer; SSI*: Surgical site infection; CSOM*: Chronic suppurative otitis media; DM*: Diabetes mellitus; HTN*: Hypertension; MTb*: *Mycobacterium tuberculosis*
*Some of study patients share more than one co-morbid condition and predisposing factor, so sum of them was more than n=342
Other*- Furuncles, carbuncles, osteomyelitis, empyma, Fournier's gangrene, necrotising fasciitis etc.,

(7; 2%), and urethral discharge (3; 1%) [Table/Fig-1]. A clinical evaluation of patients revealed that diabetes mellitus was the most common co-morbidity, present in 62 (18%) cases. The co-existence of diabetes and hypertension was also highly prevalent, affecting 55 (16%) patients, while hypertension alone was observed in 15 (4%), trauma in 14 (4%), and *Mycobacterium tuberculosis* infection in 10 (3%). Lifestyle analysis showed that smoking was the most common addiction (121; 35%), followed by alcoholism (108; 32%). A considerable number of patients (87; 25.4%) had both habits. Associations between co-morbidities (diabetes mellitus, hypertension, their co-existence, trauma, and tuberculosis) and lifestyle factors (smoking, alcoholism, and their co-existence) with pyogenic infections were analysed, with p-value <0.05 considered statistically significant [Table/Fig-1]. Among patients with infected wounds, the co-existence of diabetes and hypertension was the most common comorbidity (39; 38.2%), while smoking was the predominant addiction (56; 54.9%) [Table/Fig-1].

Isolates	Number (%)
Gram Negative Bacteria (GNB)	**92 (56)**
Enterobaceterales GNB	**79 (48)**
E.coli	44 (26.8)
Klebsiella pneumonia	31 (18.9)
Klebsiella aerogens	2 (1)
Proteus mirabilis	2 (1)
Non Fermenter GNB	**13 (8)**
Pseudomonas aeruginosa	10 (6)
Acinetobacter spp.	3 (2)
Gram Positive Cocci (GPC)	**72 (44)**
S.aureus	41 (25)
Coagulase Negative *Staphylococcus*	31 (19)

[Table/Fig-2]: Organisms Isolated from pus samples% (n= 164)

Out of 164 bacterial isolates, Enterobacterales were the most prevalent GNB group (79; 48%), with *Escherichia coli* being the most frequently isolated organism (44; 27%), followed by *Klebsiella pneumoniae* (31; 19%). Other non fermenting GNB included *Pseudomonas aeruginosa* (10; 6%) and *Acinetobacter* spp. (3; 2%). Among GPC, the most common isolate was *Staphylococcus aureus* (41; 25%), followed by Coagulase-Negative Staphylococci (CONS) (31; 19%). Overall, *E. coli* and *S. aureus* were the two most prevalent pathogens [Table/Fig-2].

Of all isolates, the highest number (48; 29.2%) were recovered from infected wounds. The most common organism in these wounds was *E. coli* (16; 33.3%), followed by *S. aureus* (13; 27%) and *K. pneumoniae* (7; 14.5%). Less frequent isolates included *Klebsiella aerogenes* (2; 4.1%), *Acinetobacter* spp. (2; 4.1%), and *P. aeruginosa* (1; 2%) [Table/Fig-3].

The study found a statistically significant association (p-value <0.05) for *E. coli*, *S. aureus*, and CONS, indicating a strong correlation between these bacterial species and specific types of infections [Table/Fig-3].

The distribution of pathogens varied by department. The highest number of isolates (59; 36%) were obtained from the Surgery department, where *Klebsiella pneumoniae* was the most prevalent pathogen (18; 31%), followed by *E. coli* (13; 22%) and *S. aureus* (10; 17%). Less common isolates included *P. aeruginosa* (3; 5%) and *Acinetobacter* spp. (2; 3%). This highlights the significant presence of *K. pneumoniae* and other GNB in surgical settings.

Isolates (n=164)	Type of Pyogenic infections										
	Infected wound 48 (29.2%)	NHU* 22 (13.4%)	Abscess 20 (12.1%)	Pyothorax 17 (10.3%)	CSOM* 13 (7.9%)	SSI* 12 (7.3%)	Burn wound 11 (6.7%)	Discharging sinuses 11 (6.7%)	Other 7 (4.2%)	Urethritis 3 (1.8%)	Chi-square value	p-value*
***E.coli* 44 (27%)**	16 (33.3)	8 (36.3)	5 (25)	4 (23.5)	00	2 (16.6)	3 (27.2)	2 (18.1)	2 (28.5)	2 (66.6)	10.435	0.0012
***K. pneumoniae* 31 (19%)**	7 (14.5)	5 (22.7)	4 (20)	4 (23.5)	2 (15.3)	3 (25)	2 (18.1)	2 (18.1)	2 (28.5)	00	2.577	0.1084
***K.aerogens* 2 (1%)**	2 (4.1)	00	00	00	00	00	00	00	00	00	NC*	NC*
***P.mirabilis* 2 (1%)**	00	00	00	00	2 (15.3)	00	00	00	00	00	NC*	NC*
***P. aeruginosa* 10 (6%)**	1 (2)	1 (4.5)	00	00	3 (23)	2 (16.6)	2 (18.1)	00	1 (14.2)	00	NC*	NC*
***A. baumanii* 3 (2%)**	2 (4.1)	00	00	00	00	00	00	00	1 (14.2)	00	NC*	NC*
***S. aureus* 41 (25%)**	13 (27)	5 (22.7)	6 (30)	2 (11.7)	3 (23)	3 (25)	3 (27.2)	4 (36.3)	1 (14.2)	1 (33.3)	3.379	0.0660
CONS 31 (19%)	7 (14.5)	3 (13.6)	5 (25)	7 (41.1)	3 (23)	2 (16.6)	1 (9)	3 (27.2)	00	00	10.6804	0.0011

[Table/Fig-3]: Association of Isolates based on Type of Infection %(n=164).

Department	Total no. 164 (%)	Enterobacterales GNB 79 (48%)				Non fermenter GNB 13 (8%)		GPC 72 (44%)	
		E.coli 44 (%)	*Klebsiella pneumoniae* 31 (%)	*Klebsiella aerogens* 2 (%)	*P. mirabilis** 2 (%)	*P. aeruginosa** 10 (%)	*Acinetobacter spp.* 3 (%)	*S. aureus* 41 (%)	CONS* 31 (%)
Surgery	59 (36)	13 (22)	18 (31)	00	00	3 (5)	2 (3)	10 (17)	13 (22)
Orhto*	32 (20)	7 (22)	00	00	00	00	1 (3)	14 (44)	10 (31)
O/G*	28 (17)	7 (25)	3 (11)	00	00	7 (25)	00	3 (11)	8 (29)
ENT*	20 (12)	11 (55)	00	00	2 (10)	00	00	7 (35)	00
Dermatology	10 (6)	3 (30)	00	00	00	00	00	7 (70)	00
ICU*	7 (4.2)	00	7 (100)	00	00	00	00	00	00
Medicine	3 (2)	00	3 (100)	00	00	00	00	00	00
Pul.Medicine*	3 (2)	3 (100)	00	00	00	00	00	00	00
Paediatrics	2 (1.2)	00	00	2 (100)	00	00	00	00	00
Total	164	44	31	2	2	10	3	41	31

[Table/Fig-4]: Department wise distribution of Isolates %(n=164).
CONS: Coagulase negative staphylococcus, *P.mirabilis*-Proteus mirabilis, P.aeruginosa-*Pseudomonas aeruginosa*
Ortho- Orthopedic, O/G*-Obstetrics and Gynecology, ENT- Ear nose and Throat, ICU-Intensive care unit, Pul.medicine- Pulmonary medicine

In samples from ICUs (7; 4.2%), *Klebsiella pneumoniae* was the predominant causative pathogen, which may be attributed to the fact that ICU patients are typically critically ill and immunocompromised [Table/Fig-4].

A significant proportion of GNB exhibited MDR (37; 40.2%) and XDR (31; 33.6%). In contrast, GPC showed a similar rate of MDR (34; 47.2%), but no XDR strains were detected. Among specific bacteria, *Staphylococcus aureus* isolates showed an alarming MDR rate of 34 (82.9%), with no XDR strains detected. Among GNB, the highest percentage of MDR was observed in *Escherichia coli* (24; 54.5%), while the highest percentage of XDR was found in *Klebsiella pneumoniae* (11; 35%) [Table/Fig-5].

Isolates	MDR 71 (%)	XDR 31 (%)
Gram Negative Bacteria (GNB) (n=92)	37 (40.2)	31 (33.6)
E. coli (44)	24 (54.5)	10 (22.7)
Klebsiella pneumoniae (31)	11 (35.4)	11 (35.4)
P. aeruginsa (10)	1 (10)	4 (40)
Acinetobacter spp.(3)	1 (33.3)	2 (66.6)
Klebsiella aerogens (2)	00	2 (100)
P. mirabilis (2)	00	2 (100)
Gram Positive Cocci (n=72)	34 (47.2)	00
S. aureus (41)	34 (82.9)	00

[Table/Fig-5]: Distribution of Isolates as MDR and XDR [7].

This finding highlights a serious concern regarding drug resistance, particularly in GNB and specific strains such as *S. aureus* and *E. coli*. These isolates showed the highest susceptibility to minocycline, meropenem, and ertapenem-41 (93%) and 25 (81%) each-followed by cefoperazone-sulbactam (40; 91%). *K. pneumoniae* demonstrated the highest susceptibility to minocycline, meropenem, and ertapenem (25; 81%) each, followed by piperacillin-tazobactam, cefoperazone- sulbactam, imipenem, amikacin, and tobramycin (22; 70%) each. *Pseudomonas aeruginosa* showed the highest susceptibility to meropenem (8; 80%), followed by piperacillin–tazobactam (7; 70%) and tobramycin (7; 70%) [Table/Fig-6].

Among *S. aureus* isolates, 24 (59%) were identified as MRSA. The highest antimicrobial susceptibility was observed with vancomycin, linezolid, and levofloxacin (24; 100%) each, followed by gentamicin (17; 71%). Inducible Clindamycin Resistance (ICR) was detected in 5 (21%) *S. aureus* isolates [Table/Fig-7].

Antimicrobial agents	Enterobacterales GNB (n=79)				Non fermenter GNB (n=13)	
	E.coli 44 (%)	*Klebsiella pneumoniae* 31 (%)	*Enterobacter aerogens* 2 (%)	*Proteus mirabilis* 2 (%)	*Pseudomonas aeruginosa* 10 (%)	*Acinetobacter* spp. 3 (%)
Ampicillin-Sulbactam	31 (70)	20* (64.5)	-	1* (50)	-	1* (33)
Amoxclav	30 (68)	9* (30)	-	1* (50)	-	-
Piperacillin-Tazobactam	34 (77)	22* (70)	1* (50)	1* (50)	7* (70)	1* (33)
Cefoxitin	14* (32)	9* (30)	-	00*	-	-
Ceftazidime	27* (61)	16* (52)	00*	00*	4* (40)	-
Cefuroxime	24* (55)	9* (30)	00*	00*	-	-
Cefotaxime	14* (32)	9* (30)	00*	00*	-	00
Ceftriaxone	13* (30)	9* (30)	00*	00*	-	00
Cefoperazone-Sulbactam	40 (91)	22* (70)	1* (50)	00*	-	-
Cefepime	20* (45)	9* (30)	00	00*	3* (30)	1* (33)
Imipenem	37 (84)	22* (70)	2* (100)	1* (50)	6* (60)	1* (33)
Meropenem	41 (93)	25* (81)	2* (100)	2* (100)	8* (80)	1* (33)
Ertapenem	41 (93)	25* (81)	2* (100)	2* (100)	-	-
Ciprofloxacin	20* (45)	6* (19)	00	00*	5* (50)	1* (33)
Levofloxacin	24* (55)	9* (30)	1* (50)	00*	6* (60)	1* (33)
Tetracycline	30 (68)	19* (61)	1* (50)	-	-	-

Minocycline	41 (93)	25* (81)	2* (100)	-	-	2* (67)
Amikacin	34 (77)	22* (70)	2* (100)	1* (50)	-	1* (33)
Gentamicin	27* (61)	19* (61)	1* (50)	1* (50)	-	1* (33)
Tobramicin	27* (61)	22* (70)	1* (50)	1* (50)	7* (70)	2* (67)
Aztreonam	31 (70)	19* (61)	1* (50)	1* (50)	5* (50)	-
Cotrimoxazole	24* (55)	9* (30)	00*	00*	-	00*

[Table/Fig-6]: Antimicrobial susceptibility pattern of Gram Negative Bacteria (GNB) % (n=92).
*As per CLSI, the number of isolates less than 30 is not significant. However, this data has been presented here for epidemiological reasons, so that it can be later on pooled in a different meta-analysis.

Antimicrobial agents	MRSA 24 (59%)	MSSA 17 (41%)
Benzyle penicillin	12 (50)	13 (76)
Chloramphenicol	5 (21.4)	15 (88)
Ciprofloxacin	10 (42)	14 (82)
Levofloxacin	24 (100)	15 (88)
Erythromycin	12 (50)	14 (82)
Clindamycin	12 (50)	15 (88)
Gentamicin	17 (71)	16 (94)
Linezolid	24 (100)	17 (100)
Teicoplanin	24 (100)	17 (100)
Vancomycin	24 (100)	17 (100)
Tetracyclin	12 (50)	17 (100)
Cotrimoxazole	9 (38)	15 (88)
Inducible Clindamycin resistant (ICR)	5 (21)	00

[Table/Fig-7]: Antimicrobial susceptibility pattern of *Staphylococcus aureus* % (n=41).

DISCUSSION

In the present study, culture positivity was 164 (48%), which correlates with findings by Devi KD et al., (30.9%) and Wajid M et al., (43.3%) [14,17]. However, some studies have reported higher culture positivity rates [6,18]. In this study, the isolation rate of GNB (92; 56%) was higher than that of GPC (72; 44%), consistent with earlier reports [6,18]. The majority of samples were obtained from male patients (174; 51%), compared to female patients (168; 49%), findings that are similar to previous studies [18,19]. The highest culture positivity was observed in the Surgery Department (59; 36%), followed by Orthopaedics (32; 20%), Obstetrics and Gynaecology (28; 17%), ENT (20; 12%), Dermatology (10; 6%), and ICU (7; 4.2%). Comparable results were reported by Bankar N et al., [20].

In the present study, the most common co-morbidity was Diabetes Mellitus (DM) (62; 18%), followed by the co-existence of DM with Hypertension (55; 16%), and Hypertension alone (15; 4.3%). Similar findings were reported by Kar M et al., who identified DM (25; 35.67%) as the predominant comorbidity [21]. Pre-existing DM was associated with poorer clinical outcomes. It is estimated that 693 million people will have DM by 2045, making it one of the most significant global health challenges of the 21st century [22]. This poses a major concern in infectious diseases, as DM increases susceptibility to various infections [4,23].

In this study, the most common addiction was smoking (121; 35.53%), followed by alcohol consumption (108; 32%), and combined smoking and alcohol use (87; 25.4%), which aligns with findings from other studies [23]. Previous studies have also reported smoking as a risk factor for pyogenic infections [21,24]. The associations between co-morbidities and addictions with pyogenic infections are presented in [Table/Fig-1]. Among patients with infected wounds, the co-existence of DM and Hypertension was the most frequent co-morbidity (39; 38.2%), followed by DM alone (17; 16.6%), Hypertension (4; 3.9%), *Mycobacterium tuberculosis* (3; 2.9%), and Trauma (2; 1.9%). The most common addiction was smoking (56; 54.9%), followed by combined smoking and alcohol use (45; 44.1%), and alcohol alone (44; 43.1%). Associations of co-morbidities (DM, hypertension, trauma, tuberculosis) and addictions (smoking, alcoholism, and their co-existence) with pyogenic infections were statistically significant (p-value <0.05). Similar associations of DM, tuberculosis, and smoking were reported by Pathak A et al., [25].

In this study, the most frequently isolated organism was *E. coli* (44; 26.8%), followed by *S. aureus* (41; 25%), *K. pneumoniae* (31; 18.9%), *P. aeruginosa* (10; 6%), *Acinetobacter* spp. (3; 2%), *K. aerogenes* (2; 1%), and *Proteus mirabilis* (2; 1%), consistent with earlier studies [9,21]. Among GPC, *S. aureus* (41; 25%) was the most frequent isolate, followed by Coagulase-Negative Staphylococci (CONS) (31; 19%), similar to findings reported in previous studies [6,18]. Mixed growth was observed in 3 (0.87%) samples in the present study, which is consistent with previous reports [14]. Several studies have associated mixed bacterial growth with poor wound care, increased microbial persistence, ineffective antimicrobial therapy, and unfavourable patient outcomes [14].

A study from Mysuru, Karnataka reported 30.07% MDR GNB among pyogenic infections [26]. In the present study, the prevalence of MDR and XDR among GNB was 37 (40.2%) and 31 (33.6%), respectively. However, a study by Ingale H, reported higher rates of MDR (68.8%) and XDR (47.2%) in GNB isolates [27].

Multidrug-Resistant (MDR) Gram-Negative Bacilli (GNB): *E. coli* was the most predominant MDR GNB, accounting for 24 (54.5%) of isolates, followed by *K. pneumoniae (*11; 35.4%), and both *Acinetobacter spp.* (1; 33.3%) and *P. aeruginosa* (1; 10%).

Extensively Drug-Resistant (XDR) Gram-Negative Bacilli (GNB): Among XDR GNB, *Klebsiella aerogenes* 2 (100%) and *Proteus mirabilis* 2 (100%) showed complete resistance, followed by *Acinetobacter* spp. 2 (66.6%), *P. aeruginosa* 4 (40%), *K. pneumoniae* 11 (35.4%), and *E. coli* 10 (22.7%). A study by Devi KD et al., and Kavya V et al., reported higher MDR rates in *Acinetobacter baumanni*i, at 2 (66.7%) and 27 (16.2%) respectively. The findings of the present study align with these reports [14,26].

Ingale H et al., reported extremely high MDR (63; 91.3%) and XDR (43; 62.3%) rates among *E. coli* isolates [27]. Similarly, other studies also reported higher MDR *E. coli* isolation rates, 33.3% and 43 (25.9%) by Chakraborty A et al., and Kavya V et al., respectively [18,26]. Previous research consistently shows high levels of drug resistance in *K. pneumoniae*. Kavya V et al., reported nearly half (48.12%) of isolates as MDR. Ingale H et al., found high rates of both MDR (69%) and XDR (42.8%), while Kalita JM et al., reported an even higher MDR rate of 74.79% [26-28].

Ingale H, also found significant resistance in *P. aeruginosa*, reporting MDR rates of 42.5% and XDR rates of 33.7%. In contrast, other studies have shown variable MDR rates ranging from 9.6% to 61.9% (Kavya V et al., 16 [9.6%]; Devi KD et al., 5 [16.7%]; and Soni M et al., 61.9%, respectively) [14,26,29]. In contrast to the study by Ingale H, which reported MDR and XDR rates of 67% and 11.3% for *S. aureus* [27], the present study found a significantly higher MDR rate of 82.9% but no XDR strains.

The high prevalence of MDR and XDR bacteria in pyogenic infections represents a critical public health concern, driven by multiple factors. The inappropriate and excessive use of antibiotics exerts strong selective pressure, enabling resistant

strains to proliferate. Pyogenic pathogens such as *P. aeruginosa*, *Acinetobacter baumannii*, and MRSA readily acquire and transfer resistance genes. Additionally, their capacity to form biofilms provides physical protection from both antibiotics and host immune responses, complicating treatment and promoting resistance. Healthcare environments are major reservoirs for MDR and XDR pathogens. Previous hospitalisation, use of medical devices, and inadequate infection control practices facilitate the transmission of resistant bacteria among patients.

E. coli strains demonstrated high susceptibility to carbapenems- Meropenem and Ertapenem 41 (93%) each- and Minocycline 41 (93%), followed by Cefoperazone-Sulbactam 40 (91%). However, susceptibility markedly decreased for commonly used Third-Generation Cephalosporins (TGCs) such as Ceftriaxone 13 (30%) and Cefotaxime 14 (32%). These findings align with a study from Odisha, which reported high susceptibility to the carbapenem group (Imipenem and Meropenem, 92%) and Cefoperazone-Sulbactam (80%), but reduced susceptibility to Ceftriaxone (36%). Previous studies have also reported higher susceptibility to carbapenems [21,30] and lower susceptibility to routinely used TGCs [21].

The antimicrobial susceptibility pattern of *Klebsiella pneumoniae* showed high sensitivity to Meropenem, Ertapenem, and Minocycline (25; 81% each). For TGCs- Ceftriaxone and Cefotaxime—the susceptibility was 9 (30%) each, while Ciprofloxacin showed the lowest susceptibility at 6 (19%). Similar susceptibility patterns for carbapenems were reported from Odisha, with Meropenem (80%); however, susceptibility to Ceftriaxone (65%) and Ciprofloxacin (70%) was higher than that found in the present study [30]. Conversely, another study reported lower susceptibility patterns than those observed here [21].

Antimicrobial Susceptibility Pattern of *P. aeruginosa*

The antimicrobial susceptibility pattern of *P. aeruginosa* showed significantly reduced sensitivity to carbapenems- Meropenem 8 (80%) and Imipenem 6 (60%)- and markedly decreased susceptibility to anti-pseudomonal cephalosporins, including Ceftazidime 4 (40%) and Cefepime 3 (30%). Sensitivity to Piperacillin-Tazobactam and Tobramycin was 7 (70%) each. A previous study reported higher susceptibility to Meropenem (94%) and lower susceptibility to Imipenem (53%), Piperacillin-Tazobactam (67%), and Ceftazidime (47%), findings that correlate with the present study [30]. Compared to the current findings, another study reported a lower susceptibility pattern [21].

Acinetobacter spp.

Acinetobacter spp. isolates demonstrated low susceptibility to carbapenems- Imipenem and Meropenem 1 (33%) each- but showed better sensitivity to Minocycline and Tobramycin 2 (67%) each. Previous studies have reported higher susceptibility to Imipenem and Meropenem (93% each) [30].

The high resistance observed to TGCs and fluoroquinolones in *E. coli* and *K. pneumoniae* is a significant concern and is likely due to widespread ESBL production. This pattern aligns with the continued high susceptibility to carbapenems and Piperacillin-Tazobactam. A notable observation is the much higher susceptibility to Minocycline compared to Tetracycline, suggesting a specific resistance mechanism less effective against Minocycline. Overall, the data indicate a high burden of MDR organisms, particularly ESBL producers, though ESBL production was not directly detected in this study.

Methicillin-Resistant *Staphylococcus aureus* (MRSA)

In this study, MRSA accounted for 24 (59%) isolates, while MSSA comprised 17 (41%). These findings are consistent with a previous study reporting MRSA prevalence at 51.86% [21]. However, other studies have reported lower MRSA rates-151 (13.26%) by Kalita JM et al., 37.3% by ICMR AMRSN, and 40% as reported by the Indian Network for Surveillance of Antimicrobial Resistance (INSAR) group [28,31,32]. In India, the prevalence of MRSA ranges from 40% to 70% among *S. aureus* isolates, with variations observed between hospital and community settings [33].

All MRSA isolates in this study were susceptible to Vancomycin, Teicoplanin, Linezolid, and Levofloxacin 24 (100%) each. Inducible Clindamycin Resistance (ICR) was detected in 5 (21%) *S. aureus* isolates. *S. aureus* is a common commensal organism found on the skin and mucous membranes, and MRSA can colonise these sites, increasing the risk of infection. MRSA produces toxins and enzymes that facilitate tissue invasion and damage. Its multidrug resistance poses a challenge in clinical management. Healthcare workers can serve as carriers, contributing to the spread of MDR MRSA within hospital settings.

Clinical Implications and Antibiogram Significance

The study provides an invaluable "antibiogram"- a snapshot of local antimicrobial resistance patterns. This information is crucial in clinical settings. The observed high resistance to TGCs, once considered reliable antibiotics, indicates that standard empirical treatment protocols may now be ineffective. This resistance can lead to adverse outcomes such as prolonged illness and increased mortality.

These findings necessitate changes in clinical practice. Physicians managing severe pyogenic infections should consider using more potent, last-resort agents such as carbapenems from the outset or include them as part of combination therapy. Furthermore, identifying patient risk factors- such as underlying co-morbidities and lifestyle habits- can enable a more targeted and cautious approach to treatment in high-risk individuals.

Limitation(s)

The present study was conducted at a single centre and, therefore, reflects data from a limited geographical area regarding the distribution of aetiological agents, co-morbid conditions, and predisposing factors associated with pyogenic infections. A multicentre study would provide more comprehensive insights and aid in formulating effective antimicrobial stewardship policies for better management of such infections.

CONCLUSION(S)

This study found that pyogenic infections are predominantly caused by GNB, with *E. coli* being the most common pathogen. A significant finding is the alarming rise in antimicrobial resistance, including MDR and XDR strains among GNB. The study also highlights the highest burden of MDR among *S. aureus* isolates and the emergence of highly resistant pathogens such as *Acinetobacter* spp. and *K. pneumoniae*, which pose major therapeutic challenges. These findings are critical for clinicians, providing essential guidance for revising empirical treatment strategies to improve patient outcomes. To address this growing threat, the study recommends regular updates to local empirical treatment protocols, implementation of robust Antimicrobial Stewardship Programs (ASP) with continuous surveillance and mandatory culture testing, and strengthening infection control measures. Future research should focus on the molecular characterisation of resistance genes, identification of community sources of resistant bacteria, and evaluation of the impact of ASPs on resistance trends and patient outcomes.

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