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UROPATHOGENS ISOLATED AND THEIR ANTIBIOTIC SUSCEPTIBILITY PROFILES FROM A TERTIARY CARE HOSPITAL IN NORTHERN INDIA

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ABSTRACT Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, with increasing antimicrobial resistance presenting significant therapeutic challenges. This study examines the current profile of uropathogens isolated from hospital settings and their antibiotic susceptibility patterns. The study aims to analyse the distribution of uropathogens in hospital settings and evaluate their antimicrobial resistance patterns to guide empirical therapy decisions. This cross-sectional observational study conducted at Dr. Baba Saheb Ambedkar Medical College and Hospital, New Delhi, from July 2022 to December 2023, assessed the antimicrobial resistance (AMR) profiles of uropathogens isolated from clinical samples. A total of 15,020 samples screened revealed 20.36% culture positivity. Gram-negative bacteria predominated, with Escherichia coli and Klebsiella pneumoniae as principal isolates exhibiting multidrug resistance, including resistance to cephalosporins and fluoroquinolones, though high efficacy was retained by last-line agents such as colistin and polymyxin. Gram-positive isolates, mainly Staphylococcus aureus and Enterococcus spp., showed declining sensitivity to critical antibiotics including vancomycin and linezolid, reflecting an alarming resistance trend that threatens last-resort treatment options. Drugs like gentamicin and clindamycin demonstrated moderate efficacy against S. aureus. Seasonal variations in isolate prevalence were noted, with peaks during warmer months. The findings underscore the urgent need for robust antimicrobial stewardship programs, regular surveillance of resistance patterns, and revision of empirical therapy guidelines to effectively manage UTIs in hospital settings amid escalating AMR challenges.

KEYWORDS : Urinary Tract Infections (UTIs), Gram-negative Bacteria, Gram-positive Bacteria, antimicrobial resistance (AMR), Multidrug Resistance (MDR), Antibiotic Susceptibility Testing

1. INTRODUCTION

Urinary tract infections (UTIs) remain among the most prevalent bacterial infections encountered in clinical practice, frequently leading to hospital admissions and posing significant public health challenges globally.[1] With an estimated 150 million people affected annually worldwide, these infections contribute substantially to healthcare burdens, encompassing millions of emergency department visits and hospitalizations each year.[2] Despite their commonality, untreated UTIs can escalate to severe conditions such as pyelonephritis and urosepsis, which carry considerable morbidity and mortality rates, particularly in vulnerable populations.[3] Moreover, urinary tract infections are a leading cause of gram-negative sepsis in hospitalized patients, highlighting the critical need for prompt diagnosis and effective treatment to mitigate severe outcomes.[4] The global burden of UTIs is substantial, with 404.6 million cases reported in 2019, and the economic impact is equally significant, with an estimated annual societal cost of $3.5 billion in the United States alone.[5,6] This pervasive clinical issue necessitates a comprehensive understanding of the uropathogens involved and their susceptibility to antimicrobial agents, especially within hospital environments where antibiotic resistance patterns can differ significantly from community settings[7-9]. This growing concern is further compounded by the escalating rates of antimicrobial resistance, which limit therapeutic options and complicate patient management, underscoring the urgent need for continuous surveillance of resistance patterns among uropathogens[10]. This necessitates a regular assessment of the microbiological agents causing UTIs and their antimicrobial resistance profiles to guide tailored empirical antibiotic responses and strengthen infection control strategies[11,12]. This paper, therefore, aims to provide an updated review of the most common uropathogens isolated from hospital settings and their current antibiotic susceptibility profiles, offering crucial insights for effective clinical management and informing antimicrobial stewardship programs.[13,14] This critical assessment is essential for developing evidence-based guidelines that optimize patient outcomes while simultaneously combating the global threat of antibiotic resistance.[15] This manuscript will analyse the findings from 2022-2023 to highlight emerging trends in uropathogen distribution and resistance, providing a contemporary perspective on the challenges faced in hospital-acquired urinary tract infections.

2. MATERIALS AND METHODS:

2.1. Study Design:

This study used a cross-sectional observational design to assess the antibiotic susceptibility profiles of uropathogens from patients at Dr. Baba Saheb Ambedkar Medical College and Hospital in New Delhi, between July 2022 and December 2023. As the present study includes standard laboratory isolates, approval from the Institutional Ethical Committee was not required.

2.2. Sample Collection and Screening:

Midstream urine samples were collected in sterile universal containers and processed within two hours of collection. If processing was delayed, samples were stored at 2 to 8°C for up to six hours. Samples were plated on Blood Agar and MacConkey Agar (Himedia, India) using the semi-quantitative calibrated loop method (1 L)[16] and incubated aerobically overnight at 37°C. Significant bacteriuria was defined as pure growth of an isolate with a count of at least 10^5 colony forming units (CFU) per millilitre. Samples with growth of three or more isolates were considered contaminated and required repeat sample collection. Bacterial isolates were identified using conventional methods.[17] Antimicrobial sensitivity testing (AST) was performed on Mueller Hinton agar (Himedia, India) using the Kirby-Bauer technique according to CLSI guidelines, with Escherichia coli (ATCC 25922), Staphylococcus aureus (ATCC 25923) and Pseudomonas aeruginosa (ATCC 27853) as control strains.[18] The following antibiotic discs and concentrations were used: Amikacin (AMK, 30 µg), Ciprofloxacin (CIP, 30 µg), Sulphamethoxazole/ Trimethoprim (SXT, 25 µg), Cefotaxime (CTX, 30 µg), Cefepime (FEP, 30 µg), Ampicillin (AMP, 25 µg), Colistin (COL, 25 µg), Ceftazidime (CAZ, 30 µg), Ceftriaxone (CRO, 30 µg), Gentamicin (GEN, 30 µg), Imipenem (IPM, 10 µg), Linezolid (LNZ, 30 µg), Vancomycin (VAN, 30 µg), Teicoplanin (TEC, 30 µg), Piperacillin plus Tazobactam (TZP, 30 + 6 µg), Meropenem (MEM, 10 µg), Azithromycin (ATM, 30 µg), Tetracycline (TCY, 30 µg), Polymyxin B (POL, 300 U), Nitrofurantoin (NIT, 30 µg), Erythromycin (ERY, 15 µg), Cefoxitin (FOX, 30 µg), Clindamycin (CLI, 10 µg), and high-level Gentamicin (GEH, 120 µg), all from Himedia Laboratories (India).

2.3. Statistical Analysis

Data was collected based on drug sensitive patterns of patients which was fed in an Excel sheet. The data were analysed and was presented in the form of tables and figures.

3. RESULTS

A total of 15,020 samples were screened during the period between July, 2022 and December, 2023, of which 6211 (41.35%) were male while 8809 (58.65%) were female. Of the 15,020 samples screened, 3058 (20.36%) were reported culture positive. Of the total 3058 positive samples 2080 (68.01%) were from female patients and 978 (31.98%) were from males. Overall positivity was higher in females at 23.6% (2080/8809) than males at 15.7% (978/6211)

From the samples found culture positive, 2479 (81.07%) isolates were found to be Gram negative bacteria, 187 (6.11%) were Gram positive bacteria while 392 (12.82%) were reported fungi (Fig. 1).

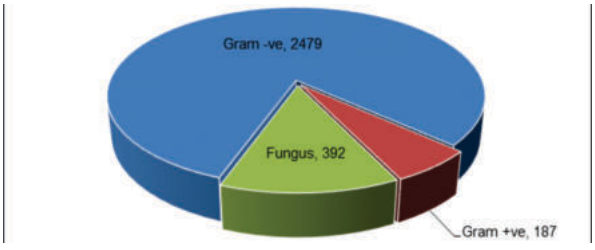

Fig. 1. Graph Showing the Distribution of Culture Positivity Among the Isolates

Among the Gram-negative isolates, the most common isolate found was Escherichia coli (n=1720, 56.25%) followed by Klebsiella pneumoniae (n=311, 10.17%), Providentia stuartii (n=122, 3.99%), Citrobacter sps. (n=103, 3.37%), Pseudomonas aeruginosa (n=92, 3.01%), Proteus mirabilis (n=66, 2.16%), Acinetobacter sps. (n=34, 1.11%), Proteus vulgaris (n=19, 0.62%). Klebsiella oxytoca, Morganella morganii and Serratia marcescens were also reported, but in least numbers with 7 (0.23%), 4 (0.13%) and 1 (0.03%) isolates respectively. From the 187 (6.11%) Gram positive isolates, Staphylococcus aureus was found predominant with 105 (3.43%) isolates followed by Enterococcus sps. with 82 (2.68%) isolates. In the fungal isolates, Candida albicans was reported in majority with 223 (7.29%) isolates followed by non-albicans Candida with 169 (5.53%) isolates (Table 1).

Table 1. Distribution of Different Isolates from the Study

Microorganism	No. of isolates	% of total samples (n=15,020)	% of culture positive isolates (n=3,058)
Gram negative Bacteria (n=2,479)			
Escherichia coli	1720	11.45	56.25
Klebsiella pneumoniae	311	2.07	10.17
Providentia stuartii	122	0.81	3.99
Citrobacter sps.	103	0.69	3.37
Pseudomonas aeruginosa	92	0.61	3.01
Proteus mirabilis	66	0.44	2.16
Acinetobacter sps.	34	0.22	1.11
Proteus vulgaris	19	0.13	0.62
Klebsiella oxytoca	7	0.05	0.23
Morganella morganii	4	0.03	0.13
Serratia marcescens	1	0.01	0.03
Gram positive Bacteria (n=187)			
Staphylococcus aureus	105	0.70	3.43
Enterococcus sps.	82	0.55	2.68
Fungi (n=392)			
Candida albicans	223	1.48	7.29
Non-albicans Candida	169	1.10	5.53

From the distribution pattern of the isolates throughout the year, a notable increase was observed in the total number of isolates in 2023 when compared to 2022, with overall rising trends for most organisms. The highest monthly counts of isolates were observed in the months from July to October each year (Table 2). E. coli was reported with largest number of isolates in both the years with 595 (19.46%) and 1125 (36.79%) isolates in 2022 and 2023 respectively, with peak isolation during monsoon and post-monsoon months ranging between July and November. Similar pattern was observed for K. pneumoniae with rising counts in 2023 with 206 (6.74%) in comparison to 105 (3.43%) isolates in 2022, again peaking mid-year and towards the end of the year. C. albicans also showed consistently high incidence rates, with a clear upward trend from 2022 with 71 (2.32%) to 2023 with 152 (4.97%) isolates. Similar trend was observed for non-albicans Candida and P. aeruginosa. Some species such as Enterococcus sps. (ENT), Providencia stuartii (PRS), Staphylococcus aureus (SAU) and Acinetobacter (ABA) were present throughout the year with sporadic peaks. K. oxytoca, M. morganii and S. marcescens were detected infrequently with no clear monthly pattern (Table 2).

Table 2: Table showing the Distribution Pattern of the Clinical Isolates from the UTI Subjects During the Period 2022-2023

Organism	Month / year	JAN	FEB	MAR	APR	MAY	JUNE	JULY	AUG	SEP	OCT	NOV	DEC	TOTAL
	Gram Negative Bacteria:													
ABA	2022	-	-	-	-	-	-	2	2	1	3	7	0	15
	2023	1	1	0	0	1	2	6	4	1	1	1	1	19
CIB	2022	-	-	-	-	-	-	0	0	11	0	6	6	23
	2023	0	3	6	3	2	4	9	18	11	13	4	7	80
ECO	2022	-	-	-	-	-	-	136	109	106	63	86	95	595
	2023	59	44	23	37	101	159	151	175	130	101	69	76	1125
ENT	2022	-	-	-	-	-	-	13	4	5	8	14	5	49
	2023	1	2	2	2	2	1	6	1	7	2	3	4	33
KLP	2022	-	-	-	-	-	-	24	17	15	22	14	13	105
	2023	2	3	6	4	19	19	22	43	22	22	20	24	206
KOX	2022	-	-	-	-	-	-	0	4	3	0	0	0	7
	2023	0	0	0	0	0	0	0	0	0	0	0	0	0
MMO	2022	-	-	-	-		-	0	0	2	1	0	0	3
	2023	0	1	0	0	0	0	0	0	0	0	0	0	1
PAE	2022	-	-	-	-	-	-	3	1	6	3	3	1	17
	2023	2	1	1	2	5	6	12	13	11	9	8	5	75
PMI	2022	-	-	-	-	-	-	5	3	1	5	2	7	23
	2023	1	2	0	0	4	8	7	12	3	2	2	2	43
PVU	2022	-	-	-	-	-	-	1	0	1	0	3	1	6
	2023	0	1	1	0	1	2	2	4	1	0	1	0	13
PRS	2022	-	-	-	-	-	-	9	9	11	3	7	10	49
	2023	3	0	1	4	6	9	7	8	11	5	8	11	73
SMA	2022	-	-	-	-	-	-	0	0	0	1	0	0	1
	2023	0	0	0	0	0	0	0	0	0	0	0	0	0
	Gram positive bacteria :													
ENT	2022	-	-	-	-	-	-	13	4	5	8	14	5	49
	2023	1	2	2	2	2	1	6	1	7	2	3	4	33
SAU	2022	-	-	-	-	-	-	0	4	6	3	3	3	19

	2023	4	2	4	2	8	10	18	13	8	8	6	3	86
	Fungal isolates													
CAL	2022	-	-	-	-	-	-	15	17	11	16	6	6	71
	2023	8	4	4	12	12	10	16	18	15	24	17	12	152
NAC	2022	-	-	-	-	-	-	11	10	20	9	11	9	70
	2023	4	6	4	0	9	12	10	17	20	8	3	6	99
Total		85	70	52	66	170	242	485	506	439	332	304	307	3058

ABA - Acinetobacter sps., CAL – C. albicans, NAC – Non-albicans Candida, CIB – Citrobacter sps., ECO – E. coli, ENT – Enterococcus sps., KLP – K. pneumoniae, KOX – K. oxytoca, MMO – M. morganii, PAE – P. aeruginosa, PMI - P. mirabilis, PVU – P. vulgaris, PRS – P. stuartii, SAU – S. aureus, SMA – S. marcescen

The drug sensitivity or antibiotic susceptibility profiles also revealed interesting results. In the Gram-negative bacteria, the sensitivity rates for E. coli, K. pneumoniae and Citrobacter sps. against AMK increased substantially in 2023, indicating improved susceptibility. In E. coli, the sensitivity for AMK was seen in 99 (16.64%) isolates in 2022 while it was seen in 625 (55.56%) isolates in 2023 while in K. pneumoniae the sensitivity for AMK was seen in 37 (35.24%) and 133 (64.56%) isolates in 2022 and 2023, respectively. The CIP sensitivity remained low for most isolates, with slight improvement was observed for some organisms. Acinetobacter sps., showed an increased sensitivity pattern in the two years compared with 1 (6.67%) isolate in 2022 and 7 (36.84%) isolates in 2023 where as for P. aeruginosa, P. stuartii similar pattern was found. With the SXT drug, moderate sensitivity was observed in E. coli while fluctuations were observed for other isolates suggest persistent resistance. Sensitivity rates for CTX and FEP remained very low or zero for virtually all isolates, while FEP data was found inconsistent, with some high rates likely due to small sample sizes. COL and POL sensitivity was found very high across organisms for these reserve antibiotics, maintaining their critical role against multi-drug resistant isolates specifically in E. coli, K. pneumoniae, P. aeruginosa and P. stuartii. For GEN, improved sensitivity was observed for E. coli and several other isolates. Other antibiotics like MEM, IPM, TZP showed variable effectiveness across organisms, with some moderate improvements noted. In the high-level Gentamicin (GEH) panel, only E. coli and K. pneumoniae were sensitive, while VAN, TEC, TCY, ERY, FOX and CLI showed no effect on the sensitivity patterns of the UTI isolates (Table 3).

Table 3: Table Showing the Drug Susceptibility Profiles of Gram-negative Bacteria

Org		ABA		CIB		ECO		KLP		KOX		MMO		PAE		PMI		PVU		PRS		SMA	
Year		2022	2023	2022	2023	2022	2023	2022	2023	2022	2023	2022	2023	2022	2023	2022	2023	2022	2023	2022	2023	2022	2023
No of isolates Drug		15	19	23	80	595	1125	105	206	7	0	3	1	17	75	23	43	6	13	49	73	1	0
AMK	No.	1	11	0	47	99	625	37	133	4		0	0	8	40	5	24	1	7	15	34	0	
	%	6.67	57.89	0	58.75	16.64	55.56	35.24	64.56	57.14		0	0	47.06	53.33	21.74	55.81	16.67	53.85	30.61	46.58	0	
CIP	No.	1	7	0	15	0	124	0	61	0		0	0	9	21	0	13	0	2	21	13	0	
	%	6.67	36.84	0	18.75	0	11.02	0	29.61	0		0	0	52.94	28.00	0	30.23	0	15.38	42.86	17.81	0	
SXT	No.	4	9	0	23	185	393	56	69	2		1	0	0	0	7	10	3	2	0	9	1	
	%	26.67	47.37	0	28.75	31.09	34.93	53.33	33.50	28.57		33.33	0	0	0	30.43	23.26	50	15.38	0	12.33	100	
CTX	No.	2	1	0	0	22	0	0	0	0		0	0	0	0	2	0	0	0	0	0	0	
	%	13.33	5.26	0	0	3.7	0	0	0	0		0	0	0	0	8.7	0	0	0	0	0	0	
FEP	No.	4	0	0	0	138	0	58	0	2		3	0	11	0	8	0	4	0	26	0	1	
	%	26.67	0	0	0	23.19	0	55.24	0	28.57		100	0	64.71	0	34.78	0	66.67	0	53.06	0	100	
AMP	No.	2	0	0	6	19	72	5	6	0		0	0	0	0	4	16	1	1	9	20	0	
	%	13.33	0	0	7.5	3.19	6.4	4.76	2.91	0		0	0	0	0	17.39	37.21	16.67	7.69	18.37	27.4	0	
COL	No.	0	0	0	18	595	1125	105	206	7		0	0	17	74	0	0	0	0	47	73	0	
	%	0	0	0	22.5	100	100	100	100	100		0	0	100	98.67	0	0	0	0	95.92	100	0	
CAZ	No.	0	2	0	0	0	0	0	0	0		0	0	4	17	0	0	0	0	11	22	0	
	%	0	10.53	0	0	0	0	0	0	0		0	0	23.53	22.67	0	0	0	0	22.45	30.14	0	
CRO	No.	6	4	0	19	119	253	49	73	2		1	0	0	0	13	20	3	6	0	0	1	
	%	40	21.05	0	23.75	20	22.49	46.67	35.44	28.57		33.33	0	0	0	56.52	46.51	50	46.15	0	0	100	
GEN	No.	4	11	0	40	323	714	54	105	6		3	0	6	33	16	18	2	6	28	38	0	
	%	26.67	57.89	0	50	54.29	63.47	51.43	50.97	85.71		100	0	35.29	44	69.57	41.86	33.33	46.15	57.14	52.05	0	
GEH	No.	0	0	0	0	0	141	0	10	0		0	0	0	0	0	0	0	0	0	0	0	
	%	0	0	0	0	0	12.53	0	4.85	0		0	0	0	0	0	0	0	0	0	0	0	
IPM	No.	4	1	0	25	259	450	41	88	1		1	0	0	0	11	25	3	9	0	0	1	
	%	26.67	5.26	0	31.25	43.53	40	39.05	42.72	14.29		33.33	0	0	0	47.83	58.14	50	69.23	0	0	100	
LNZ	No.	0	6	0	17	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	
	%	0	31.58	0	21.25	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	
VAN	No.	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	
	%	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	
TEC	No.	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	
	%	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	
TZP	No.	6	11	0	0	0	0	0	0	0		0	0	11	48	0	0	0	0	38	53	0	

	%	40	57.89	0	0	0	0	0	0	0		0	0	64.71	64	0	0	0	0	77.55	72.6	0
MEM	No.	6	8	0	0	0	0	0	0	0		0	0	8	33	0	0	0	0	20	35	0
	%	40	42.11	0	0	0	0	0	0	0		0	0	47.06	44	0	0	0	0	40.82	47.95	0
ATM	No.	3	1	0	0	0	0	0	0	0		0	0	11	38	0	0	0	0	22	28	0
	%	20	5.26	0	0	0	0	0	0	0		0	0	64.71	50.67	0	0	0	0	44.9	38.36	0
TCY	No.	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
POL	No.	0	0	0	0	86	0	0	0	0		0	0	17	74	0	0	0	0	49	72	0
	%	0	0	0	0	14.45	0	0	0	0		0	0	100	98.67	0	0	0	0	100	98.63	0
NIT	No.	1	0	0	1	467	197	55	27	1		0	0	0	1	0	0	0	0	0	0	0
	%	33.33	0	0	1.25	78.49	17.51	52.38	13.11	14.29		0	0	0	1.33	0	0	0	0	0	0	0
ERY	No.	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
FOX	No.	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
CLI	No.	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0
	%	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0

ABA - Acinetobacter sps., CIB – Citrobacter sps., ECO – E. coli, KLP – K. pneumoniae, KOX – K. oxytoca, MMO – M. morganii, PAE – P. aeruginosa, PMI - P. mirabilis, PVU – P. vulgaris, PRS – P. stuartii, SMA – S. marcescens; AMK - Amikacin, CIP – Ciprofloxacin, SXT – Sulphamethoxazole/Trimethoprim, CTX – Cefotaxime, FEP – Cefepime, AMP – Ampicillin, COL – Colistin, CAZ – Ceftazidime, CRO – Ceftriaxone, GEN - Gentamicin, GEH – high-level Gentamicin, IPM – Imipenem, LNZ – Linezolid, VAN – Vancomycin, TEC – Teicoplanin, TZP – Piperacillin plus Tazobactam, MEM – Meropenem, ATM – Azithromycin, TCY – Tetracycline, POL – Polymyxin B, NIT – Nitrofurantoin, ERY – Erythromycin, FOX – Cefoxitin, CLI – Clindamycin

In the Gram-positive isolates, Enterococcus sps. showed high sensitivity to LNZ and VAN with 49 (100%) and 48 (97.96%) of isolates, respectively in 2022 but the sensitivity profiles dropped substantially in 2023 to 16 (48.48%) and 12 (36.36%) isolates, respectively. The sensitivity of S. aureus to LNZ remained fairly effective, with sensitivities in 19 (100%) and 64 (74.42%) isolates in 2022 and 2023, respectively while the sensitivity profiles with VAN revealed 18 (94.74%) and 77 (89.53%) sensitive isolates in 2022 and 2023, respectively. CLI and SXT showed moderate and stable to slightly improved effectiveness while NIT showed varied sensitivity in the years studied. GEN and GEH sensitivities were found moderate in S. aureus and Enterococcus sps. Ampicillin sensitivity was moderately low and also decreased in the UTI isolates during the study period (Table 4).

Table 4: Table Showing the Drug Susceptibility Profiles of Gram-positive Bacteria

Org		ENT		SAU	
Year		2022	2023	2022	2023
No of isolates		49	33	19	86
Drug					
AMK	No.	0	8	0	0
	%	0	24.24	0	0
CIP	No.	0	0	0	5
	%	0	0	0	5.81
SXT	No.	0	0	7	40
	%	0	0	36.84	46.51
CTX	No.	0	0	0	0
	%	0	0	0	0
FEP	No.	0	0	0	0
	%	0	0	0	0
AMP	No.	28	7	2	0
	%	57.14	21.21	10.53	0
COL	No.	0	0	0	4
	%	0	0	0	4.65
CAZ	No.	0	0	0	0
	%	0	0	0	0
CRO	No.	0	0	0	0
	%	0	0	0	0
GEN	No.	0	4	9	35
	%	0	12.12	47.37	40.7
GEH	No.	14	6	0	0
	%	28.57	18.18	0	0
IPM	No.	3	7	0	0
	%	6.12	21.21	0	0
LNZ	No.	49	16	19	64
	%	100	48.48	100	74.42
VAN	No.	48	12	18	77
	%	97.96	36.36	94.74	89.53
TEC	No.	47	20	4	0
	%	95.92	60.61	21.05	0
TZP	No.	0	1	0	0
	%	0	3.03	0	0
MEM	No.	0	0	0	0
	%	0	0	0	0
ATM	No.	0	0	0	0
	%	0	0	0	0
TCY	No.	7	2	0	0
	%	14.29	6.06	0	0
POL	No.	0	0	0	0
	%	0	0	0	0
NIT	No.	37	6	16	13
	%	75.51	18.18	84.21	15.12
ERY	No.	0	0	5	20
	%	0	0	26.32	23.26
FOX	No.	0	0	7	23
	%	0	0	36.84	26.74
CLI	No.	0	0	10	46
	%	0	0	52.63	53.49

ENT – Enterococcus sps., SAU – S. aureus; AMK - Amikacin, CIP – Ciprofloxacin, SXT – Sulphamethoxazole/Trimethoprim, CTX – Cefotaxime, FEP – Cefepime, AMP – Ampicillin, COL – Colistin, CAZ – Ceftazidime, CRO – Ceftriaxone, GEN - Gentamicin, GEH – high-level Gentamicin, IPM – Imipenem, LNZ – Linezolid, VAN – Vancomycin, TEC – Teicoplanin, TZP – Piperacillin plus Tazobactam, MEM – Meropenem, ATM – Azithromycin, TCY – Tetracycline, POL – Polymyxin B, NIT – Nitrofurantoin, ERY – Erythromycin, FOX – Cefoxitin, CLI – Clindamycin

4. DISCUSSION

The present study highlights the evolving antibiotic resistance patterns of clinically significant pathogens, primarily Gram-negative and Gram-positive pathogens, isolated over recent years. The findings reveal alarming trends in resistance that are consistent with global and regional reports, underscoring the pressing threat antimicrobial resistance (AMR) poses to effective clinical management.

4.1. Seasonality and Patterns

The majority of organisms in the present study were isolated between the months of June through October, suggesting seasonality possibly linked to hospital admission patterns or environmental factors. For Gram-negative bacteria such as E. coli, K. pneumoniae, P. aeruginosa

and Acinetobacter sps., a clear seasonal pattern emerges with higher infection rates typically in warmer months, especially during summer and monsoon seasons in tropical regions[19,20]. This increase is linked to factors such as elevated humidity and temperature that favour bacterial growth and survival in hospital environments, combined with increased patient admissions and invasive device utilization during these periods. In Gram-positive bacteria like S. aureus and Enterococcus infections, seasonal trends tend to be less pronounced but remain evident, reflecting different epidemiological and transmission dynamics. Studies report increase in S. aureus infections during winter months in temperate regions, likely influenced by increased respiratory viral infections leading to secondary bacterial infections.[21] Such seasonal surges are often accompanied by increased empirical antibiotic use, inadvertently driving resistance selection pressure.[22-24] The lower environmental stability of Gram-positive pathogens compared to Gram-negative pathogens may underlie the less marked seasonality in community-acquired infections. The majority of research indicates that Candida infections tend to peak during warmer, more humid months primarily in summer and monsoon seasons in tropical regions aligning with optimal fungal growth conditions.[25-28] Similarly, studies report a relative increase in NAC prevalence during colder months, possibly linked to antifungal selection pressure, nosocomial transmission, and healthcare worker colonization.[29,30]

4.2. Drug Sensitivity Patterns

The data obtained from the present study indicate increasing trends in drug resistance across several clinically important pathogens, highlighting the need for enhanced surveillance and targeted interventions for infection control.

In Gram-negative bacteria, this study revealed the predominance of E. coli and K. pneumoniae as leading uropathogens and nosocomial agents exhibiting multidrug resistance (MDR). These results are consistent with those reported[13, 28, 31,32] where E. coli accounted for the majority of urinary tract infections. The widespread resistance to cephalosporins (including CTX and FEP) and fluoroquinolones (CIP) observed here aligns closely with studies made elsewhere[33,34] Citrobacter and Acinetobacter sps. also demonstrated persistent resistance to several drug classes except the last-line agents COL and POL. COL and POL maintain high efficacy in our study, The effectiveness of colistin and polymyxin remains very high (>95%) across all tested Gram-negative isolates, supporting their role as valuable last-resort drugs.[35,36] This mirrors global concerns raised by recent surveillance studies,[37,38] reinforcing cautious stewardship of these agents. Our data indicate improved susceptibilities toward aminoglycosides, such as amikacin and gentamicin, which somewhat alleviate the therapeutic predicament. One of the studies made similarly highlight aminoglycosides as valuable adjuncts in combination therapy targeting MDR Gram-negative bacteria.[39-41] Nonetheless, the significant dependency on carbapenems and polymyxins of which the latter being last-resort agents remains concerning. Recent studies alerted to the emergence of colistin resistance even among carbapenem-resistant isolates, emphasizing that the current susceptibility of these agents should not lead to complacency.[42,43]

The present data reveals a concerning trend of rapidly developing antimicrobial resistance in both Enterococcus and S. aureus isolates. The emergence of vancomycin resistance and the declining effectiveness of reserve antibiotics like linezolid highlight an urgent need for antimicrobial stewardship programs, infection control measures, and continued surveillance of resistance patterns.

The resistance profile noted for Enterococcus spp. reveals troubling reductions in sensitivity to LIN and VAN, correlative with reports describing the swift expansion of vancomycin-resistant enterococci (VRE) globally.[44-46]Vancomycin and linezolid remain highly effective for S. aureus but saw reduction in Enterococcus susceptibility. For S. aureus, the retention of good susceptibility to glycopeptides and oxazolidinones aligns with regional antibiogram data.[47,48] Both organisms showed growing resistance to nitrofurantoin and many first-line agents. Both Enterococcus spp. and S. aureus show declining linezolid sensitivity, threatening one of the last-line antibiotics for Gram-positive infections. Surveillance studies indicate that despite initially high susceptibility rates (>99%), there is a documented rise in linezolid-resistant Gram-positive organisms globally.[49,50] Drugs like GEN and CLI showed some improvement but remain moderate in efficacy for S. aureus. Studies made elsewhere also support our data.[51-53]

The antimicrobial resistance (AMR) landscape highlighted by our data reflects a critical and escalating global health concern, aligned with the broader patterns observed in India and worldwide over the past decade. The persistent high prevalence of resistant Gram-negative bacteria, alongside the emerging resistance in Gram-positive cocci, signals formidable challenges to empirical treatment regimens and infection control in clinical settings.

The observed resistance patterns from the present study emphasize the importance of updating local empiric therapy guidelines. Several recent reviews advocate for measures including antimicrobial stewardship programs (ASPs), enhanced diagnostic precision, and restriction of broad-spectrum antibiotics to mitigate AMR escalation.[50,54-56] Implementation of these strategies has shown measurable declines in resistance in various regions.[57-62]

Our study is limited by its retrospective design and institution-specific data, which may not fully generalize to other settings. However, the congruence of local data with national and international resistance patterns substantiates the broader applicability of our conclusions. Prospective, multicentre genomic epidemiological studies are needed to unravel resistance mechanisms further and inform novel therapeutic approaches.[63,64]

5. CONCLUSION

There is a clear trend toward increasing multidrug resistance in key Gram-negative pathogens. While certain antibiotics still retain high efficacy, the decreasing sensitivity to most first-line and second-line agents is concerning and highlights the need for careful antibiotic stewardship and ongoing resistance surveillance.

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7. Conflicts of Interest

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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