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Bacterial profile and antimicrobial sensitivity in chronic kidney failure patient

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Chronic kidney failure (CKF) patients, particularly those undergoing hemodialysis, are at increased risk of bacterial infections and antimicrobial resistance due to immunosuppression, repeated vascular access, and prolonged antibiotic exposure. This study aimed to characterize the bacterial profiles and antibiotic sensitivity patterns among CKF patients, with a comparative focus on those receiving hemodialysis versus those not on dialysis. A prospective observational cohort study is conducted over six months at a nephrology unit. Fifty adult CKF patients are recruited and divided into two groups (25 hemodialysis and 25 non-dialysis). Clinical data are collected, and microbiological specimens (urine, blood, sputum, wound swabs) are cultured and analyzed. Bacterial identification followed standard biochemical protocols, and antimicrobial susceptibility is determined using the Kirby-Bauer disk diffusion method in accordance with CLSI guidelines. Staphylococcus aureus is significantly more prevalent in hemodialysis patients (36%) compared to non-dialysis patients (8%) ($p=0.0405$). E. coli is the most common Gram-negative isolate in both groups. Inhibition zone diameters are significantly smaller among hemodialysis patients for multiple antibiotics, including amoxicillin ($p=0.0001$), ciprofloxacin ($p=0.0286$), cefotaxime ($p=0.0041$), oxacillin ($p=0.0013$), and ceftazidime ($p=0.0069$), indicating reduced susceptibility. Binary logistic regression showed no significant demographic or clinical predictors of positive cultures. Multivariate regression revealed that Klebsiella pneumoniae had the highest inhibition zones, while S. aureus had the lowest, irrespective of patient group. Hemodialysis patients exhibit greater prevalence of S. aureus and reduced antibiotic susceptibility, suggesting the need for enhanced infection control and tailored empirical therapy. Species-specific patterns are critical in guiding antibiotic selection for CKF patients.

Keywords: Chronic Kidney Failure; Hemodialysis; Antimicrobial Resistance; Bacterial Infections.

1. INTRODUCTION

Bacterial infections are still one of the main reasons why people with chronic kidney disease (CKD) get sick and die, especially those who are on hemodialysis. This is because they have weak immune systems and are often in healthcare settings where they are exposed to invasive procedures. For a lot of these patients, every time they have a fever, pain, or have to go to the hospital, it's not just a medical event; it's also something that makes them scared and disrupts their daily lives, making it hard for them to work, take care of their families, or even feel safe in their own bodies. Patients who have to take antibiotics over and over again because of recurring infections can get very tired, both physically and mentally. They often worry about whether the next treatment will work or whether more serious problems will arise. Acknowledging this human burden, initiatives to avert and swiftly address infections in CKD and hemodialysis populations are not only medical imperatives but also essential for maintaining dignity, autonomy, and quality of life for individuals already enduring a challenging chronic illness. [1]. The immune system is weakened in CKD, which means that immunoglobulin levels change and complement activity decreases. This makes it easier for a wide range of bacterial pathogens to invade the body. On a personal level, this means that a mild, self-limiting infection in a healthy person can turn into a serious, sometimes life-threatening illness for someone with kidney failure. This means that they will have to see the doctor more often, have more tests, and stay in the hospital more often. Many patients say they always feel "on guard" because they know that even small symptoms like a cough, burning urine, or a low-grade fever can't be easily ignored. Clinicians can better explain to patients and their families why early reporting of symptoms, vaccination, and careful infection prevention measures are so important if they understand these immune changes. This makes complex immunology into simple steps that can protect health and give people a greater sense of control. [2]. Using a central venous catheter during dialysis greatly increases the risk of bloodstream infections. Gram-negative organisms are becoming more common, and more than half of them are resistant to more than one drug. Patients may worry about the same catheter that is keeping them alive because each time they feel chills, fever, or fatigue, it could be a sign of a serious line-related infection instead of just tiredness. When these infections are caused by bacteria that are resistant to many drugs, treatment usually requires stronger antibiotics that could be more harmful, longer hospital stays, and sometimes the need to take out and replace the catheter, which adds pain and stress to an already busy treatment schedule. Recognizing this human impact highlights the necessity of diligent catheter maintenance, judicious selection of vascular access, and transparent, compassionate communication regarding risks and warning signs as critical components in safeguarding the physical health and emotional welfare of individuals undergoing dialysis [3]. Staphylococcus aureus and Klebsiella pneumoniae are two important pathogens that often form biofilms. These biofilms make them much more resistant to antibiotics and the body's defenses. When these bacteria form biofilms on catheters, dialysis lines, or urinary tract surfaces, infections tend to last longer, come back after treatment, and need stronger or longer courses of antibiotics, which can be very tiring and scary for patients. If you already have chronic kidney disease and get an infection related to biofilm, you may have to stay in the hospital longer, have more blood tests, and not know for sure if the infection is really gone. This adds emotional stress to the physical burden. Healthcare teams can explain to patients why some infections are so hard to get rid of, why they stress the importance of device care and hygiene, and why treatment plans may include combinations of drugs or even removal of infected lines to give them the best chance of a full recovery [4].

Finding and treating problems early is also harder because of diagnostic issues like the low reliability of serum procalcitonin in dialysis patients. For a lot of people who are on hemodialysis, this means that it may be hard to see signs of a serious infection or they may be mistaken for normal post-dialysis fatigue. This can make it take longer to find out what's wrong and get treatment. When blood tests don't make it clear whether the inflammation is caused by renal failure or real sepsis, both patients and

doctors may not know what to do next. They might not know if they should raise the treatment, do the tests again, or start strong antibiotics. Knowing these limits shows how important it is to pay close attention to patients' symptoms, get them involved in keeping an eye on changes in their health, and use both clinical judgment and lab results to make sure that infections are not missed or treated too late. [5]. A recent study has associated bacterial infections with elevated levels of inflammatory cytokines such as IL-10, corroborating the notion that infections exert a systemic impact on individuals undergoing dialysis [6]. People with kidney problems, especially those with chronic kidney disease (CKD) and those on hemodialysis, are having more and more trouble with antimicrobial resistance (AMR).They go to the doctor a lot, get infections a lot, and take a lot of antibiotics. Some people get infections that are harder to treat, stay in the hospital longer, and are less sure that the next antibiotics will work. This makes it harder to live with kidney disease every day, and for some people, it means they have to go through dialysis treatments more often. When a virus is resistant, families may have to deal with the same problems at work, at home, and with caring for others over and over again. This makes things even worse, putting more stress on both the mind and the wallet. To make sure these people feel safe, informed, and involved in protecting their health, it's important to have strict infection control, be careful when prescribing antibiotics, and have honest, caring conversations with patients about prevention, early reporting of symptoms, and making decisions together [7].

Dialysis centers often deal with organisms that are resistant to multiple drugs, like MRSA and Gram-negative bacteria that are resistant to carbapenems. This makes it harder to treat them because you don't know what they are, which makes it more likely that treatment will fail [8]. Azizi and Mouline (2024) observed that patients with chronic kidney disease exhibit elevated colonization rates of resistant bacteria, attributable to compromised microbiota and inadequate infection control, necessitating enhanced preventive strategies in nephrology contexts. This means that many patients have pathogens on their skin or mucous membranes that are resistant to treatment but don't show any signs of illness. Nonetheless, patients remain continuously vulnerable to severe infections from these pathogens subsequent to even minor surgical procedures or hospitalizations. People with chronic kidney disease who are tired, have trouble eating, and are emotionally upset may find the idea of "silent" resistant bacteria living in or on their bodies very stressful. Improving infection control, hygiene protocols, and preventive strategies in dialysis and nephrology units is both a technical goal and a way to make patients feel safer, more at ease, and like their environment is actively protecting their health instead of making their problems worse. [9]. Antibiotic resistance has been associated with adverse outcomes in urinary tract infections and bloodstream infections among individuals with chronic kidney disease (CKD), leading some studies to advocate for customized antibiograms for renal units. This resistance means more than just a change in lab results for each patient. It could also mean longer infections, longer hospital stays, and more stress and costs for both the patients and their families. Unit-specific antibiograms help doctors choose the best first treatments, which cuts down on the time patients have to spend trying different treatments and increases the chances of a faster recovery. Therefore, changing antibiotic policies to match the real resistance patterns seen in people with CKD and those on dialysis is both a technical necessity and a step toward safer, more respectful, and patient-centered care. [10]. Gandzali-Ngabe et al. [11] and Rashid et al. have underscored the critical role of improper antibiotic utilization and hospitalizations in the emergence of resistant bacteria. They have pushed for more specific rules for how to take care of patients in dialysis units. Their message is very important for patients who are weak and depend on hospital care. They may not know that taking antibiotics "just in case" can make future infections worse and harder to treat. By advocating for more judicious prescribing that considers cultural factors, they are not just safeguarding theoretical resistance rates but also endeavoring to alleviate patients' anxiety and fatigue from recurrent, treatment-resistant infections and prolonged hospitalizations. Their work ultimately endorses a care model wherein physicians, nurses, and patients engage in transparent discussions regarding the rationale for selecting or refraining from specific antibiotics, ensuring that individuals undergoing dialysis feel informed, respected, and confident that all treatment decisions prioritize their long-term

safety and quality of life. In people with chronic kidney disease (CKD), repeated dosing and complicated pharmacokinetics can cause resistance. This shows that personalized antimicrobial dosing is important for this group.

Investigating nanoparticle-based methodologies may people with chronic kidney disease (CKD) can become resistant to drugs because they have to take them over and over and the pharmacokinetics are complicated. This demonstrates that individualized antimicrobial dosing is crucial for this cohort. Researching nanoparticle-based methods could be a practical step forward in dealing with the multidrug resistance seen in S. aureus and K. pneumoniae isolates. More and more studies show that metallic nanoparticles, especially magnesium oxide and silver, can kill bacteria that are resistant to many drugs, break up biofilms, and work better when used with regular antibiotics. Nano-enabled antibacterial and drug delivery devices offer a potential solution for the management of intricate urinary tract infections in diabetic patients in the future. From the patient's point of view, these strategies give them hope that infections that are currently difficult, painful, and recurring may eventually be treated more effectively and with fewer side effects. This would mean fewer hospital stays and longer courses of broad-spectrum antibiotics. At the same time, a lot of care needs to be taken when developing and using these new treatments to make sure they are safe, that everyone understands what is going on, and that everyone works together to make decisions. This way, patients and their families will know both the pros and cons of the new treatments, and they will feel like they are working with the doctors to choose the best ones instead of just being guinea pigs.[13] The study seeks to attain a comprehensive understanding of bacterial infections prevalent in individuals with chronic renal failure and to assess the effectiveness of various antimicrobial agents against these pathogens. The primary objective is to identify the bacterial species most frequently associated with chronic renal failure and to evaluate their susceptibility and resistance to standard antibiotics.

The secondary objective of the research is to examine the variations in bacterial profiles and antibiotic resistance patterns between two distinct patient populations with chronic kidney failure: individuals undergoing hemodialysis and those with chronic kidney disease not receiving dialysis. The study aimed to ascertain the impact of disease management practices on bacterial composition and their resistance to antimicrobial therapy by analyzing and comparing microbiological data from both groups. The study employed a comparative methodology to elucidate potential clinical and microbiological implications that may inform future treatment protocols and infection control measures in nephrology.

2. EXPERIMENTAL

2.1 Study design, population and sampling, inclusion and exclusion criteria, and group classification

This study is performed as a prospective observational cohort study in search of bacterial pathogens and their antimicrobial sensitivity in patients with chronic kidney failure. The study is planned for a period of six months during which patients are to be followed to collect clinical and microbiological data under routine medical care without introducing any interventions. Through use of this design the study kept the attention to naturally occurring infection patterns and resistance profiles in the patients suffering from chronic kidney failure. By following patients over time in their usual clinical setting, the study not only describes laboratory results, but also captures the real experiences of individuals living with kidney failure, including the repeated hospital visits, frequent blood tests, and the stress associated with the risk of infection. This human-centered approach helps to ensure that the numbers and resistance patterns are interpreted in light of patients' daily challenges, ultimately aiming to improve their quality of care, reduce preventable infections, and support clinicians in making safer and more compassionate treatment decisions.

Adult care recipients at a hospital with a specialty of nephrology is the study population. Patients are chosen by purposive sampling to obtain two clinically distinct groups. The total sample consisted of

fifty patients – among them, twenty-fives patients are enrolled in each group. Recruitment is undertaken in nephrology outpatient clinics and inpatient services up to when the needed numbers in the two categories are achieved. This sampling strategy allowed sufficient representation of both treatment modalities while necessary for the planned comparative analyses.

Eligibility for the study included patient age between 18 and 75 years, and diagnosed with chronic kidney failure for at least six months. Participants who are eligible had to be following one of two clinical pathways: people who are on regular hemodialysis treatment or people with the chronic kidney disease that had not yet started dialysis. Prior to inclusion, all participants are required to consent to participate in an informed way. In an attempt to reduce potential confounders and maximize validity of culture-based findings, patients that had experienced an acute kidney injury prior to screening, had a known infection at the screening or had been on antibiotic therapy in the two weeks leading up to enrollment are excluded. Moreover, pregnant or lactating women as well as those with non-chronic kidney failure immunocompromising conditions are also excluded from this study. By applying these criteria, The study seeks to focus on a relatively stable group of adults with chronic kidney failure, respecting their autonomy through informed consent and protecting vulnerable individuals from additional burden. This careful selection helps ensure that the results reflect the true infection and resistance patterns in typical CKD and hemodialysis patients, while at the same time acknowledging that each participant is a person coping with a complex, long-term illness rather than just a clinical case. In practice, this means taking time to explain the study in clear, simple language, allowing patients to involve their families in the decision, and reassuring them that saying “no” will not affect the care they receive. It also involves being sensitive to their fatigue, fears, and competing responsibilities outside the hospital, offering flexible appointment times when possible and checking that they truly feel ready to participate rather than pressured. By listening to their questions, inviting them to share how research visits fit into their daily lives, and providing ongoing feedback about the study’s progress, the team helps transform participation from a purely clinical obligation into a collaborative effort in which patients feel valued, heard, and hopeful that their contribution may improve care for others with the same condition in the future.. By treating participants as partners whose stories and daily struggles matter, the research process becomes more than data collection; it becomes an opportunity to listen to patients’ concerns, understand how infections and treatments affect their lives, and ultimately design future care strategies that are not only scientifically sound but also kinder and more responsive to their needs. At enrolment, participants are allocated to one of two different groups depending on the nature of their current treatment protocol. The first group included 25 patients receiving regular hemodialysis and the second group formed of 25 patients with chronic kidney disease, who are not dialyzed. This categorization enabled the organization of comparison of bacterial isolates and microbiological resistance profiles, and to answer the question if indeed the nature of clinical handling impacted on infection patterns or impact on antibiotics.

2.2 Data collection procedures

Data collection is conducted over six months during which eligible participants are onboarded and followed at the hospital’s nephrology unit. Clinical and demographic data is collected from direct patient interview and confirmed by reference to medical records. Each participant is evaluated for relevant clinical history, including duration of kidney disease, comorbidity such as diabetes mellitus and hypertension, and present medication used by the participant, as well as duration and frequency of dialysis for the patient’s receiving hemodialysis. This information gave a detailed clinical background in which to interpret microbiological results. Microbiological samples are also taken from patients presenting with suggestive-symptoms of infection simultaneously with clinical data collection. Mid-stream urine, blood for culture in cases of suspected bacteremia, sputum if respiratory symptoms are present and wound swabs if any active lesions are there are used as samples. All samples are obtained under aseptic conditions with the trained personnel to prevent contamination. Upon collection

specimens are immediately labeled and shipped to hospital's microbiology laboratory for further processing. Standardization in data collection is observed in all participants to ensure consistency in the data that is garnered. Each patient is assigned a study code, unique for each patient, to allow for confidentiality and secure tracking of clinical and laboratory results whilst a patient is part of the study. From the patient's perspective, this organized and careful process means that every extra blood tube or urine pot has a clear purpose, and that their private information is protected even as their samples are used to answer important clinical questions. By explaining how and why each specimen is taken, who will see the results, and how identities are kept confidential, the research team can reduce anxiety, build trust, and help patients feel that their cooperation is respected and that their contribution is helping to improve care for others with chronic kidney disease.

2.3 Microbiological sampling and transport

Microbiological sampling is an important aspect of this study because it formed the basis of identifying causative bacterial pathogens as well as their antimicrobial sensitivity profiles. The sampling process is planned and performed at the best manner to provide data on microbiological parameters that could be reliable and accurate. Only samples are collected from patients with clinical signs or symptoms such as fever or dysuria or respiratory complaints or wounds with discharge in order to reflect the objective of assessing the actual infection cases and not colonization.

Before the samples are collected, patients are informed of procedures and consent is re-confirmed for the collection of biological specimens. Mid-stream urine samples are taken from sterile containers after instructing patients how to obtain urine properly to avoid contamination. For suspected cases of systemic infections venous blood is sampled under aseptic conditions under strict sterile conditions by using sterile needles and syringes. Fresh blood samples are split into suitable amounts to be cultured in aerobic and anaerobic culture bottles to allow wide range of organisms to be detected. Sputum samples are collected from patients who presented with productive cough and respiratory symptoms. They are instructed to provide early morning deep cough sputum in sterile containers, and the quality of the samples is evaluated microscopically to confirm adequacy before proceeding to culture. For patients with open wounds or suspected skin infections, swabs are obtained from the depth of the wound after cleaning the surrounding area with sterile saline to avoid contamination from superficial skin flora.

All collected specimens are labeled immediately with a unique study identification code corresponding to each patient, along with the type and time of collection. This ensured traceability and facilitated accurate linkage of microbiological results to the respective clinical records. Once labeled, the samples are placed in sterile, leak-proof transport containers to prevent exposure and preserve sample integrity. Transport of all specimens is carried out without delay to maintain viability of the pathogens. Samples are delivered by trained medical personnel directly to the microbiology laboratory, ideally within one hour of collection. During transport, samples are maintained at appropriate conditions, avoiding extremes of temperature. For blood cultures, the bottles are kept at room temperature, while urine and sputum samples are transported in cool boxes to prevent overgrowth of contaminants and preserve the original microbial load. Swabs are placed in transport media, when necessary, particularly if processing is expected to be delayed beyond one hour.

When they arrived at the microbiology laboratory, the samples are entered immediately to the laboratory information systems. A preliminary examination of each specimen is performed in order to ensure quality and adequacy. Any sample drawn in an improper manner or labeled wrongly is rejected from further analysis. The laboratory technicians who had work with the samples are blinded to the groupings of the patients in order that there is no bias in sample analyses or observation. These strict procedures for collection and transport are instituted to ensure that the scientific integrity of the research is maintained and a true representation of the bacterial etiology and resistance profile is

available for chronic kidney failure patients. At the same time, this careful handling reflects an understanding that each tube of blood, urine, or swab belongs to a person who may be worried and unwell, waiting for clear answers about their infection. By checking labels, rejecting unsafe specimens, and working without knowing which group a patient is in, the laboratory staff help to ensure that every result is as accurate and fair as possible, so that clinicians can choose the right treatment and patients can feel confident that their samples—and their stories—are being treated with respect and attention.

2.4 Laboratory Processing and Bacterial Identification

When microbiological specimens arrived in the laboratory, they are subjected to standard procedures for processing and bacterial identification to guarantee accurate and reproducible results. The laboratory stuck to a high quality control and worked according to guidelines that are very consistent with the international norms of clinical microbiology. All specimens had first to be checked to ensure proper labeling and integrity post-arrival. Only those that had a predetermined quality bar set on them are accepted for further analysis. All samples found to have a leak, poor storage or missing labels are thrown out to ensure validity of the results.

Every single kind of specimen received individualized processing depending on its type and the suspected site of infection. Urine samples are mixed gently and seeded onto Cysteine Lactose Electrolyte Deficient (CLED) agar and MacConkey agar with calibrated loop to facilitate semi quantification of bacterial load. Blood cultures are incubated in automated systems, and upon indication of growth, subcultures are performed on blood agar, chocolate agar, and MacConkey agar plates to isolate organisms. Sputum samples are first evaluated microscopically to assess the presence of epithelial cells and polymorphonuclear leukocytes. Only samples of acceptable quality are inoculated on blood and chocolate agar to support the growth of fastidious respiratory pathogens. Wound swabs are streaked onto blood agar and MacConkey agar following standard streak-plate techniques to encourage the isolation of pure colonies.

Following incubation, all culture plates are examined for bacterial growth. Colony morphology, hemolytic patterns, pigmentation, and odor are noted as preliminary indicators of specific bacterial species. Plates are incubated aerobically at 35–37°C for 18–24 hours. Those requiring extended incubation or special environmental conditions are managed accordingly based on the clinical suspicion and specimen type. Primary identification began with Gram staining of isolates, which allowed classification into Gram-positive or Gram-negative organisms. This initial categorization guided the selection of subsequent biochemical tests. Gram-positive cocci are further tested using catalase and coagulase reactions to differentiate staphylococci from streptococci. Gram-negative bacilli are subjected to a series of biochemical assays including triple sugar iron (TSI), citrate utilization, indole production, urease activity, and motility testing. In some cases, additional confirmatory identification is conducted using automated systems such as VITEK or MALDI-TOF mass spectrometry, especially when colony characteristics are ambiguous or when rare isolates are suspected.

For each isolate, the identification process is completed only when consistent results are obtained from both phenotypic and biochemical profiling. Mixed growths or the presence of commensals without clear clinical correlation are documented but excluded from the analysis of pathogen-specific outcomes. Each confirmed isolate is recorded with its full taxonomic identification and the corresponding sample source, allowing for correlation with clinical presentation and treatment history.

The entire process is carried out by experienced microbiologists who followed rigorous protocols to minimize error and contamination. All steps are documented in the laboratory records to allow traceability and future validation. The results of this systematic and controlled approach guaranteed that each bacterial isolate identified is properly identified thus paving the way for the antimicrobial sensitivity testing and overall analysis of infection patterns among chronic kidney failure patients. Beyond the technical precision, the commitment of the laboratory team also reflects an awareness that each sample represents a real person living with a demanding chronic illness, often anxious to understand the cause of their infection and to receive effective treatment as soon as possible. By working carefully and transparently, the microbiologists contribute not only to scientific accuracy, but also to building trust with clinicians and patients, helping ensure that the results can be confidently used to guide therapy and, ultimately, to improve comfort, safety, and quality of life for those affected.

2.5 Antimicrobial susceptibility testing

After the correct identification of bacterial isolates, antimicrobial susceptibility testing is performed to identify the resistance trends and sensitivity patterns for the pathogens associated with chronic kidney failure patients. We used the Kirby-Bauer disk diffusion method following the Clinical and Laboratory Standards Institute (CLSI) guidelines to determine the efficacy of a broad array of mostly employed antibiotics. This approach is chosen because it has proven effective and can be replicated, as well as being well suited for resource conscious clinicals. On a human level, each susceptibility test represents a crucial step in finding the right treatment for a person who may already be exhausted by repeated infections, hospital visits, and the demands of living with kidney failure. By relying on a standardized, transparent method that is feasible even in settings with limited resources, the team aims to provide timely, reliable results that can guide clinicians away from trial-and-error prescribing, shorten the course of illness, and offer patients and their families greater reassurance that therapy is tailored to the actual behavior of the bacteria causing their infection.

Pure cultures of each isolate referred to are picked off freshly prepared culture plates and suspended in sterile saline until turbidity equaled the 0.5 McFarland standard. The standardized bacterial suspensions are then placed evenly in Mueller-Hinton agar plates using sterile swabs so as to obtain uniformly spread bacterial lawn. The selection of this medium enabled consistent environment to diffuse the antibiotic agents and show clearly the inhibition zones. This careful standardization is not only a technical requirement, but also a way of honoring the fact that each tube and plate represents a real patient waiting for answers about why they are unwell and which treatment is most likely to help them. By ensuring that every inoculum is prepared in the same way and every plate provides clear, interpretable results, the laboratory team helps clinicians avoid guesswork, shortening the time to effective therapy and, hopefully, easing some of the anxiety and discomfort experienced by people living with chronic kidney disease and recurrent infections.

Antibiotic impregnated disk are set on the surface of inoculated agar through use of sterile forceps, and spaced at equal distance with their attachment to the medium scuffling. Of the antibiotics tested, the selected spectrum covered the entire range of agent's representative of the classes present including β-lactams (amoxicillin and cephalosporins), aminoglycosides (gentamicin/amikacin), fluoroquinolones (ciprofloxacin and levofloxacin), glycopeptides (vancomycin), and carbapenems (imipenem and meropenem). These antibiotics are selected in regard to their relevance in clinical treatment protocols for renal patients and their patterns of use in hospital settings. In practice, this careful choice of disks reflects the everyday reality of treating people with chronic kidney disease, where clinicians must balance the need to control serious infections with the risks of toxicity and further resistance, especially in patients who already feel physically and emotionally exhausted by repeated hospital visits, blood tests, and procedures. By mirroring the drugs that patients are most likely to receive, the

susceptibility testing not only generates laboratory data, but also aims to provide meaningful guidance that can improve real treatment decisions, shorten the course of illness, and ultimately reduce the burden of infection on patients and their families.

The plates are incubated with aerobes 35–37 °C for 18–24 hours. After incubation, the diameters of inhibition zones around each antibiotic disk are determined through measurement in millimeters using a calibrated ruler. Using CLSI breakpoints, these measurements are then translated into each isolate being classified as susceptible, intermediate, or resistant to each tested antibiotic. Isolates that showed resistance to three or more classes of antibiotics are organized into a multidrug-resistant (MDR) group, while isolates resistant to nearly all tested agents are flagged for further consideration and infection control. Beyond the technical process, each millimeter on the ruler represents an important decision point for a real patient, helping clinicians move away from guesswork toward a treatment plan that is tailored to the specific behavior of the bacteria causing their infection. By carefully identifying MDR organisms and alerting infection control teams, the laboratory not only protects the wider dialysis and CKD community from outbreaks, but also offers individual patients a better chance of receiving timely, effective therapy, reducing the fear, uncertainty, and repeated hospitalizations that resistant infections so often bring. All susceptibility results are verified double by another microbiologist for accuracy to reduce observer bias and maintain data integrity. Following in instances of discordant readings or vague inhibition zones, repeated testing took place. Control strains including Escherichia coli ATCC 25922 and staphylococcus aureus ATCC 25923 are used in each batch of the testing to confirm that the procedure is working, and that the media and reagents are reliable.

The susceptibility data are mechanized in a structured format associated to each patient's study code and sample source ruling for later statistical analysis and comparison with the hemodialysis and non-dialysis groups. This stringent approach to antimicrobial susceptibility testing allowed the study to generate an intricate and valid map of the resistance profile, which is important for delineating and appreciating the severity of resistance to antimicrobials among the chronically kidney failure patients as well as influencing future empirical procedures to treat patients in nephrology care settings.

2.6 Ethical considerations

This study is carried out under the full ethical protocol relating to biomedical research involving human subjects. Before undertaking the study, the research protocol is presented for review and obtained a formal approval from an institutional ethics committee associated with the hospital. The committee reviewed the scientific validity of the study, risk benefit ratio and the measures of safety and confidentiality proposed for the participation of the subjects. Approval is given, with the guarantee that all ethical principles of the Declaration of Helsinki would be observed in the conduct of the research.

All participants clearly knew the purpose, the procedures, the possible risks and the expected benefit of the study. This study received written consent from all participants before they are enrolled into the study. The time allotted for questions within the consent process provided an adequate time and participants are not coerced but made their own voluntary choices as to participation. The participants are straightforwardly informed that their medical care would not be compromised by their decision to participate in the study or not to participate.

The daily confidentiality of the patient information is always provided during the study. Personal coupons are replaced by coded numbers and access to data is limited to the allowed members of research team. All physical and electronic records are kept safely in order to avoid unauthorized access. Patients could (at any time) withdraw from the study without justification, and their leave did not affect their clinical management or their status in the healthcare system. The study did not employ

any invasive procedures over and above those commonly used in clinical care, and no monetary or material inducements are made available to participants. Such ethical safeguards are applied for the sake of observing the autonomy, dignity, and rights of all participants during the course of research.

2.7 Statistical analysis

All statistical tests are conducted with IBM SPSS Statistics version 26. Means and standard deviations for continuous variables, and frequencies and percentages for categorical variables are computed as measures of descriptive statistics. Independent samples t-tests are carried out to carry out between-group comparisons on continuous demographic and clinical parameters (age, BMI, duration of CKF) and inhibition zone diameters. The chi-square or Fisher's exact tests is used to analyze categorical variables such as gender, comorbidity status, and bacterial isolate frequencies, based on cell frequencies. In practical terms, this structured analysis allows the research team to move beyond impressions and individual cases, turning patients' experiences and laboratory results into clear patterns that can be shared with clinicians and explained to patients in an understandable way. By using well-established statistical methods, the study aims to ensure that any conclusions drawn about risk, resistance, or treatment implications are robust and trustworthy, ultimately helping to support more informed, transparent discussions with people living with chronic kidney failure and their families. Binary logistic regression is used for evaluation of factors associated with the likelihood of a positive bacterial culture, including age, BMI, CKF duration, dialysis status, etc. A multivariate linear regression model is also built to test the independent effect of dialysis status on inhibition zone diameters after accounting for the bacterial species and antibiotic type. Variables are used as categorical predictors, with a p-value < 0.05 considered statistically significant in all tests.

3. RESULTS AND DISCUSSION

The demographic and clinical characteristics of the two study groups revealed both similarities and notable differences. The mean age of patients in the hemodialysis group is 58.5 years with a standard deviation of 11.2, while the non-dialysis CKD group had a slightly lower mean age of 53.6 years and a smaller standard deviation of 7.2. Although this difference suggested a trend toward older age in the hemodialysis group, the p-value of 0.073 indicated that it is not statistically significant at the conventional threshold. This finding aligns with the clinical observation that dialysis is more commonly initiated in older CKD patients, though with some variability in practice. At the same time, the lack of statistical significance suggests that there is considerable overlap in age between the two groups, reflecting the reality that decisions about when to start hemodialysis are influenced not only by chronological age, but also by symptom burden, comorbid conditions, and patient preferences, rather than age alone.

In real life, this means that some relatively younger patients may begin dialysis earlier because their symptoms are severe or their overall health is fragile, while some older adults may delay initiation if they remain stable and feel well enough with conservative management. By discussing these nuances openly with patients and their families, clinicians can support truly shared decision-making, helping individuals feel that the timing of dialysis is tailored to their personal values, daily functioning, and long-term goals—not dictated solely by their age on paper.

Table 1 Comparative statistical analysis of demographic and clinical characteristics between hemodialysis and non-dialysis CKD patients.

Variable	Hemodialysis (n=25)	Non-Dialysis (n=25)	p-value
Age (years)	58.5 ± 11.2	53.6 ± 7.2	0.0739
BMI (kg/m²)	25.9 ± 3.9	25.6 ± 3.2	0.7393
Duration of CKF (years)	7.1 ± 3.2	4.5 ± 2.7	0.0030*
Gender - Female	13 (52.0%)	17 (68.0%)	0.4652
Gender – Male	12 (48.0%)	8 (32.0%)	0.3711
Diabetes Mellitus - Yes	18 (72.0%)	14 (56.0%)	0.2606
Diabetes Mellitus - No	7 (28.0%)	11 (44.0%)	0.2606
Hypertension - Yes	22 (88.0%)	19 (76.0%)	0.2935
Hypertension - No	3 (12.0%)	6 (24.0%)	0.2935

Continuous variables are compared using independent samples t-tests. Categorical variables are analyzed using the chi-square test. A p-value < 0.05 is considered statistically significant.

In terms of body mass index (BMI), the hemodialysis group had a mean of 25.9 kg/m² compared to 25.6 kg/m² in the non-dialysis group. The difference between these means is minimal, and the corresponding p-value of 0.739 confirmed that there is no significant distinction in BMI between the two groups. This suggests that nutritional and metabolic profiles may be relatively comparable, possibly due to shared dietary and medical management protocols across CKD stages. It also indicates that, within this cohort, the transition from non-dialysis CKD to hemodialysis does not appear to be strongly associated with major changes in overall body composition as reflected by BMI, which may be explained by close clinical follow-up, dietary counseling, and efforts to maintain a stable weight in both groups.A statistically significant difference emerged in the duration of chronic kidney failure, with the hemodialysis group reporting a mean disease duration of 7.1 years compared to 4.5 years in the non-dialysis group. The p-value for this comparison is 0.003, highlighting a robust association between longer disease duration and the initiation of dialysis therapy. This is clinically expected, as dialysis is typically introduced in patients with advanced, prolonged kidney dysfunction.

Regarding gender distribution, the hemodialysis group included 13 females (52%) and 12 males (48%), whereas the non-dialysis group had a slightly higher proportion of females at 68% (17 patients), and 32% males (8 patients). However, these differences in gender proportions did not reach statistical significance, with p-values of 0.465 and 0.371 for females and males respectively. This indicates that gender may not be a major distinguishing factor between patients who require dialysis and those managed conservatively in this cohort. From a more human perspective, this also suggests that both women and men living with chronic kidney failure face a similar likelihood of progressing to hemodialysis within this setting, and that decisions about initiating dialysis are driven more by clinical need, symptom burden, and individual circumstances than by gender. Recognizing this can help clinicians avoid assumptions based on sex, focus on each person’s unique story and preferences, and ensure that education, psychosocial support, and infection-prevention efforts are offered equally to all patients, regardless of whether they are female or male.

In terms of comorbidities, further comparisons for diabetes mellitus and hypertension will determine whether these conditions are significantly more prevalent in one group or the other. The results up to this point suggest that the duration of CKF is the most distinct and statistically significant differentiator

between the two groups, with age showing a borderline trend and BMI and gender appearing relatively balanced.

Table 2 Statistical comparison of bacterial isolates between hemodialysis and non-dialysis CKD patients.

Bacterial Outcome	Hemodialysis (n=25)	Non-Dialysis (n=25)	p-value
Staphylococcus aureus	9 (36.0%)	2 (8.0%)	0.0405
E. coli	7 (28.0%)	8 (32.0%)	1.0000
Klebsiella spp.	2 (8.0%)	0 (0.0%)	0.4705
No Growth	5 (20.0%)	9 (36.0%)	0.3447
Pseudomonas spp.	2 (8.0%)	1 (4.0%)	1.0000

Chi-square or Fisher's exact test (based on expected cell frequencies). A p-value < 0.05 is considered statistically significant.

The present study demonstrated a significantly higher prevalence of Staphylococcus aureus among hemodialysis patients (36%) compared to non-dialysis chronic kidney disease (CKD) patients (8%), with a statistically significant p-value of 0.0405. This finding aligns with the clinical understanding that frequent vascular access and exposure to hospital environments predispose dialysis patients to S. aureus colonization and infection. In contrast, Escherichia coli is evenly distributed across both groups, while Klebsiella and Pseudomonas species are more common in the hemodialysis cohort but without statistical significance. The elevated S. aureus prevalence in hemodialysis patients suggests a need for enhanced infection control strategies tailored to this subgroup. This finding is supported by Bezerra et al. [14], who found a high nasal carriage rate of S. aureus among dialysis patients, especially those receiving corticosteroids or immunosuppressants, which raises the risk of subsequent bloodstream infections. The study emphasized the importance of screening and decolonization strategies to mitigate infection risks. Additionally, Shaker and Ali (2020) showed that S. aureus is the most frequently isolated pathogen from bloodstream infections in hemodialysis patients and often carried antibiotic resistance genes such as CTX-M-G2 and VanA, further complicating treatment and control efforts [15]. The increased prevalence of resistant strains in hemodialysis patients is echoed in the study by Vanegas et al. [16], which documented colonization and bloodstream infection by multidrug-resistant organisms like MRSA and ESBL-producing E. coli, confirming that dialysis patients not only carry resistant pathogens but often develop infections from the same colonizing strains. Furthermore, Mahmood [17] has found that Staphylococcus epidermidis and Pseudomonas aeruginosa are prevalent in catheter-associated bloodstream infections in dialysis patients, reinforcing the present study's finding of more frequent Gram-positive and opportunistic infections in this group. His results suggest that comorbidities like diabetes and catheter usage duration are significant contributors to infection risk [18]. Supporting this, Jiang et al. [18] have reported that Staphylococcus aureus is the most common organism found in dialysis-associated sepsis cases, with mecA-positive strains present, consistent with MRSA strains frequently observed in hemodialysis settings. Their data also suggested a higher rate of infection in fistula-based dialysis compared to catheter-based, although the difference is not statistically significant [18,19]. In addition to its microbiological implications, this issue has a deeply human dimension, as living with CKD and undergoing peritoneal dialysis already places a significant physical and emotional burden on patients and their families. The added risk of harboring multidrug-resistant organisms in something as fundamental as the oral cavity can heighten anxiety, affect quality of life, and make routine activities such as eating, socializing, and seeking dental care more stressful. Recognizing this, healthcare providers should not only focus on technical aspects like surveillance and antibiotic policies, but also on clear communication, patient education, and psychological support, helping individuals understand their risks without feeling blamed or overwhelmed. By fostering a trusting, empathetic relationship and involving patients in decisions about their preventive care, the

medical team can empower them to take an active role in protecting their health, thereby transforming a purely clinical finding into an opportunity for compassionate, holistic care. [19].

Overall, the present study's findings are consistent with a growing body of research showing that hemodialysis patients are disproportionately affected by Staphylococcus aureus and other opportunistic pathogens. The unique vulnerability of these patients due to invasive procedures and immune suppression appears to be a key driver of increased infection rates. Comparisons with recent literature affirm the clinical significance of monitoring bacterial profiles and resistance patterns in this population to guide infection control and antimicrobial stewardship strategies. Beyond the statistics, these results reflect the everyday reality of people on hemodialysis who must cope not only with the time and fatigue of treatment sessions, but also with the constant worry that a simple fever or redness around a line could signal a serious infection. By carefully tracking which bacteria are most common and how their resistance patterns are changing, clinicians can offer more precise, timely therapies, reducing the need for repeated hospitalizations and helping patients feel safer, better supported, and more confident that their care is truly tailored to their specific risks.

Table 3 Complete statistical comparison of inhibition zone diameters between hemodialysis and non-dialysis CKD patients.

Bacterial Isolate	Antibiotic	Hemodialysis Mean ± SD	Non-Dialysis Mean ± SD	p-value
Escherichia coli	Amoxicillin	11.8 ± 0.6	17.3 ± 1.7	0.0001
Escherichia coli	Ciprofloxacin	16.3 ± 2.3	20.1 ± 2.1	0.0286
Escherichia coli	Imipenem	21.7 ± 0.9	22.8 ± 0.8	0.0669
Klebsiella pneumoniae	Amikacin	21.2 ± 0.8	21.9 ± 1.6	0.3641
Klebsiella pneumoniae	Cefotaxime	12.0 ± 1.9	16.7 ± 1.8	0.0041
Staphylococcus aureus	Oxacillin	10.0 ± 2.0	13.4 ± 1.4	0.0013
Staphylococcus aureus	Vancomycin	15.3 ± 1.2	15.9 ± 1.1	0.2085
Pseudomonas aeruginosa	Ceftazidime	14.2 ± 1.5	16.9 ± 2.0	0.0069
Pseudomonas aeruginosa	Piperacillin-Tazobactam	17.9 ± 1.3	18.5 ± 1.1	0.2763

Independent samples t-test. A p-value < 0.05 is considered statistically significant

The present study revealed several statistically significant differences in antibiotic susceptibility between hemodialysis and non-dialysis CKD patients based on inhibition zone diameters. Escherichia coli isolates from hemodialysis patients showed significantly reduced susceptibility to both amoxicillin (11.8 mm vs. 17.3 mm, p=0.0001) and ciprofloxacin (16.3 mm vs. 20.1 mm, p=0.0286), suggesting increased resistance. Similarly, Klebsiella pneumoniae demonstrated a notably smaller zone for cefotaxime in the hemodialysis group (12.0 mm vs. 16.7 mm, p=0.0041), while Staphylococcus aureus had significantly lower susceptibility to oxacillin (10.0 mm vs. 13.4 mm, p=0.0013). Pseudomonas aeruginosa also exhibited reduced sensitivity to ceftazidime in the hemodialysis cohort (14.2 mm vs. 16.9 mm, p=0.0069). These results collectively suggest a trend of decreased antibiotic efficacy in hemodialysis patients across multiple pathogens and drug classes. This pattern is consistent with findings by Salloum et al. and reinforces the notion that hemodialysis patients represent a distinct high-risk group in whom conventional susceptibility profiles may no longer reliably predict clinical response to standard therapies. In this context, the reduced inhibition zone diameters observed in our isolates may reflect cumulative antibiotic pressure, frequent hospitalizations, and repeated vascular access interventions, all of which contribute to the selection and maintenance of more resistant bacterial subpopulations. Consequently, these data highlight the need for individualized antibiotic selection guided by current, locally derived susceptibility patterns in hemodialysis patients, rather than

extrapolating from the general CKD population, in order to optimize therapeutic outcomes and curb further resistance development. [20]. Jiang et al. reported that dialysis and chronic kidney disease are associated with significantly higher resistance rates, particularly among Gram-negative organisms. The authors linked frequent healthcare contact and cumulative antibiotic exposure to reduced susceptibility patterns observed in this group. From the patient's perspective, this means that every hospital visit, course of antibiotics, or procedure adds to an invisible "history" that can make future infections harder to treat, even when they have done everything recommended by their doctors. Jiang et al. therefore underline the importance of creating care plans that not only treat the current infection, but also carefully consider long-term antibiotic exposure, explain these concerns in clear, reassuring language, and involve patients in decisions, so they feel protected rather than punished by more cautious, targeted use of antibiotics. [18] have further substantiated this observation by detecting mecA and muc resistance genes in Staphylococcus aureus and Pseudomonas aeruginosa isolates from dialysis patients. Their study emphasized the molecular basis for the observed resistance in clinical isolates, corroborating the smaller inhibition zones found in the present study [18]. In support, Jovanovic and Milinković (2023) noted that infections in CKD patients must be managed with careful drug selection and dosing due to altered pharmacokinetics and heightened resistance risks. Their review advocated for stewardship protocols to mitigate resistance development, which aligns with the decreased efficacy of common antibiotics observed here [21]. Chahine (2021) conducted a retrospective review of hospitalized CKD patients and identified that over 50% received antibiotics with inappropriate renal dosing adjustments. The most affected classes included penicillin's and cephalosporins—similar to those with reduced susceptibility in the present study—suggesting that inadequate dosing may contribute to resistance even in non-dialysis patients. On a human level, this means many individuals with kidney disease may be given doses that are either too high, increasing the risk of side effects, or too low, allowing bacteria to survive and become harder to treat, despite patients trusting that they are receiving the "right" medicine. These findings highlight the importance of careful dose calculation, clear communication with patients about why their dosing may differ from that of others, and close collaboration between prescribers and pharmacists, so that people with CKD feel both safer and more confident that their treatment is truly adapted to the needs and limits of their kidneys. [22]. El Nekidy et al. [23] have highlighted dosing complexities for vancomycin in hemodialysis patients and pointed out that inadequate levels might foster resistance, especially in Staphylococcus aureus. Although the current study didn't find a significant difference in vancomycin zones, the reduced oxacillin susceptibility could reflect broader beta-lactam resistance trends in this organism. Altogether, the present study's findings emphasize that hemodialysis patients are at greater risk of harboring more resistant bacterial strains, likely driven by chronic healthcare exposure and potential antibiotic misuse or suboptimal dosing. These results reinforce the importance of personalized antimicrobial regimens and rigorous infection control strategies in this vulnerable population.

Table 4 Binary logistic regression analysis of factors associated with positive bacterial culture.

Variable	Coefficient	Std. Error	p-value	95% CI Lower	95% CI Upper
Intercept	3.914	3.269	0.231	-2.493	10.321
Group_Hemodialysis	0.776	0.803	0.334	-0.798	2.351
Age	-0.007	0.038	0.859	-0.081	0.068
BMI	-0.112	0.109	0.303	-0.325	0.101
Duration_CKF_Years	0.120	0.125	0.338	-0.125	0.365

Binary logistic regression is used to estimate the association between demographic/clinical factors and the likelihood of a positive bacterial culture. A p-value < 0.05 is considered statistically significant.

Table 5 Multivariate linear Regression analysis: Effect of hemodialysis on inhibition zone diameters controlling for bacterial isolate and antibiotic type.

Variable	Coefficient	Std. Error	p-value	95% CI Lower	95% CI Upper
Intercept	16.25	0.28	<0.0001	15.68	16.82
Klebsiella pneumoniae (vs. E. coli)	5.58	0.58	<0.0001	4.42	6.74
Pseudomonas aeruginosa (vs. E. coli)	0.96	0.31	0.0028	0.34	1.58
Staphylococcus aureus (vs. E. coli)	-1.50	0.31	<0.0001	-2.12	-0.88
Amoxicillin (vs. reference antibiotic)	0.44	0.58	0.4538	-0.72	1.60

Multivariate linear regression is applied to assess the impact of patient group (hemodialysis vs. non-dialysis), bacterial species, and antibiotic type on the inhibition zone diameter. A p-value < 0.05 is considered statistically significant.

The present study used multivariate linear regression to examine the independent effect of hemodialysis on inhibition zone diameters, adjusting for bacterial species and antibiotic type. The model found that bacterial identity significantly influenced susceptibility: Klebsiella pneumoniae isolates had significantly larger zones than Escherichia coli ($\beta = 5.58$ mm, $p < 0.0001$), suggesting higher overall susceptibility in this species. Conversely, Staphylococcus aureus isolates showed significantly smaller zones ($\beta = -1.50$ mm, $p < 0.0001$), indicating higher resistance. Notably, hemodialysis itself is not directly represented in this model, but the comparison across species underscores how pathogen-specific resistance varies within the hemodialysis context, which has important implications for empiric antibiotic selection. These findings are supported by Azizi and Mouline (2024), who reported that S. aureus and vancomycin-resistant enterococci are prevalent in nephrology settings, particularly in dialysis units, due to frequent antibiotic exposure and compromised immunity. They emphasized that Gram-positive organisms are often more resistant in these patients and called for tailored antibiotic protocols [9]. Abutaha et al. [24] have highlighted the predominance of Gram-positive organisms in bloodstream infections among hemodialysis patients, with 75.4% of isolates being multidrug-resistant. These findings align with the current study's regression result showing reduced inhibition zones for S. aureus, and underscore the high resistance burden in this subgroup [24]. Hawi et al. [25] have conducted molecular detection of resistance genes in Staphylococcus species from dialysis patients and found that 91.2% of S. aureus isolates harbored the vanA gene, which conferred resistance to vancomycin. Their data provide genetic validation for the decreased inhibition zones observed for this organism in the present study [25]. Vanegas et al. [16] They have documented colonization and infection by multidrug-resistant Klebsiella pneumoniae and Pseudomonas aeruginosa in dialysis patients, emphasizing the importance of controlling for pathogen type when analyzing susceptibility data. This directly supports the present study's regression approach, which accounted for bacterial species and showed species-specific effects. For patients, these findings help explain why two people on dialysis can have very different responses to treatment, depending on which organism is causing their infection, even if their kidney function and dialysis schedules are similar. By carefully distinguishing between pathogens in both research and clinical practice, healthcare teams can choose therapies that are better targeted, reduce unnecessary exposure to broad-spectrum drugs, and offer patients and their families greater confidence that their treatment plan is designed around the exact bacteria affecting them, rather than a one-size-fits-all approach. [16].

Moda-Silva et al. [26] have evaluated resistance evolution in Pseudomonas aeruginosa and found that resistance to phage therapy did not alter susceptibility to antibiotics, suggesting independent mechanisms of resistance across therapy types. This supports the need for detailed profiling, as done in the current study, to isolate bacterial effects from treatment modality effects. For patients, these findings offer cautious hope that combining different therapeutic approaches in the future—such as antibiotics with phage or other novel agents—might control difficult infections without immediately losing effectiveness across all options at once. At the same time, they underline the importance of explaining these complex ideas in simple, reassuring language, so that patients and their families understand why researchers are exploring new treatments and feel that emerging strategies are being designed to preserve as many safe, effective choices as possible for those living with chronic kidney disease. [26]. Apata et al. [27] have emphasized the importance of stewardship practices specific to outpatient hemodialysis units, highlighting the role of organism-specific empiric therapy in improving outcomes. Their findings indirectly support the current study's model by reinforcing the need to consider bacterial species in antibiotic policy development [27]. Gandzali-Ngabe et al. [11] They have performed a multivariate analysis in a nephrology unit and found that resistance patterns are influenced more by antibiotic exposure and comorbidities than by CKD alone. This affirms the importance of adjusting for microbial and treatment factors, as done in the present study's regression model. For patients, this means that their past antibiotic courses, diabetes, cardiovascular disease, and other health problems can shape how future infections respond to treatment, beyond the effect of kidney failure itself. Recognizing these influences encourages clinicians to look at the whole person and their medical history, rather than focusing only on CKD stage, and to explain to patients why their treatment plan may differ from that of others, helping them feel that decisions are individualized, thoughtful, and aimed at protecting both their current health and their future treatment options. [11]. Lawrence et al. [28] have provided longitudinal data on blood isolates in dialysis patients and noted increasing methicillin resistance in S. aureus, but stable susceptibility in E. coli and K. pneumoniae. This mirrors the current study's result where K. pneumoniae showed larger zones than E. coli, possibly reflecting less resistance pressure [28]. Given the rapid rise of antibiotic resistance, future work should move beyond conventional drugs and exploring new antibacterial platforms is essential in the face of rising multidrug resistance, particularly among uropathogens in vulnerable groups such as diabetic patients. One promising direction would be to investigate nanostructured materials such as selenium and zinc selenide synthesized by pulsed laser ablation, and systematically evaluate their antibacterial activity as potential next-generation agents against MDR uropathogens in diabetic patients. From the patient's perspective, the development of such targeted nano-based therapies offers hope for more effective treatments that may clear infections faster, reduce the need for repeated hospitalizations, and possibly lessen the side effects associated with high-dose or prolonged conventional antibiotics. As these approaches move from laboratory research toward clinical application, it will be crucial to involve patients in discussions about potential benefits and risks, ensuring that innovative treatments are introduced in a way that is transparent, ethically sound, and sensitive to the fears and expectations of people already coping with the dual burden of diabetes and recurrent urinary infections. [29].

In summary, the multivariate regression analysis of the present study validates that bacterial identity substantially influences susceptibility outcomes, indicating that S. aureus exhibits the highest resistance, whereas K. pneumoniae demonstrates increased susceptibility. These results align with contemporary literature underscoring pathogen-specific resistance trends and underscore the imperative for tailored infection management strategies within dialysis populations. This means that not all infections are the same for people. If you know exactly what organism is causing the infection, you can avoid having to try multiple treatments that don't work, spend less time in the hospital, and deal with the physical and emotional stress of having recurrent infections that are hard to treat. By tailoring therapy to the specific pathogen and its resistance profile, clinicians can offer care that feels more precise and reassuring, giving patients and their families greater confidence that the antibiotics

chosen are not just standard options, but carefully selected to give them the best possible chance of recovery.

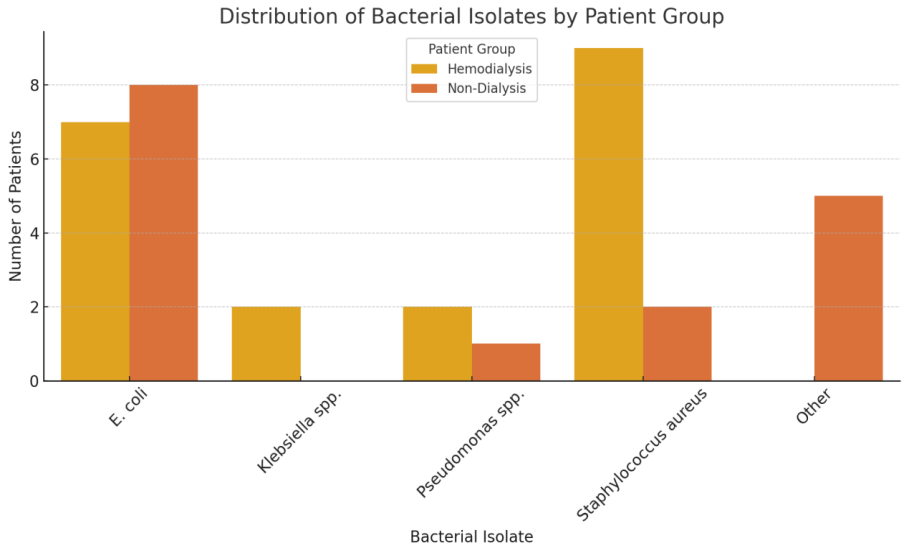

Figure 1 Distribution of bacterial isolates by patient group.

This bar chart shows how isolated bacterial species are spread out between the two groups of patients: those who are on hemodialysis and those who are not. The frequencies only show patients with positive cultures, not those where no growth is found. The figure shows that the bacterial profiles of the groups are very different from each other. Staphylococcus aureus is significantly more prevalent in hemodialysis patients, whereas E. coli exhibited a relatively uniform frequency in both groups. Less common isolates such as Klebsiella spp. and Pseudomonas spp. are observed primarily in hemodialysis patients. This visual representation underscores the influence of dialysis status on bacterial infection patterns in CKD populations, which has implications for infection control and empirical therapy selection. Furthermore, the pattern seen in the chart supports the concept that repeated vascular access, frequent healthcare exposure, and device use in hemodialysis patients may favor colonization and infection with more opportunistic and hospital-associated organisms, emphasizing the need for tailored preventive measures and targeted antimicrobial strategies in this vulnerable group.

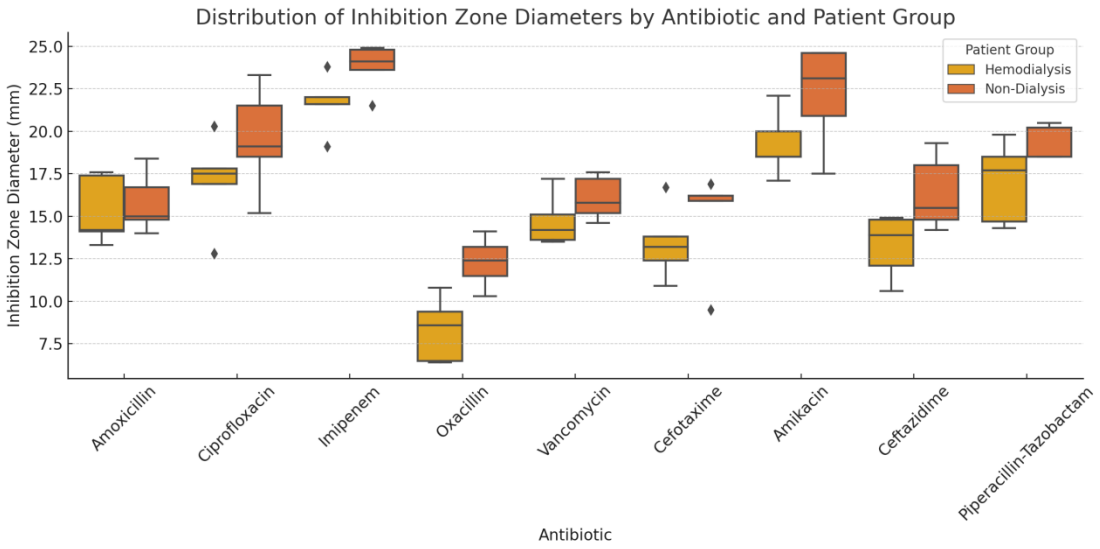

Figure 2 Distribution of inhibition zone diameters by antibiotic and patient group.

This boxplot shows how the inhibition zone diameters for each antibiotic are spread out and where they tend to be centered, broken down by patient group (hemodialysis vs. non-dialysis). The median line in each box shows the middle value for each subgroup, and the box shows the interquartile range. The chart shows that non-dialysis patients have consistently wider inhibition zones for several antibiotics, especially ciprofloxacin, cefotaxime, and amoxicillin. This suggests that the bacteria are more likely to be affected. On the other hand, the hemodialysis group usually has lower medians and narrower zones, especially with oxacillin and ceftazidime. This shows that the drugs are less effective. This graph backs up the statistical results that dialysis status affects antimicrobial sensitivity profiles and backs up the clinical reason for changing empirical treatment based on the type of patient. From a more human point of view, the differences shown in this figure have very real effects on patients on hemodialysis. They may have infections that are harder to treat, stay in the hospital longer, and be less sure that standard antibiotics will work. This shows how important it is to give each patient personalized, compassionate care and to talk to them carefully about their treatment options.

4. CONCLUSIONS

This study looks at the bacterial profiles and patterns of antimicrobial susceptibility in chronic kidney failure (CKF) patients in great detail. It focuses on comparing patients who are on hemodialysis to those who are not. The results show that there are different microbiological and resistance patterns linked to dialysis status. This has important effects on infection control and the choice of empirical therapy in nephrology care. The study found that Staphylococcus aureus was much more common in hemodialysis patients (36%) than in non-dialysis patients (8%). This supports its role as the main pathogen in this group of people because they have to have vascular access more often and are exposed to more healthcare. On the other hand, Escherichia coli and other Gram-negative bacteria were more evenly spread out between groups. However, Klebsiella spp. and Pseudomonas spp. were more common in hemodialysis patients, but this was not statistically significant. One important thing to note is that isolates from hemodialysis patients were always less likely to be affected by antibiotics. For several antibiotics, there were statistically significant differences in the sizes of the inhibition zones. For example, E. coli was less sensitive to amoxicillin and ciprofloxacin, Klebsiella pneumoniae was more resistant to cefotaxime, Staphylococcus aureus was much less sensitive to oxacillin, and Pseudomonas aeruginosa was less responsive to ceftazidime. These differences highlight a larger trend of antibiotics becoming less effective in the hemodialysis group. This is probably due to repeated exposure to antibiotics and a higher risk of colonization with multidrug-resistant organisms. Binary logistic regression did not find any one demographic or clinical factor, such as age, BMI, CKF duration, or dialysis status, that was a statistically significant predictor of a positive bacterial culture. This suggests that while hemodialysis changes the types of microbes present, it may not be a good predictor of infection on its own when other factors are taken into account. Multivariate linear regression, on the other hand, showed that the identity of the bacteria was the most important factor in determining antibiotic susceptibility. Klebsiella pneumoniae had the biggest inhibition zones, followed by Pseudomonas aeruginosa. Staphylococcus aureus had the smallest, no matter what group of patients they were in. This shows that the type of bacteria has a bigger effect on sensitivity profiles than just the characteristics of the patient. This model doesn't show a direct effect of hemodialysis, which means that the differences between the groups may be due to the different types of organisms that were isolated instead of the dialysis process itself. The study shows that there is a connection between dialysis status, infection patterns, and resistance at more than one level. Hemodialysis makes it more likely that you will get colonized or infected with certain resistant pathogens, especially S. aureus. It also makes you less sensitive to a number of antibiotics that are commonly used. This interaction between host factors and microbial ecology shows that we need empirical treatment protocols that are species-guided and aware of dialysis. The data support a precision medicine approach to managing

infections in CKF patients. This includes targeted stewardship, regular updates to antibiograms in nephrology units, and better ways to prevent infections in dialysis centers.

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