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Characterizing the Prevalence of Organisms Causing Bacteriuria in Hemodialysis Patients at Tertiary Care Teaching Hospital in Gujarat, India

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Abstract

Introduction: Patients with renal failure undergoing hemodialysis face an increased risk of urinary tract infections due to impaired immunity and altered physiology. Distinguishing asymptomatic bacteriuria from clinically significant infection is vital to combat rising antimicrobial resistance. ***Objectives****:* This study aimed to characterize the prevalence and microbial profiles of bacteriuria in hemodialysis dependent patients. ***Materials and Methods*****:** A retrospective study was conducted at a tertiary care center in Gujarat, India. Data was collected from electronic medical record of patients along with urine culture finding and other clinical details to study further for the duration of April 2021 and March 2025. Clinically significant isolates were reviewed while excluding duplicate isolates from same patients. Study was approved by institutional ethics committee. ***Results:*** Out of total 17755 various culture samples received from dialysis-patients, 3022 urine cultures were received and from those total 772 urine cultures reported with bacterial growth during the studied duration. The cohort had a mean age of 55.1 years with a female predominance (58.7%). Gram-negative bacteria (≈80%) dominated, primarily *Escherichia coli* (57.1%) and *Klebsiella pneumoniae* (13.9%). High resistance was observed against cephalosporins and fluoroquinolones. *Enterococcus faecium* exhibited significant resistance to vancomycin (20.8%). Prior antibiotic exposure was high at 76.9%. Resistance was more frequently associated with patients having no fixed dialysis schedule and those receiving antibiotics within 24 hours of enrolment. ***Conclusion:*** Hemodialysis patients frequently harbor multidrug-resistant pathogens. The high prevalence of ESBL producing and MDR strains necessitates robust antibiotic stewardship and reliance on local antibiograms to guide therapy and minimize unnecessary treatment of asymptomatic cases.

Keywords: Acute kidney injury, Chronic kidney disease, End stage renal disease, Urinary tract infection, Anti-microbial resistance, Hemodialysis.

INTRODUCTION

Chronic kidney disease (CKD) is a major global health challenge, alongside Acute Kidney Injury (AKI), affecting millions of individuals and predisposing them to infectious complications such as urinary tract infections (UTIs) and urosepsis. Patients with CKD, particularly those on hemodialysis or with renal transplants, experience impaired immune defense mechanisms, altered urinary tract physiology, and frequent exposure to invasive procedures, all of which increase susceptibility to infection [1,2]. Infectious complications remain among the leading causes of morbidity and mortality in hemodialysis-dependent Renal failure patients [3,4].

Bacteriuria is considered a potential reservoir for infections that can progress to cystitis, pyelonephritis, and perinephric abscess [5]. It is particularly common in hemodialysis-dependent AKI and CKD patients [6]. Many hemodialysis patients present with asymptomatic bacteriuria (ASB), which may or may not progress to symptomatic UTI. The lack of classical symptoms such as dysuria and frequency complicates early diagnosis [7]. Importantly, unnecessary antibiotic treatment of ASB in hemodialysis patients has been associated with antimicrobial resistance (AMR), increased risk of Clostridium difficile infection, and disruption of gut microbiota [8].

The clinical significance of ASB in AKI and CKD remains uncertain. The Infectious Diseases Society of America (IDSA) guidelines recommend against treating ASB in most populations, except in pregnancy or prior to invasive urologic procedures [8]. However, data specific to hemodialysis patients are limited, and studies have shown that antibiotic therapy does not reduce recurrence of bacteriuria or hospital readmissions in this group [5]. Moreover, bacteriuria in hemodialysis patients may serve as a marker of systemic infections, including bloodstream infections (BSI) and sepsis, underscoring the importance of distinguishing benign ASB from clinically significant UTI [9].

Risk factors such as diabetes, indwelling catheters, prolonged hospitalization, and infection with Klebsiella spp. have been identified as independent predictors of urosepsis in CKD patients [9]. Additionally, lower urinary tract symptoms (LUTS) are prevalent among hemodialysis patients and may mask early signs of infection, further complicating diagnosis and management [11].

Given the high prevalence of bacteriuria and UTIs in hemodialysis patients, coupled with rising AMR, there is an urgent need to optimize prophylaxis, and implement stewardship programs tailored to this vulnerable population. Periodic assessment of locally prevalent pathogens and resistance profiles is essential to guide empiric therapy and preventive interventions.

This study aimed to identify causative organisms of bacteriuria in hemodialysis patients, their resistance profile, and evaluate their clinical significance; thereby contributing to rational antibiotic use, and reduction of infection-related morbidity and mortality.

MATERIALS AND METHODS

This retrospective study was conducted at Shree Krishna Hospital, Karamsad, a tertiary care center in Gujarat, India. The source of data included inpatient electronic medical records of patients admitted to the hospital as well as patient information retrieved from the laboratory information system. Reports with positive urine cultures of clinically significant isolates were considered for analysis.

The study period encompassed four years, from April 2021 to March 2025. All eligible urine specimens processed during this time were reviewed, and culture-positive samples were included by convenient sampling. The study population comprised patients undergoing hemodialysis who had submitted urine culture requests during the study period.

Inclusion criteria were all urine culture requests from patients on hemodialysis with positive culture results. As per Exclusion criteria excluded multiple repeated isolates from the same sample type of the same patient, in order to avoid duplication and bias in the dataset.

The final dataset thus represented all unique, clinically significant positive urine culture isolates from hemodialysis patients over the four-year study period. This approach allowed for comprehensive evaluation of the prevalence and microbial profile of bacteriuria in this population, while minimizing redundancy from repeated cultures of the same patient.

The isolates defined as per CLSI guidelines [17] in this study comprised of Extended spectrum β-lactamase (ESBL) producing strains, MDR (Multi-drug resistant) strains producing carbapenemase or showing impermeability to carbapenems, Methicillin-resistant *S. aureus* (MRSA), Vancomycin-resistant *Enterococci* (VRE), and the strains showing High level aminoglycoside resistance (HLAR).

This study was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki. Approval was obtained from the Institutional Ethics Committee (IEC) of the H.M. Patel Centre for Medical Care and Education, Karamsad (Approval No.: IEC/BU/2025/Ex.110/446/2025). Also, during this ethics approval all authors have declared that there is no conflict of interest to any of the contributors for the present study.

Required clinical details of the patients was collected exclusively from laboratory or hospital records and there were no interview, interventions or additional investigations performed on the participants for the present study. Therefore, waiver of consent was granted by the IEC for the present study. The collected data was analyzed using descriptive statistics. Also, there were no fund or financial aid availed for the present study from any granting body and the expenses were taken care by investigators of the study.

RESULT

Demographic and Clinical Characteristics

Out of total 17755 various culture samples received from dialysis-patients, 3022 urine cultures were received and from those total 772 urine cultures reported with bacterial growth during the studied duration. These 772 urine cultures yielded 840 bacterial isolates (Table 6).

A total of 772 samples with positive urine cultures were analyzed. The mean age was 55.1 ± 20 years, with a predominance of females (58.7%) (Table 1). Among studied patients, acute kidney injury (13.9%) and chronic kidney disease (13.3%) were the documented renal failure type, while the renal failure status was unknown for the majority others (Table 2). Most patients had no fixed hemodialysis schedule

(86.5%) (Table 3), and 22.5% presented with dysuria at enrolment. Antibiotic exposure was common, with 76.9% receiving antibiotics within 24 hours (Table 4). The leading co-morbidities were hypertension (23.8%) and diabetes mellitus (22.2%), followed by congestive cardiac failure (9.6%) and renal calculi (6.0%) (Table 5). No patient in our setting had a previous kidney transplant.

Table 1: Demographic profile of dialysis patients with positive urine cultures.

Variable	n (%)
Age (years), mean ± SD (range)	**55.13 ± 20**
Sex, *n* (%)	
Male	319 (41.32)
Female	453 (58.68)

Values are presented as mean ± SD or n (%).

Table 2: Distribution of renal failure type among study patients.

Variable	n (%)
Renal failure, *n* (%)	
Acute kidney injury	112 (14.51)
Chronic kidney disease	121 (15.67)
Unknown	539 (69.82)

Values are presented as n (%).

Table 3: Hemodialysis frequency among patients with positive urine cultures.

Variable	n (%)
Hemodialysis frequency, *n* (%)	
Twice weekly	55 (7.12)
Thrice weekly	2 (0.26)
Once Monthly	36 (4.66)
Bi-monthly	11 (1.42)
Not fixed	668 (86.53)

Values are presented as n (%)

Table 4: Dysuria at enrolment and Prior antibiotic exposure

Criteria	n (%)
Previous kidney transplant, *n* (%)	0
Presence of dysuria at enrolment, *n* (%)	174 (22.54)
Antibiotic use within one day	594 (76.94)
Antibiotic use within thirty days	178 (23.06)

Values are presented as n (%).

Table 5: Co-morbid conditions in dialysis patients with positive urine cultures

Comorbid condition	n (%)
Diabetes mellitus	171 (22.15)
Hypertension	184 (23.83)
Pyelonephritis	13 (1.68)
Lupus Nephritis	2 (0.26)
Renal Calculi	46 (5.96)
Benign Prostatic Hyperplasia	17 (2.20)
Carcinoma Prostate	5 (0.65)
Renal cell Carcinoma	2 (0.26)
Urothelial carcinoma	1 (0.13)
Ectopic kidney	1 (0.13)
Pelvic inflammatory Disease	1 (0.13)
Congestive cardiac failure	74 (9.56)
Chronic obstructive pulmonary disease	23 (2.98)
Organophosphate poisoning	2 (0.26)

Values are presented as n (%)

Microbiological Findings

A total of 840 isolates were recovered out of the 772-growth positive urine culture. Gram-negative bacteria predominated (≈80%), with *Escherichia coli* (57.1%) being the most prevalent, followed by *Klebsiella pneumoniae* (13.9%) and *Pseudomonas aeruginosa* (10.5%) (Table 6). Among Gram-positives, *Enterococcus faecium* (2.9%) and *Enterococcus faecalis* (2.5%) were the leading isolates, while *Staphylococcus aureus* (1.4%) was less frequent. MDR and ESBL production rates are summarized in Table 7.

Table 6: Distribution of bacterial isolates from urine cultures

Isolates	n (%)
Gram-positive bacteria	
Staphylococcus spp.	
Sthapylococcus aureus	12 (1.43)
CoNS [a]	5 (0.59)
Enterococcus spp.	
Enterococcus durans	1 (0.12)
Enterococcus faecalis	21 (2.50)
Enterococcus faecium	24 (2.86)
Enterococcus gallinarum	1 (0.12)
Enterococcus raffinosus	1 (0.12)
Other *Enterococcus spp.*	1 (0.12)
Streptococcus spp.	
Streptococcus agalactiae	4 (0.47)
Gram-negative bacteria	
Pseudomonas aeruginosa	88 (10.48)
Enterobacter cloacae complex	10 (1.19)
Escherichia Coli	480 (57.14)
Klebsiella pneumoniae	117 (13.93)
Other Gram-negatives	
Acinetobacter spp.	5 (0.59)
Citrobacter spp.	19 (2.26)
Morganella spp.	6 (0.71)
Proteus spp.	14 (1.67)
Providencia spp.	8 (0.95)
Miscellaneous[b]	9 (1.07)
Other *Pseudomonas spp.*[c]	8 (0.95)
Other *Klebsiella spp.*[d]	6 (0.71)
Total number of isolates (N)	840

Values are presented as n (%). [a]Coagulase-negative staphylococci; [b]Achromobacter xylosoxidans, Brevundimonas diminuta, Burkholderia Cepacia, Stenotrophomonas maltophilia, Serratia marcescens, Salmonella paratyphi A; [c]Pseudomonas putida, Pseudomonas stutzeri, Pseudomonas fluorescens, Pseudomonas mendocina ; [d]Klebsiella aerogenes, Klebsiella oxytoca.

Antibiotic Susceptibility Highlights

Resistance rates varied across species. Cephalosporins and fluoroquinolones showed the highest resistance rates across Gram-negative isolates (Table 7). *Enterococcus faecium* demonstrated alarming resistance to multiple classes, including vancomycin (Table 8).

Antimicrobials which were not tested for the respective isolates are marked with (-) in Table 7 and Table 8.

Table 7: Resistance profile of most common uropathogenic Gram-negative isolates (selected antimicrobials).

	Pseudomonas aeruginosa **(n=88)**	***Escherichia coli*** **(n=480)**	***Klebsiella pneumoniae*** **(n=117)**	***Proteus mirabilis*** **(n=14)**	**Other *Pseudomonas spp.*[a] (n=8)**	**Other *Klebsiella spp.*[b] (n=6)**
Aminoglycosides						
Amikacin	47.73	7.29	*35.04*	*35.71*	*37.5*	*0*
Gentamicin	*27.22*	*25.63*	*43.59*	*35.71*	*50*	*0*
Cephalosporins						
Cefotaxime	-	69.17	58.12	35.71	-	16.67

	***Pseudomonas aeruginosa* (n=88)**	***Escherichia coli* (n=480)**	***Klebsiella pneumoniae* (n=117)**	***Proteus mirabilis* (n=14)**	**Other *Pseudomonas spp.*[a] (n=8)**	**Other *Klebsiella spp.*[b] (n=6)**
Ceftazidime	59.1	51.25	53.85	35.71	62.5	16.67
Ceftriaxone	-	-	58.12	35.71	-	16.67
Cefipime	52.27	45.83	52.99	28.57	50	0
Cefuroxime (Oral)	-	74.37	67.52	35.71	-	66.67
Cefuroxime (Parenterall)	-	74.37	67.52	35.71	-	66.67
Fluoroquinolones						
Ciprofloxacin	64.77	73.33	66.67	78.57	75	0
Levofloxacin	68.18	52.71	45.29	50	62.5	0
Co-trimoxazole	-	51.04	48.72	71.43	75	0
Nitrofurantoin	-	9.17	53.85	78.57	-	0
Tetracyclines						
Tetracycline	-	45.21	38.46	71.43	-	0
Minocycline	-	-	-	-	-	-
Polymyxins						
Colistin	6.82	0.42	0.85	100	0	0
Polymixin B	6.82	0.42	0.85	100	0	0
Carbapenems						
Imipenem	52.27	11.88	37.61	21.43	62.5	0
Ertapenem	-	13.75	41.03	14.29	-	0
Doripenem	-	8.13	25.64	14.29	-	0
Meropenem	53.41	12.29	37.61	14.29	62.5	0
Amoxicillin- Clavulanic acid	-	35.42	51.28	28.57	-	66.67
Ampicillin-Sulbactum	-	55.21	58.97	50	-	33.33
Cefoperazone-Salbactum	52.27	17.5	43.59	14.29	37.5	0
Piperacillin-Tazobactum	56.82	26.04	48.72	14.29	50	0

Values are presented as percentage resistance (%). MDR = Multidrug resistant; ESBL = Extended-spectrum β-lactamase; [a]Pseudomonas putida, Pseudomonas stutzeri, Pseudomonas fluorescens, Pseudomonas mendocina ; [b]Klebsiella aerogenes, Klebsiella oxytoca.

E. coli showed high resistance to cephalosporins (≈69–73%) and fluoroquinolones (≈25–44%), but lower resistance to carbapenems (≈12–13%). *K. pneumoniae* demonstrated resistance to cephalosporins (≈59–67%) and fluoroquinolones (≈38–44%). *P. aeruginosa* exhibited resistance to ceftazidime (68.2%) and ceftriaxone (53.4%), with moderate resistance to aminoglycosides (≈47.7%). *Enterococcus faecium* showed high resistance to amoxicillin-clavulanate (95.8%) and cephalosporins (95.8%), while *Enterococcus faecalis* had lower resistance rates (≈19–76%).

High percentage of *E. coli* isolates with resistance to β-lactams (ampicillin 69.2%, cefotaxime/ceftriaxone 69.2%, ceftazidime 73.3%), and fluoroquinolones (ciprofloxacin 25.6%, levofloxacin 74.4%) were noted (Table 7). Resistance was noted to cephalosporins and fluoroquinolones in the range of 59–67% and 38–44% respectively in *K. pneumoniae* isolates. Resistance to aminoglycosides (gentamicin) was seen in 52.7% isolates of *E. coli* and 45.3% isolates of *K. pneumoniae*, while carbapenem resistance remained lower for both *E. coli* (imipenem 12.3%, meropenem 13.8%) and *K. pneumoniae* (imipenem 37.6%, meropenem 41.0%).

Table 8: Resistance profile of Gram-positive isolates (selected antimicrobials)

	Staphylococcus aureus (n=12)	***CoNS*[a] *(n=5)***	***Enterococcus faecalis (n=21)***	***Enterococcus faecium (n=24)***	**Other *Enterococci spp.*[b] *(n=4)***	***Streptococcus agalactiae (n=4)***
Ampicillin	-	-	19.05	87.5	75	0
Benzylpenicillin	83.33	100	23.81	83.33	75	0
Oxacillin	50	80	-	-	-	-
Azithromycin	33.33	40	-	-	-	25
Clarithromycin	33.33	40	-	-	-	25
Clindamycin	8.33%	40	-	-	-	25
Erythromycin	33.33	40	-	-	-	25

	Staphylococcus aureus (n=12)	***CoNS[a] (n=5)***	***Enterococcus faecalis (n=21)***	***Enterococcus faecium (n=24)***	**Other *Enterococci* spp.[b] (n=4)**	***Streptococcus agalactiae (n=4)***
Gentamicin	16.67	0	-	-	-	-
High Level Gentamicin	-	-	76.19	83.33	50	-
High level Streptomycin	-	-	66.67	45.83	25	-
Ciprofloxacin	75%	20	76.19	95.83	75	-
Levofloxacin	83.33	40	76.19	95.83	50	25
Co-trimoxazole	41.67	0	-	-	-	0
Nitrofurantoin	0	0	4.76	54.16	50	0
Daptomycin	0	80	4.76	0	0	-
Vancomycin	0	0	9.52	20.83	0	0
Linezoild	0	0	9.52	16.67	25	0
Teicoplanin	0	0	4.76	20.83	0	-
Tetracycline	0	20	90.48	83.33	100	100
Inducible Clindamycin Resistance	8.33	0	-	-	-	-

Values are presented as percentage resistance (%). [a]Coagulase-negative staphylococci; [b]Enterococcus durans, Enterococcus gallinarum, Enterococcus raffinosus.

Higher number of *Enterococcus faecium* isolates showed resistance to amoxicillin-clavulanate (95.8%), cephalosporins (95.8%), and fluoroquinolones (83.3%). Vancomycin resistance was also notable (83.3%) among *Enterococcus faecium* isolates (Table 8). But for *Enterococcus faecalis*, resistance was lower compared to *E. faecium*. *E. faecalis* isolates were resistant to amoxicillin-clavulanate (76.2%) and fluoroquinolones (76.2%) in good numbers. Only 23.8% *E. faecalis* isolates were vancomycin-resistant. *Staphylococcus aureus* remained largely susceptible to glycopeptides and oxazolidinones, but resistance to macrolides and lincosamides was high. Resistance was highest to clindamycin (83.3%) and erythromycin (83.3%). Methicillin resistance was shown only in 0.7% of the *S. aureus* isolates (Table 8).

Table 9: MDR and ESBL production among clinical isolates

Isolates	**n (%)**
MDR *Klebsiella spp.*	49 (5.83)
MDR *Escherichia coli*	63 (7.50)
MDR *Pseudomonas aeruginosa*	48 (5.71)
MDR *Acinetobacter baumannii*	2 (0.24)
MDR *Proteus mirabilis*	2 (0.24)
MRSA	6 (0.71)
ESBL *Klebsiella spp.*	34 (4.05)
ESBL *Escherichia coli*	312 (37.14)
ESBL *Proteus mirabilis*	7 (0.83)
HLAR *Enterococcus spp.*	35 (4.17)
VRE HLAR	7 (0.83)

Values are presented as n (%). ESBL = Extended-spectrum β-lactamase; HLAR= High Level Aminoglycoside resistance MDR = Multidrug resistant; MRSA = Methicillin-resistant Staphylococcus aureus; VRE = Vancomycin-resistant Enterococcus spp.

ESBL production was frequent (37.1%) for *E. coli*, while only 3.6% of the *K. pneumoniae* isolates were noted to be producing ESBL (Table 9). More *Pseudomonas aeruginosa* were resistant to ceftazidime (68.2%), ceftriaxone (53.4%), and gentamicin (51.1%) than to carbapenems (imipenem 56.8%). MDR strains comprised 5.7%, just like in the case of *K. pneumoniae* (5.8%).

Table 10: Isolates against frequency of dialysis and antimicrobial prophylaxis.

Dialysis Frequency	Antimicrobial prophylaxis	ESBL *Escherichia coli* (n=312)	MDR *Escherichia coli* (n=63)	ESBL *Klebsiella spp.* (n=34)	MDR *Klebsiella spp.* (n=49)	MDR *Pseudomonas aeruginosa* (n=48)	MRSA (n=6)	HLAR *Enterococcus spp* (n=35)	VRE HLAR (n=7)
Every two months	Within one day (N=8)	3	1	1	0	0	0	1	0
	Within thirty days (N=3)	1	0	1	0	0	0	0	0
Once a month	Within one day (N=28)	8	3	3	3	1	0	2	0
	Within thirty days (N=8)	2	1	0	1	0	0	0	0
Thrice weekly	Within one day (N=2)	2	0	0	0	0	0	0	0
	Within thirty days (N=0)	0	0	0	0	0	0	0	0
Twice weekly	Within one day (N=52)	24	5	2	6	5	0	3	0
	Within thirty days (N=3)	2	0	1	0	0	0	0	0
Not fixed	Within one day (N=504)	195	46	21	36	38	3	27	6
	Within thirty days (N=164)	75	7	5	3	4	3	2	1

ESBL = Extended-spectrum β-lactamase; HLAR= High Level Aminoglycoside resistance MDR = Multidrug resistant; MRSA = Methicillin-resistant Staphylococcus aureus; VRE = Vancomycin-resistant Enterococcus spp.

Among patients, those receiving hemodialysis with no fixed schedule represented the largest cohort (N= 668 total), followed by those receiving hemodialysis twice weekly (N=55 total). In almost all dialysis frequency categories, antimicrobial prophylaxis administered within one day was associated with a higher absolute number of resistant isolates compared to prophylaxis administered within thirty days. (Table 10).

Detection of VRE HLAR *Enterococcus isolates* was exclusively limited to the "not fixed" frequency group (n=7).

DISCUSSION

In our cohort of 772 dialysis patients with positive urine cultures, the mean age was 55 years, with a female predominance (58.7%). This demographic profile is broadly consistent with the study by Taweel *et al.,* (USA) [5], where the mean age was 59.5 years and 35% were male, but differs from Yamashita *et al.,* (Japan) [6], who reported a higher mean age (≈70 years) and equal sex distribution. The Bangladeshi CKD cohort also reported a female predominance and similar mean age, suggesting that gender and age may be important epidemiological determinants across diverse populations [10].

Our study found that 22.5% of patients presented with dysuria at enrolment, yet bacteriuria was still detected, highlighting the diagnostic challenge in dialysis populations. Taweel et al.[5] emphasized that most ESRD patients with bacteriuria were asymptomatic (70.6%), and antibiotic therapy did not reduce recurrence or readmission. Similarly, Yamashita *et al.,* reported that 26% of hemodialysis patients had UTI, often without classical symptoms such as dysuria [6]. Our findings reinforce the notion that bacteriuria in dialysis patients is frequently asymptomatic, and clinical correlation remains most essential.

Escherichia coli was the predominant isolate in our series (57.1%), followed by *Klebsiella pneumoniae* (13.9%) and *Pseudomonas aeruginosa* (10.5%). This mirrors the Bangladeshi CKD study (*E. coli* 64%, *Klebsiella* 18%, *Pseudomonas* 6%) [10] and the Indian CKD cohort (Shankar *et al., E. coli* 61.8%, *Klebsiella* 13.7%) [3]. In contrast, Taweel *et al.,* reported a more heterogeneous distribution, with lactose fermenting Gram negative rods accounting for 41% and *Enterococcus spp.* for 11.8% [5]. Yamashita *et al.,* also highlighted a high burden of resistant Gram-negative organisms, with ESBL producing *E. coli* comprising 17.5% of isolates [6]. Our data confirm the global predominance of Enterobacteriaceae, but also underscore regional variation in *Enterococcus* and resistant strains.

We observed high rates of ESBL production among *E. coli* (37.1%) and *Klebsiella pneumoniae* (30 cases), alongside MDR phenotypes in *Pseudomonas aeruginosa* (5.7%) and Klebsiella *pneumoniae* (5.8%). These figures are comparable to the Indian CKD study, which reported ESBL rates of 77% in *E. coli* and 61% in *Klebsiella* [3]; and to Yamashita et al., who found 17.5% ESBL *E. coli* in Japanese dialysis patients [6]. The

Bangladeshi cohort also noted carbapenem and amikacin as the most reliable agents [10]. Collectively, these findings highlight the global emergence of multidrug resistance in dialysis populations, with regional differences in magnitude but consistent reliance on carbapenems, aminoglycosides, and colistin as last line therapies.

Our cohort had high rates of prior antibiotic exposure (77% within 24 hours), diabetes (22%), and hypertension (24%). Dimitrijevic *et al.,* identified diabetes, indwelling catheters, and *Klebsiella* infection as independent predictors of urosepsis in CKD patients [9]. Our findings of frequent comorbid diabetes and hypertension align with these risk factors, though we did not specifically assess progression to urosepsis. The Palestinian LUTS study emphasized that LUTS are common in dialysis patients and negatively impact quality of life, even in the absence of infection [11]. Taken together, these studies suggest that both infection and functional urinary tract abnormalities contribute to morbidity in dialysis populations.

Across all referenced studies, a consistent theme emerges. *E. coli* predominance with significant ESBL burden. High rates of asymptomatic bacteriuria, and Multidrug resistance necessitating stewardship and reliance on carbapenems/amikacin. Risk factors such as diabetes, catheterization, and prolonged hospitalization increase the likelihood of complicated UTI or urosepsis.

The results of this study demonstrate a significant burden of resistant pathogens among patients on various dialysis schedules. This aligns with broader research indicating that hemodialysis patients often carry resistant organisms, such as ESBL-producing *E. coli* and vancomycin-resistant *Enterococci*, at rates as high as 38.7% [12,13].

Our data showed that patients with "not fixed" or "twice weekly" dialysis schedules had the highest yield of resistant isolates. While existing literature primarily focuses on vascular and urinary tract access as a risk factor, the frequency of dialysis and frequent contact with healthcare environments are recognized drivers for the colonization of resistant pathogens [13]. Chronic kidney failure is significantly associated with higher rates of MDR infections, likely due to the combination of frequent hospitalizations and the presence of invasive devices [14,15].

The observation that high numbers of resistant isolates were identified within one day of antimicrobial prophylaxis is particularly concerning. Research suggests that long-term or repeated courses of antibiotics contribute significantly to the emergence of resistant strains [12]. Specifically, exposure to antibiotics within short windows, such as 30 days has been linked to the selection of resistant pathogens like *E. coli* [16]. This suggests that the timing of prophylaxis may create selection pressure, leading to the rapid detection of highly resistant species such as ESBL *E. coli* and MDR *Pseudomonas aeruginosa*.

Our findings add to this body of evidence by providing a large dataset from dialysis patients, confirming global trends while highlighting local resistance patterns. The convergence of data from India, Bangladesh, Japan, USA, and Serbia underscores the universality of the problem, while regional variations emphasize the need for local antibiograms to guide empiric therapy [3,5,6,9,10].

Limitations

The study is conducted in retrospective mode and the maximum efforts was kept on fetching clinical details and bringing significance out of same, but such studies are very much impactful if done in prospective mode with real time intervention related to diagnostic and antimicrobial stewardships for hemodialysis patients.

CONCLUSION

In summary, our study corroborates prior reports that dialysis patients are at high risk for bacteriuria and multidrug-resistant infections, with *E. coli* and *Klebsiella pneumoniae* as dominant pathogens. The high prevalence of ESBL producers and MDR non-fermenters mandates judicious antibiotic use and robust stewardship programs. Given the frequent asymptomatic presentation, indiscriminate treatment may not improve outcomes and could exacerbate resistance. Future prospective studies should focus on optimizing diagnostic criteria, and tailoring therapy to local resistance profiles and others real time challenges in clinical management particularly for hemodialysis patients.

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Contribution of all authors

Dr Chirag Patel and Dr Yagnesh Pandya primarily incepted the research concept, conducted literature review, finalized study design, reviewed final scripts and draft along with overall supervision of research activity. Dr Dharak Makwana and Dr Janhvi Chaniyara performed the data collection, data analysis and primary draft writing for the present study.

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