e-ISSN: 0975-9506, p-ISSN: 2961-6093

Available online on www.ijpqa.com

International Journal of Pharmaceutical Quality Assurance 2026; 17(4); 79-85

Original Research Article

Bacteremia in Chronic Kidney Disease Patients on Hemodialysis from a Tertiary Care Centre in Kerala

Soumya Rani R.[1], Nisha Majeed[2], Sreekumary P.K.[3]

[1]Assistant Professor, Department of Microbiology, Government Medical College Kottayam, Kerala, India
[2]Assistant Professor, Department of Microbiology, Government Medical College Kottayam, Kerala, India
[3]Professor & HOD, Department of Microbiology, Government Medical College Kottayam, Kerala, India

Received: 15-02-2026 / Revised: 16-03-2026 / Accepted: 19-04-2026
Corresponding Author: Dr. Soumya Rani R.
Conflict of interest: Nil

Abstract:

Background: Chronic kidney disease is emerging as a major health concern globally. CKD patients on hemodialysis are at a higher risk for developing bacteremia. This study aimed at finding out the bacteriological profile with its antibiotic susceptibility pattern in patients undergoing hemodialysis in nephrology department, Government medical college Kottayam.

Methods: This was a Descriptive study conducted over a period of one year (April 2024-March 2025) at Department of Microbiology Kottayam. Paired Blood samples collected in conventional & automated blood culture received from 235 chronic kidney disease patients on hemodialysis were processed, isolates identified & appropriate antimicrobial susceptibility testing was done.

Results: Out of 235 patients,53 patients had a positive blood culture showing the prevalence of bacteremia as 22.56%. 66% of patients were males whereas females were 33.96%. Higher incidence of bacteremia was found in patients above 50 yrs. Among the isolates 50.94% were Gram negative bacteria as compared to 49.05% Gram positive bacteria. As per our study among the gram-negative bacteria causing bacteremia, Pseudomonas aeruginosa 10 (35.71%) was the predominant organism followed by Klebsiella species 7 (25%), Acinetobacter species 4(14.29%), Elizabethkingae meningoseptica 3(10.71%), Burkholderia cepacia 2(7.14%), Stenotrophomonas maltophilia 1(3.57%), Pantoea species 1(3.57%). Out of 26 isolates of Gram-positive organisms, 7(26.92%) were Methicillin Sensitive Staphylococcus aureus, 9 (34.61%) were Methicillin Resistant Staphylococcus aureus, 6(23.07%) were Methicillin resistant Coagulase negative Staphylococci and 4(15.38%) were Enterococcus spp. Among Pseudomonas aeruginosa 60% isolates were sensitive to Ceftazidime,40% isolates were sensitive to Ciprofloxacin, Gentamicin, Amikacin, 20% isolates were sensitive to cotrimoxazole,100 % isolates are susceptible to Piperacillin Tazobactum, Imipenam & Meropenam. MRSA strains were 100% Resistant to Penicillin and Cefoxitin, 66.66% were susceptible to cotrimoxazole, 20% were susceptible to Gentamicin, 33.33% were susceptible to Erythromycin, 66.66% susceptible to Clindamycin, 88.88% were susceptible to Doxycycline, 100 % were susceptible to Vancomycin and Linezolid.

Conclusion: The increased use of antibiotics in this particular subset of patients and their recurrent exposure to the healthcare system, there has been a rise in the incidence of infections with multidrug resistant (MDR) organisms. Thus, identification of locally prevalent pathogens is important for optimal care in patients since the choice of empiric treatment or prophylactic antibiotics depends on the prevalent pathogens in a local community.

Keywords: BSI, Haemodialysis, MDR, Pseudomonas Aeruginosa.

DOI: 10.25258/ijpqa.17.4.14

Introduction

Chronic kidney disease is a major health issue worldwide. It is the end stage renal disease occurring as a complication of various diseases affecting kidney. In India sufficient data on the rate and progression of the disease is lacking. As per the study conducted by Ajay et al from various hospitals across India the prevalence of chronic kidney disease patients is about 17.2% (1). The major reasons include diabetes mellitus, hypertension and anaemia.[1] Among them nearly 6% were in the stage 3 or even worse.[1] In another study conducted by Mohan et al Diabetic nephropathy is found to be the most common cause of CKD ranging to about 31%.[2,3] This is followed by CKD of unknown etiology(16%) and also they were younger patients and were in stage V.[2] Main strategies that can delay the progression of chronic kidney disease include early identification, modification of risk factors and best interventions. Kidney dysfunction often goes

undetected in the early stages leading to late referrals and interventions.[4]

Renal replacement therapies are modalities of treatment in chronic kidney disease patients which include hemodialysis, peritoneal dialysis and renal transplantation. Hemodialysis is the most common method used to remove toxic metabolites from the body in case of renal dysfunction[5] and it is the mainstay of renal replacement therapy in developed countries (80%) and developing countries like India.[6] Infection is a common complication and an important cause of death in chronic hemodialysis patients.[7,8,9] Disruption of natural barriers, introduction of foreign bodies in blood stream and uremic dysfunction are some of the reasons for increased risk of blood stream infection in chronic hemodialysis patients.[10] Healthcare associated infections remain a major cause for repeated hospitalization and mortality among these patients. Central venous catheter is an important source of blood stream infection in chronic hemodialysis patients in whom the rate of catheter related blood stream infections range from 10 to 30%.[11]

Among the infections, bloodstream Infections (BSI) are major cause of hospitalization and mortality among hemodialysis (HD) patients. The rates of BSI among HD patients vary and are influenced by local patient and pathogen characteristics.[12] Risk of bacteremia in HD patients are 26 fold higher compared to other population.[7] Various studies concluded that Gram positive organisms are more common among the isolates obtained from blood culture in hemodialysis patients compared to Gram negative organisms.[7,13-15] Among the Gram positive organisms Staphylococcus aureus including Methicillin Resistant Staphylococcus aureus (MRSA) constitute most important pathogens causing blood stream infection in HD patients.[7]. Following Staphylococcus aureus, the next common Gram-positive bacteria include the Coagulase negative Sraphylococci.[8] Followed by these, Gram negative organisms also result in bacteremia in hemodialysis patients. [10,15] The common Gram-negative bacteria include Escherichia coli,

Klebsiella, Enterobacter, Pseudomonas, Acinetobacter. The increased and irrationale use of antibiotics have also resulted in increase in the multidrug resistant organisms causing bacteremia in HD patients.[8] So the empirical therapy should be started with antibiotics to cover both Gram positive and Gram-negative bacterial pathogens and should be changed according to the microbiological culture & sensitivity report. This points out the importance in knowing the prevalence of organisms causing blood stream infections in all tertiary care hospitals carrying out haemodialysis. Keeping this view in mind present study aimed at finding out the bacteriological profile with its antibiotic susceptibility pattern in patients undergoing haemodialysis in nephrology department, Government medical college Kottayam.

Materials & Methods

It was a descriptive study & its objectives were to determine the prevalence rate of bacteremia among hemodialysis patients, to determine the most common microrganisms causing blood stream infections in HD patients & to determine the antimicrobial susceptibility patterns of isolates obtained.

Study period was from April 2024 - March 2025. Study setting was Department of Microbiology Kottayam. The study population were 235 patients with chronic kidney disease on hemodialysis of all age groups admitted to nephrology department whose blood samples submitted to Microbiology laboratory of Government medical college, Kottayam for culture.

Sample size,

$N = (Z\alpha)^2 pq$

$d2$

$Z\alpha$ = Z value at an α error of 0.05 = 1.96

p = Proportion of bacteremia in hemodialysis patients (Proportion of bacteremia in hemodialysis patients was 18.8% in a study by Swapnan et al[16]

q = (100-p) = 81.2

d = precision = 5%

Therefore

$$N = \frac{(1.96)2 \times 18.8 \times 81.2}{5 \times 5} = 235$$

Inclusion criteria was defined as blood samples received from chronic kidney disease patients on hemodialysis admitted in nephrology department, Government medical college Kottayam. Repeat samples from the same patient was taken as exclusion criteria.

Isolation & Identification of Bacteria: Blood samples were received in Brain heart infusion broth in Conventional blood culture and in BacT /Alert aerobic blood culture bottles in automated blood culture. Conventional bottles were incubated at 37°C for 12 to 18 hours and were subcultured on alternate days to blood agar and Mac Conkey agar for 6 days. The pure growth obtained were identified by doing gram staining and other standard biochemical tests. Automated blood culture bottles were subcultured when flagged positive and identification was done similar to conventional blood cultures.

Antimicrobial Susceptibility Testing: Antimicrobial susceptibility testing were performed on all isolates from patients according to the Clinical and Laboratory Standards Institute (CLSI) [17] guidelines by Kirby-Bauer method of disk diffusion method.

Statistical Analysis: Data was coded and entered in Microsoft Excel sheet and was analysed using SPSS statistical software version 22.

Results

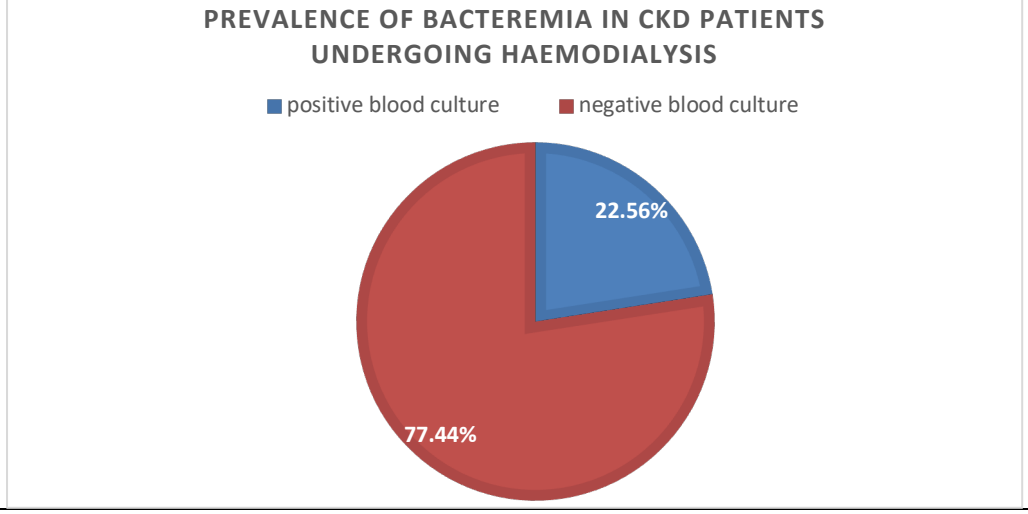

Figure 1: Prevalence of bacteremia in CKD patients

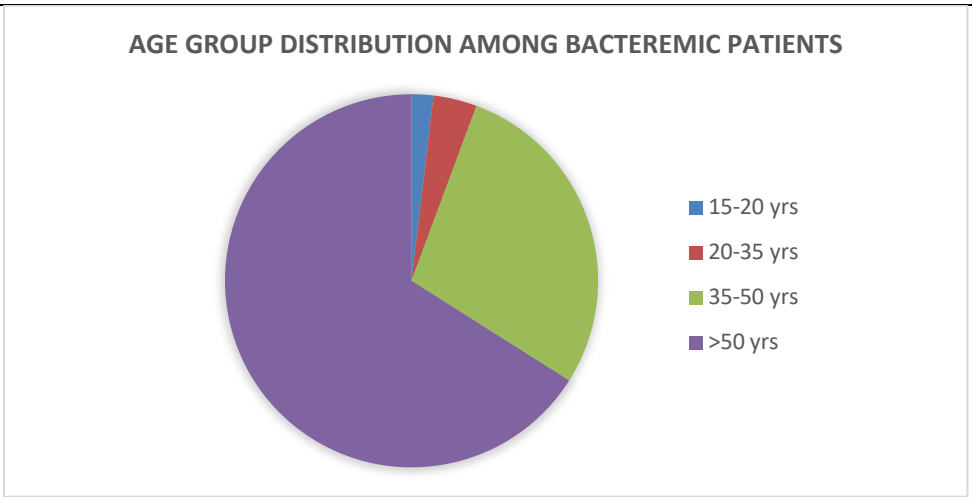

Figure 2: Age group distribution among bacteremic patients

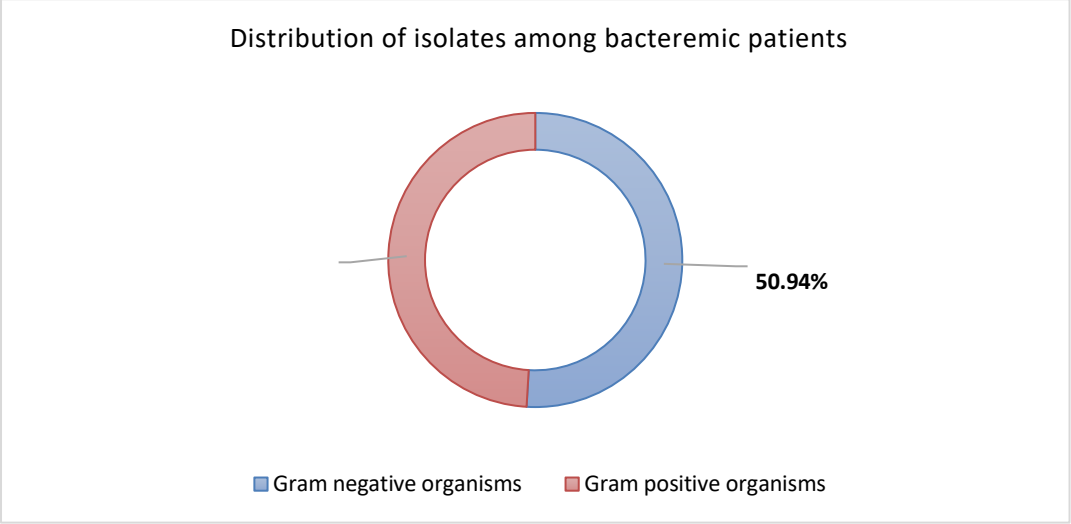

Figure 3: Distribution of isolates among bacteremic patients

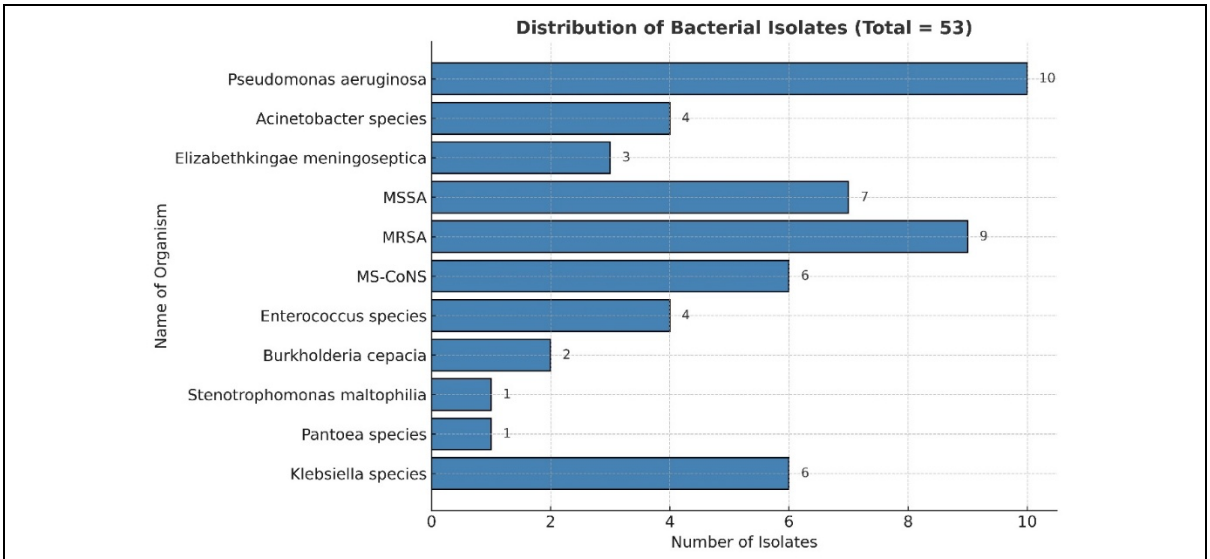

Figure 4: Distribution of bacterial isolates

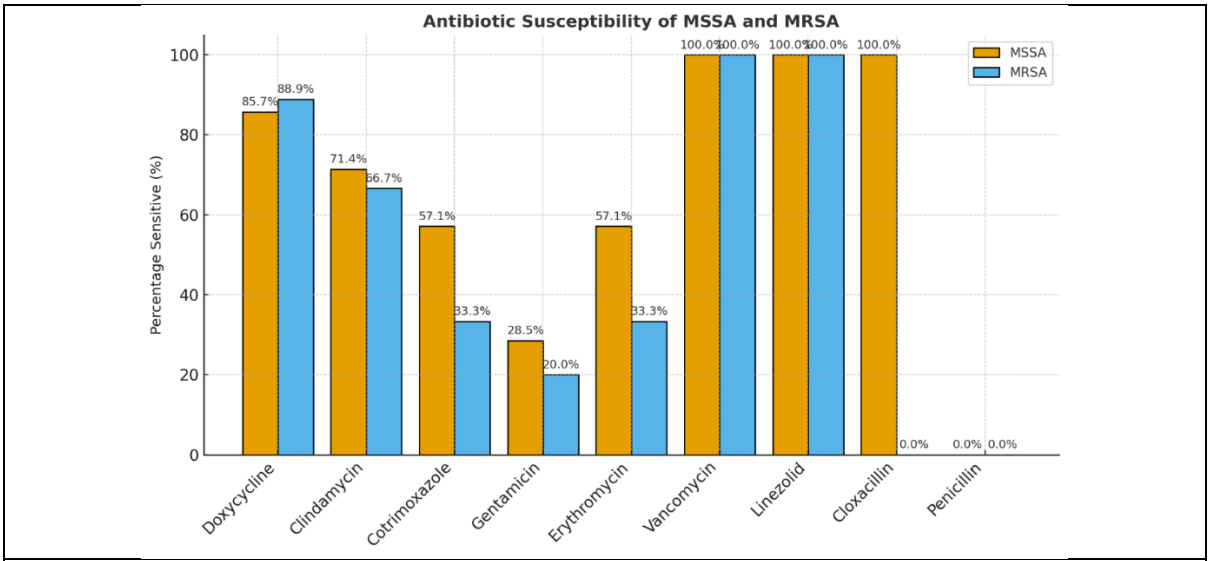

Figure 5: Antibiotic susceptibility pattern of MSSA & MRSA isolates

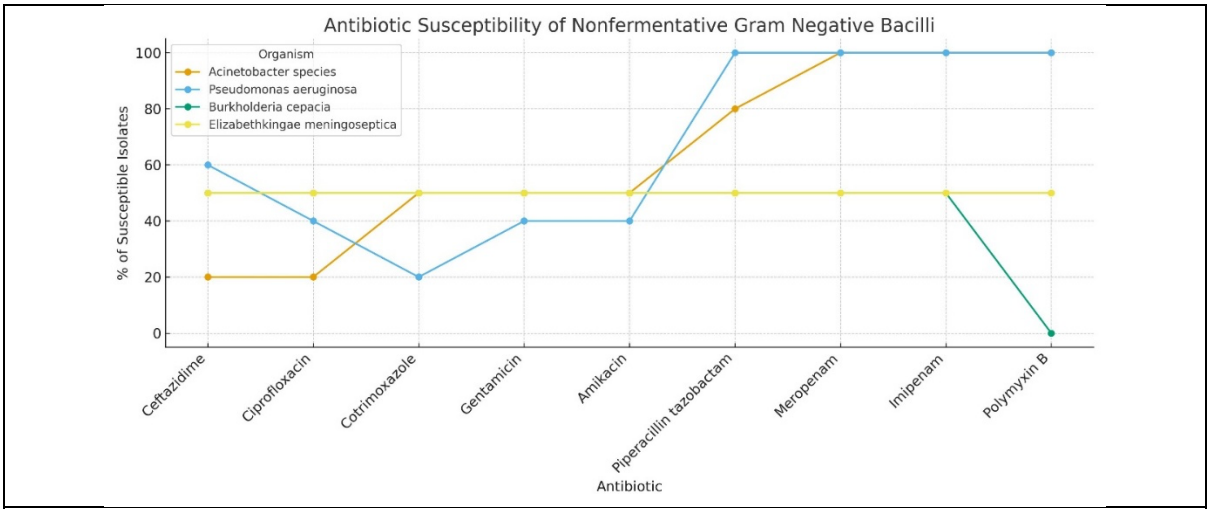

Figure 6: Antibiotic susceptibility of Nonfermentative Gram negative bacilli

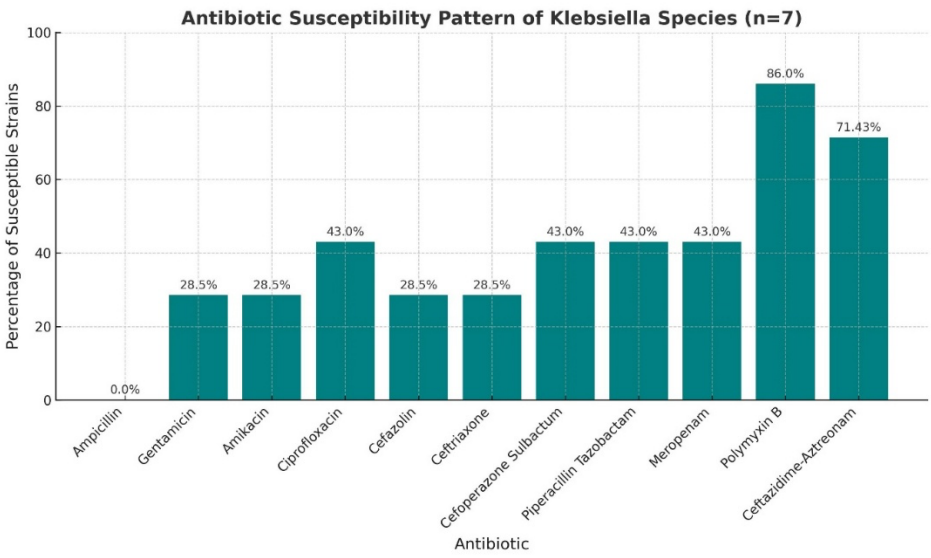

Figure 7: Antibiotic susceptibility pattern of Klebsiella species

Discussion

The incidence of bacteremia in haemodialysis patients is very high compared with its incidence in the general population. In our study a total of 235 blood samples were collected from CKD patients undergoing haemodialysis at Government medical college Kottayam who presented with clinical features suggestive of sepsis. Among these samples, 53 were positive showing a 22.56 % prevalence of bacteremia (fig. 1). The prevalence obtained is comparable to that of study conducted by Mandal S.K. Karmakar K, Sarkar K.C et al. [8,16] Among the 53 patients with positive blood culture, 35 (66%) were males and 18(33.96%) were females. The male predominance obtained in our study is similar to the study by Miri Schamroth Pravada, Yasmin Maor et al. [6,12] The above study also showed a higher incidence of bacteremia among age group above 50 years. In our study 35 of the 53 patients with positive blood culture were in the age group above 50 years (66%), 15 were in the age group 35-50 years (28.3%), 2 of them were in the age group 20-35 years (3.77%) and one was in the age group 15 - 20 years (1.89%) (fig.2). Study on CKD patients on haemodialysis by Rajapurahar M, John GT et al [2,9] showed a higher incidence of bacteremia among 41-60 yrs age.

Among the 53 isolates obtained 26 (49.05%) were Gram positive organisms. 27(50.94%) were Gram negative organisms (fig 3). A study by A Dieng et al [17,18] showed predominance of Gram-negative organisms with 59% positivity rate. Another study by Miri Schamroth Pravada, Yasmin Maor et al [6,12] showed that Gram-negative microorganisms caused 46.3% of all Blood stream infections among CKD patients. In contrast a study by Suzuki et al [3,7] showed that 1/2- 3/4 of organisms causing blood stream infection in CKD patients were Gram positive.

As per our study among the gram-negative bacteria causing bacteremia, Pseudomonas aeruginosa 10 (35.71%) was the predominant organism followed by Klebsiella species 7 (25%), Acinetobacter species 4(14.29%), Elizabethkingae meningoseptica 3(10.71%), Burkholderia cepacia 2(7.14%), Stenotrophomonas maltophilia 1(3.57%), Pantoea species 1(3.57%) (fig 4). In a study done by Parkins M.D et al [18,19] Haemodialysis is considered as a risk factor for Pseudomonas aeruginosa bacteremia. In our study out of the 28 gram negative organisms 21 (75%) were Non fermenters and 7(25%) were Glucose fermenting organisms. Among the non-fermenters predominant organism was Pseudomonas aeruginosa followed by Acinetobacter Species Elizabethkingae meningoseptica, Burkholderia cepacia, Stenotrophomonas maltophilia, Pantoea species. All of Glucose fermenting Gram negative bacilli isolated were Klebsiella species.

Out of 26 isolates of Gram-positive organisms, 7(26.92%) were Methicillin Sensitive Staphylococcus aureus, 9 (34.61%) were Methicillin Resistant Staphylococcus aureus, 6(23.07%) were Methicillin resistant Coagulase negative Staphylococci and 4(15.38%) were Enterococcus spp. A study by Suzuki et al [3,7] infers that haemodialysis patients are at a higher risk of infection with Methicillin Resistant Staphylococcus aureus. Out of 53 positive cultures Enterococcus species account for 7.55% cases. This is comparable to study by D Amato Palumbo et al [19,20] which shows a blood stream infection rate 8%.

Antibiotic susceptibility pattern of Gram-positive isolates were as follows:

All Methicillin Sensitive Staphylococcus aureus were resistant to Penicillin, 85.7% were susceptible to doxycycline,71.42% were susceptible to clindamycin, 57.14% were susceptible to cotrimoxazole, 28.5% were susceptible to Gentamicin, 57.14% were susceptible to Erythromycin100% were susceptible to Cloxacillin, Vancomycin and Linezolid.

MRSA strains were 100% Resistant to Penicillin and Cefoxitin, 66.66% were susceptible to cotrimoxazole, 20% were susceptible to Gentamicin, 33.33% were susceptible to Erythromycin, 66.66% susceptible to Clindamycin, 88.88% were susceptible to Doxycycline, 100 % were susceptible to Vancomycin and Linezolid (fig. 5).

Antibiotic susceptibility pattern of Nonfermentative Gram negative bacilli were as follows

Among Acinetobacter species 50% of isolates were sensitive to Gentamicin, Amikacin, Cotrixomazole ,20% isolates were sensitive to Ceftazidime, Ciprofloxacin, 80% isolates were sensitive to Cefoperazone Sulbactum and Piperacillin Tazobactum. 100 % isolates were sensitive to meropenem & imipenem.

Among Pseudomonas aeruginosa 60% isolates were sensitive to Ceftazidime,40% isolates were sensitive to Ciprofloxacin, Gentamicin, Amikacin,20% isolates were sensitive to cotrimoxazole,100 % isolates are susceptible to Piperacillin Tazobactum, Imipenam & Meropenam. All the isolates of Elizabethkingae meningoseptica were sensitive to Ceftazidime, Ciprofloxacin, Cotrimoxazole, Piperacillin Tazobactum & Meropenam. One isolate of Stenotrophomonas maltophila was 100% sensitive to Cotrimoxazole, Ciprofloxacin & Levofloxacin. One isolate of Burkholderia cepacia was 100% sensitive to Ceftazidime, Cotrimoxazole, Piperacillin Tazobactum & Meropenam. Other isolate was resistant to Ceftazidime, Cotrimoxazole sensitive to Piperacillin Tazobactum & Meropenam (fig. 6).

Among 7 Klebsiella species isolated, 2(28.5%) were sensitive to Gentamicin, Amikacin, Ceftriaxone.3(43%) isolates were sensitive to Ciprofloxacin, Cefoperazone Sulbactum, Piperacillin Tazobactum & Meropenam 6(86%) isolates were resistant to all antibiotics except Polymyxin B. 5(71.43%) isolates showed Ceftazidime aztreonam synergy only (fig. 7). The resistance pattern is comparable to the studies conducted by Zhou S et al. [21]

Conclusion

In our study Gram negative bacilli were the predominant group of microrganisms in our setting. Pseudomonas aeruginosa was the principal isolate followed by Methicillin Resistant Staphylococcus aureus. Our study could highlight the rising isolation of Nonfermentative gram negative bacilli when compared to fermentative gram-negative bacilli. But multidrug resistance was noted more in Klebsiella species. Understanding the bacteriological profile of bacteremia in CKD patients is crucial in guiding prompt, appropriate empirical treatment, improving patient outcomes & combating antimicrobial resistance.

References

1. Singh AK., Farag YM, Mittal BV. et al. Epidemiology and risk factors of chronic kidney disease in India – results from the SEEK (Screening and Early Evaluation of Kidney Disease) study. BMC Nephrol 2013;14:114.
2. Rajapurkar MM, John GT, Kirpalani AL, et al. What do we know about chronic kidney disease in India: first report of the Indian CKD registry. BMC Nephrol 2012;13:10.
3. Lakshminarayana GR, Sheetal LG, Mathew A, et al. Hemodialysis outcomes and practice patterns in end-stage renal disease: Experience from a Tertiary Care Hospital in Kerala. Indian J Nephrol 2017;27(1):51-7.
4. Levin A. Identification of patients and risk factors in chronic kidney disease-evaluating risk factors and therapeutic strategies. Nephrol Dial Transplant 2001;16 Suppl 7:57-60.
5. Mehmood Y, Ali I, Zahra K, et al. Hemodialysis; acute intradialytic complications found on maintenance hemodialysis in patients at a public hospital Lahore. Professional Med J 2019;26(1):45-50.
6. Hafeeq B, Gopinathan JC, Aziz F, et al. The expanding role of “Stand-Alone” hemodialysis units in chronic renal replacement therapy: A descriptive study from North Kerala. Indian J Public Health 2019;63:157-9.
7. Suzuki M, Satoh N, Nakamura M, et al. Bacteremia in hemodialysis patients. World J Nephrol 2016;5(6):489-96.
8. Rteil A, Kazma JM, El Sawda J, et al. Clinical characteristics, risk factors and microbiology of infections in patients receiving chronic hemodialysis. J Infect Public Health 2020;13(8):1166-71.
9. Naqvi SB, Collins AJ. Infectious complications in chronic kidney disease. Adv Chronic Kidney Dis 2006 ;13(3):199-204.
10. Skov Dalgaard L, Nørgaard M, Jespersen B, et al. Risk and prognosis of bloodstream infections among patients on chronic hemodialysis: a population-based cohort study. PLoS One 2015;10(4):e0124547.
11. Karthiga S, Dhanasekaran A, Someshwaran R. Bacteriological Profile and Antibiogram of Catheter Related Blood Stream Infections (CR-BSIs) among Chronic Hemodialysis Patients Attending Tertiary Care Medical College

Hospital. Int J Curr Microbiol App Sci 2018;7(11):1121-8.
12. Schamroth Pravda M, Maor Y, Brodsky K. et al. Blood stream Infections in chronic hemodialysis patients - characteristics and outcomes. BMC Nephrol 2024;25:3.
13. AbuTaha SA, Al-Kharraz T, Belkebir S, et al. Patterns of microbial resistance in bloodstream infections of hemodialysis patients: a cross-sectional study from Palestine. Sci Rep 2022;12(1):18003.
14. Berman SJ, Johnson EW, Nakatsu C, et al. Burden of infection in patients with end- stage renal disease requiring long-term dialysis. Clin Infect Dis 2004;39(12):1747-53.
15. Girndt M. Bacteraemia in haemodialysis patients--not always Staphylococcus aureus. Nephrol Dial Transplant 2015;30(7):1055-7.
16. Mandal SK, Karmakar K, Sarkar KC, et al. Isolation and identification of aerobic bacteria and their antibiogram profile in catheter related bloodstream infection among the hemodialysis patient in a tertiary care hospital. Asian Journal of Medical Sciences 2022;13(10):188-95.
17. CLSI M100 Performance standards for Antimicrobial Susceptibility testing 2025.
18. Dieng A, Niang M, Diallo AB, et al. Etiology of bacteremia under haemodialysis patients and antibiotics susceptibility profile of isolated bacteria. Journal of Bacteriology and Virology 2023;53(2):91-9.
19. Parkins MD, Gregson DB, Pitout JD, et al. Population-based study of the epidemiology and the risk factors for Pseudomonas aeruginosa bloodstream infection. Infection 2010;38(1):25-32.
20. D'Amato-Palumbo S, Kaplan AA, Feinn RS, et al. Retrospective study of microorganisms associated with vascular access infections in hemodialysis patients. Oral Surg Oral Med Oral Pathol Oral Radiol 2013;115(1):56-61.
21. Zhou S, Ren G, Liu Y, et al. Challenge of evolving Klebsiella pneumoniae infection in patients on hemodialysis: from the classic strain to the carbapenem-resistant hypervirulent one. Int J Med Sci 2022;19(3):416-24.