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# Profile of Bacteria Isolated from Patients and Surfaces in the Hemodialysis Unit of Douala General Hospital: An Analysis of 411 Samples

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## Abstract

**Background:** Hemodialysis units are particularly exposed to nosocomial infections: bacteria originating from patients, healthcare workers, or surfaces can be transmitted from one station to another, leading to severe bloodstream infections. The objective of our study was to identify the bacteria isolated from samples collected from patients and surfaces in the hemodialysis unit of Douala General Hospital. **Methods:** We conducted a descriptive cross-sectional study within the unit, during which 411 samples were collected from patients and service surfaces. The microorganisms were identified using classical bacteriological methods (direct examination, culture) and the VITEK automated system (bioMérieux). Data were analyzed using R software. **Results:** Of the 411 samples analyzed, 257 were collected from surfaces within the unit, with 98.8% testing positive, while 154 of the 163 patient samples revealed bacterial growth. Door handles were the main sampling sites (34%), followed by tables, bed feet, and headboards. Overall, 577 bacterial isolates were identified: surfaces were heavily contaminated (470 isolates), dominated by *Burkholderia cepacia* (64.8% overall, including 50.8% of surface isolates) and environmental Gram-positive cocci such as *Staphylococcus cohnii* and *S. xylosus*. Among patient samples, fermentative Gram-negative bacilli (*Escherichia coli, Klebsiella pneumoniae, Proteus mirabilis*) predominated in urine and blood cultures, while Pseudomonas aeruginosa and Acinetobacter baumannii remained major pathogens in bloodstream infections. *Staphylococcus aureus* was isolated from both patients and surfaces. **Conclusion:** Our results highlight a high level of surface contamination and a wide diversity of pathogens among patients in the hemodialysis unit of Douala General Hospital.

**Keywords**

Hemodialysis Unit, Bacterial Profile, Surface Contamination, Nosocomial Infections, Douala

## 1. Introduction

Bacteria are unicellular microorganisms lacking a true nucleus; they reproduce by binary fission, colonize virtually all ecosystems, and can become significant human pathogens [1]. Healthcare-associated infections (HAIs) remain a major burden worldwide: according to the WHO's Global Report on Infection Prevention and Control (2024), millions of patients contract an HAI daily, which prolongs hospital stays, increases healthcare costs, and contributes to antimicrobial resistance. The burden is particularly severe in low- and middle-income countries such as Cameroon, where patients are up to twenty times more likely to acquire such infections compared to high-income countries [2].

Hemodialysis units are especially vulnerable to HAIs due to the frequent use of invasive procedures and direct blood access. A multicenter study across nine hemodialysis centers reported 1.98 infectious events per 100 patient-months, with Staphylococcus aureus bloodstream infections being the most common [3]. Outbreaks linked to contaminated water or dialysate by Gram-negative bacilli are still being reported, underlining the critical importance of environmental hygiene and water quality [4]. In Nigeria, all water outlets sampled from three hemodialysis centers were contaminated with *Pseudomonas* spp. or *Moraxella* spp. [5]. Similarly, a South African cohort found that 23.9% of hemodialysis patients were colonized by multidrug-resistant organisms, particularly extended-spectrum β-lactamase-producing *Klebsiella pneumoniae* [6].

In Cameroon, and specifically in Douala, the situation is equally alarming. At the Douala General Hospital, infections at vascular access sites have been associated with a near doubling of mortality rates among patients with chronic kidney disease [7]. Despite this significant risk, published data on the microbiological profile of hemodialysis units in the region remain scarce. A recent study in Rwanda also highlighted the high incidence of catheter-related bloodstream infections, mostly caused by Gram-negative bacilli [8]. These findings reinforce the urgent need for strict adherence to international standards such as ISO 23500-1:2024, which defines microbiological requirements for the quality of water and dialysate in hemodialysis systems [9].

In this context, our study aims to bridge the global awareness of HAIs with the localized reality of Douala, by identifying the bacteria isolated from 411 samples collected within the hemodialysis unit of Douala General Hospital. The results will contribute to building a reference framework for ongoing microbiological surveillance and inform targeted infection prevention and control strategies tailored to our local setting.

## 2. Materials and Methods

### 2.1. Study Type, Period, and Population

We conducted a cross-sectional analytical study over four months, from March 8 to June 31, 2023. The study included all frequently used work surfaces and hemodialysis patients hospitalized or attending consultations or appointments during this period. Inclusion criteria involved frequently used work surfaces and hemodialysis patients with bacteriologically confirmed infections based on laboratory examinations such as urine cultures, blood cultures, or catheter tip analyses. Exclusion criteria were infrequently or unused surfaces, patients without signed informed consent, and those with non-bacterial or undocumented infections.

### 2.2. Sample Collection and Preparation

Samples were collected following a standardized protocol: surfaces were swabbed within a sterile 10 × 10 cm template using a dacron swab pre-moistened with saline, tracing horizontal-vertical “S” strokes then a diagonal pass, both before and 15 min after disinfection with a quaternary-ammonium/polyhexanide detergent-disinfectant (5-min contact time). Swabs were placed in Amies transport medium, kept at 4˚C, and plated within 4 h. Blood cultures were drawn aseptically before connection to the dialyzer, urine collected in sterile containers, catheter tips rolled on blood agar (Maki method), and ascitic fluid obtained by sterile puncture; all specimens were transported at 4˚C (blood cultures at controlled room temperature) and cultured for 24 - 48 h on blood, EMB, Chapman, CLED, or enriched chocolate agar as appropriate. Identification and susceptibility testing were performed with the VITEK 2 system using GN, GP, or NH cards and AST-N/AST-P panels, interpreted per EUCAST 2024, with weekly quality control using ATCC reference strains.

### 2.3. Bacterial Identification Using VITEK

Identification with VITEK was performed by preparing an inoculum from a selected bacterial colony emulsified in 3000 µL of saline in a hemolysis tube. The suspension was standardized to a density equivalent to 0.5 McFarland scale using a densitometer. Specific VITEK cards, chosen based on Gram staining affinity, were inserted into the inoculum and scanned into the machine using barcode recognition. After validation, cards were loaded into the machine for analysis. Electronic bacterial identification was completed within 4 - 5 hours, after which results were automatically generated.

### 2.4. Statistical Analysis

Data were entered into an Excel spreadsheet (Microsoft Office, USA) and imported into R software version 4.4.2 for Windows Professional. Categorical variables were presented as frequencies (N, n) and percentages (%) in tables and graphs.

## 3. Results

### 3.1. Distribution of Samples Collected and Their Analysis Results

The figure illustrates the distribution of the 411 samples collected: 257 from service surfaces (with 254 positive samples and 3 sterile) and 163 from patients. Among the patient samples, 68 were urine samples, 16 catheter tips, 4 urinary catheter tips (all positive for bacteria), 9 ascitic fluid samples, and 43 blood cultures, with 23 declared negative or sterile (Figure 1).

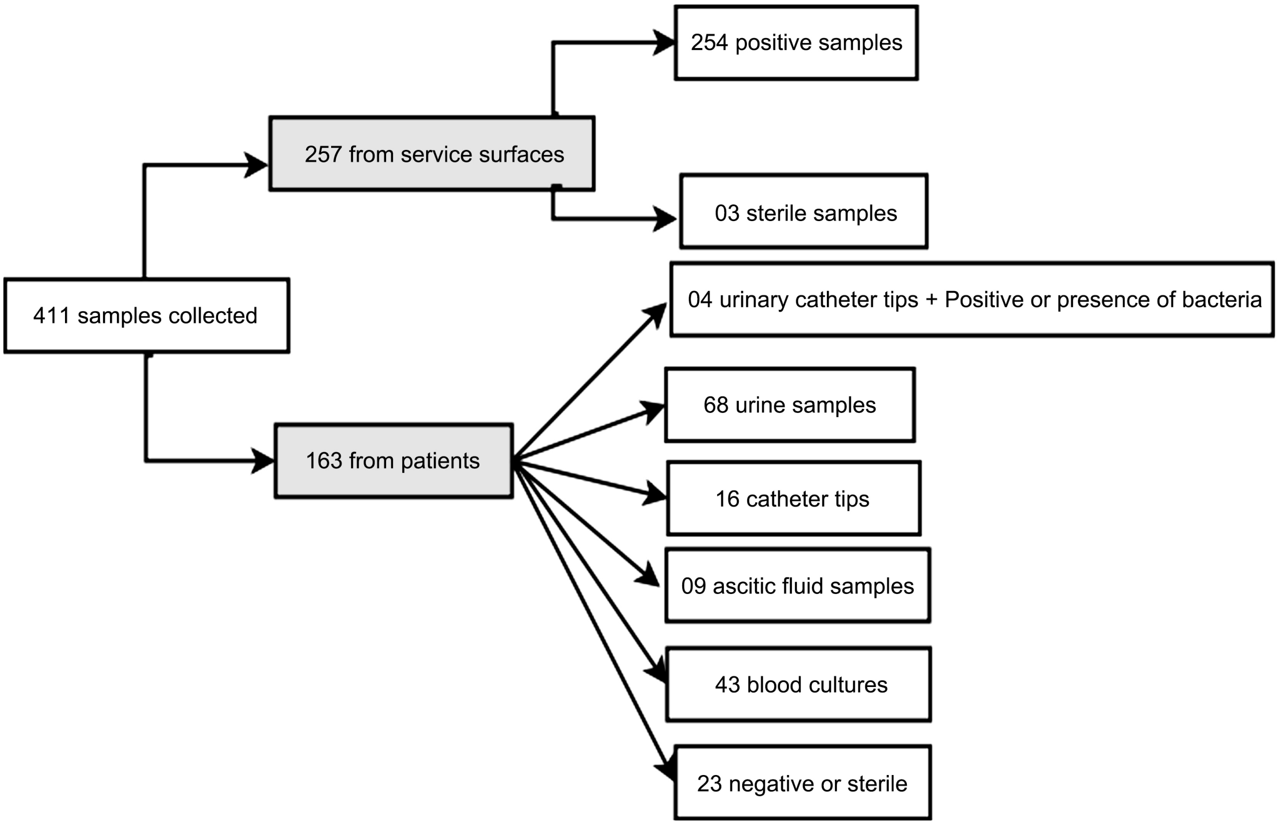

Figure 1. Distribution of samples collected and their analysis results.

### 3.2. Percentage Distribution of Surface Sampling Sites

Figure 2 shows the percentage distribution of surface sampling sites within our unit. Door handles (34%) were the most frequently sampled site, followed by tables (8.9%), bed footboards (8.1%), and bed headboards (8.1%). Other sites included remote controls (7.3%), dialysis machines (7.3%), and beds (5.7%), while less frequently sampled areas such as cabinets, weighing scales, and faucets each represented proportions below 5% (Figure 2).

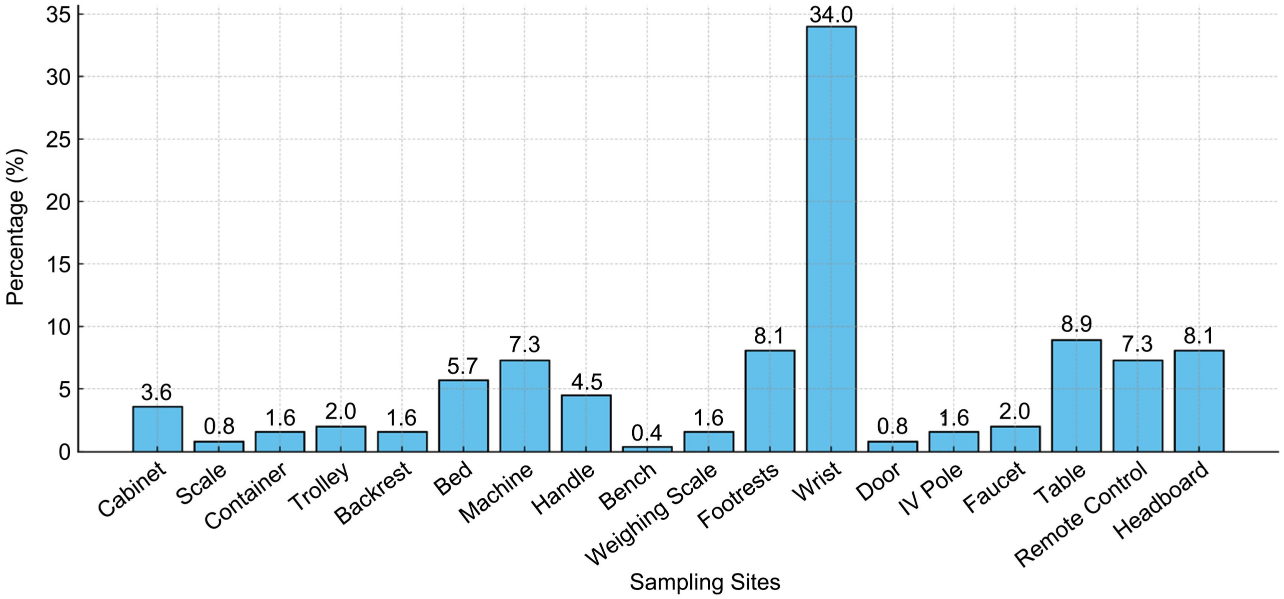

**Figure 2.** Percentage of surface sampling sites.

## 3.3. Distribution and Analysis of Bacterial Isolates from Patients and Hospital Surfaces

**Table 1** presents the distribution of bacterial isolates collected from patient samples and service surfaces. Among fermentative Gram-negative bacteria, *Escherichia coli* (11.2%), *Klebsiella pneumoniae* (13.1%), and *Proteus mirabilis* (4.67%) were predominantly isolated from patient samples. In contrast, some species such as *Klebsiella oxytoca* (1.49%) and *Serratia rubidaea* (0.58%) were exclusively found on surfaces. These findings highlight a difference in the distribution of bacterial species between patients and the environment.

**Table 1.** Bacterial profile in patients and sampled surfaces.

| Germs | Patients *n (%)* | Surfaces *n (%)* | Total *N (%)* |
|---|---|---|---|
| **Gram-Negative Fermentative Bacteria** | | | |
| *Escherichia coli* | 12 (11.2) | 0 | 12 (11.2) |
| *Klebsiella pneumoniae* | 14 (13.1) | 0 | 14 (13.1) |
| *Klebsiella oxytoca* | 0 | 7 (1.49) | 7 (1.49) |
| *Raoultella planticola* | 2 (1.86) | 0 | 2 (1.86) |
| *Enterobacter cloacae* | 6 (5.60) | 0 | 6 (5.60) |
| *Enterobacter aerogenes* | 3 (2.80) | 0 | 3 (2.80) |
| *Streptococcus pneumoniae* | 1 (0.93) | 0 | 1 (0.93) |
| *Salmonella group* | 1 (0.93) | 0 | 1 (0.93) |
| *Proteus mirabilis* | 5 (4.67) | 0 | 5 (4.67) |

**Continued**

| | | | |
|---|---|---|---|
| *Serratia odorifera* | 3 (2.80) | 0 | 3 (2.80) |
| *Serratia liquefaciens* | 2 (1.86) | 0 | 2 (1.86) |
| *Serratia rubidaea* | 0 | 8 (0.58) | 8 (0.58) |
| *Serratia marcescens* | 1 (0.93) | 0 | 1 (0.93) |
| *Pantoea spp* | 2 (1.86) | 0 | 2 (1.86) |
| *Stenotrophomonas maltophilia* | 3 (2.80) | 0 | 3 (2.80) |
| **Gram-Negative Non-Fermentative Bacteria** | | | |
| *Burkholderia cepacia* | 15 (14.01) | 239 (50.8) | 254 (64.8) |
| *Pseudomonas aeruginosa* | 4 (2.35) | 5 (1.06) | 9 (3.41) |
| *Acinetobacter baumannii* | 7 (6.54) | 0 | 7 (6.54) |
| **Gram-Positive Cocci** | | | |
| *Staphylococcus aureus* | 11 (10.3) | 5 (1.1) | 17 (11.4) |
| *Staphylococcus haemolyticus* | 7 (6.6) | 0 | 7 (6.6) |
| *Staphylococcus hominis* | 4 (3.74) | 0 | 4 (3.74) |
| *Staphylococcus cohnii* | 0 | 106 (22.5) | 106 (22.5) |
| *Staphylococcus sciuri* | 0 | 11 (2.34) | 11 (2.34) |
| *Staphylococcus xylosus* | 0 | 89 (18.9) | 89 (18.9) |
| *Kocuria rhizophila* | 4 (3.73) | 0 | 4 (3.73) |
| **Total** | **107** | **470** | **557** |

Regarding non-fermentative Gram-negative bacteria, *Burkholderia cepacia* was the dominant pathogen, accounting for 14.01% of isolates from patients and 50.8% from surfaces, representing a total of 64.8%. Pseudomonas aeruginosa (3.41%) and Acinetobacter baumannii (6.54%) were mainly identified in patient samples, underlining their significance in clinical infections.

As for Gram-positive cocci, *Staphylococcus aureus* (11.4%) was present in both patient samples (10.3%) and surface samples (1.1%). Other species, such as *Staphylococcus cohnii* (22.5%), *Staphylococcus xylosus* (18.9%), and *Staphylococcus sciuri* (2.34%), were isolated exclusively from surfaces. Conversely, bacteria such as *Staphylococcus haemolyticus* (6.6%) and *Kocuria rhizophila* (3.73%) were found exclusively in patient samples (Table 1).

### 3.4. Distribution and Analysis of Bacteria Isolated According to Different Types of Samples

Table 2 presents the distribution of the 577 bacterial isolates analyzed from various types of samples, including blood cultures, urine samples, ascitic fluids, urinary catheter tips, surfaces, and catheter tips. Among the bacteria identified, the most frequent species included *Burkholderia cepacia* (254 isolates, of which 239 were from surfaces and 8 from blood cultures), *Staphylococcus cohnii* (106 isolates, exclusively from surfaces), and *Staphylococcus xylosus* (89 isolates, also from surfaces). *Escherichia coli* (12 isolates) and *Klebsiella pneumoniae* (14 isolates) were mainly found in urine and blood cultures.

**Table 2.** Bacterial profile according to the different types of samples.

| Bacteria | Blood Culture *(n)* | Urine *(n)* | Ascitic Fluid *(n)* | Urinary Catheter Tips *(n)* | Surfaces *(n)* | Catheter Tips *(n)* | Total *(N)* |
|---|---|---|---|---|---|---|---|
| *E. coli* | 2 | 8 | 1 | 1 | 0 | 0 | 12 |
| *Klebsiella pneumoniae* | 8 | 5 | 0 | 0 | 0 | 1 | 14 |
| *Klebsiella oxytoca* | 0 | 0 | 0 | 0 | 7 | 0 | 7 |
| *Staphylococcus aureus* | 3 | 7 | 0 | 0 | 5 | 1 | 16 |
| *Staphylococcus haemolyticus* | 4 | 3 | 0 | 0 | 0 | 0 | 7 |
| *Staphylococcus hominis* | 1 | 3 | 0 | 0 | 0 | 0 | 4 |
| *Staphylococcus cohnii* | 0 | 0 | 0 | 0 | 106 | 0 | 106 |
| *Staphylococcus sciuri* | 0 | 0 | 0 | 0 | 11 | 0 | 11 |
| *Staphylococcus xylosus* | 0 | 0 | 0 | 0 | 89 | 0 | 89 |
| *Burkholderia cepacia* | 8 | 4 | 0 | 0 | 239 | 3 | 254 |
| *Kocuria rhizophila* | 0 | 4 | 0 | 0 | 0 | 0 | 4 |
| *Raoultella planticola* | 0 | 2 | 0 | 0 | 0 | 0 | 2 |
| *Pseudomonas aeruginosa* | 0 | 0 | 0 | 0 | 5 | 4 | 9 |
| *Acinetobacter baumannii* | 5 | 0 | 0 | 1 | 0 | 1 | 7 |
| *Enterobacter cloacae* | 0 | 6 | 0 | 0 | 0 | 0 | 6 |
| *Stenotrophomonas maltophilia* | 0 | 3 | 0 | 0 | 0 | 0 | 3 |
| *Salmonella group* | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| *Proteus mirabilis* | 4 | 0 | 0 | 1 | 0 | 0 | 5 |
| *Pantoea spp* | 2 | 0 | 0 | 0 | 0 | 0 | 2 |
| *Serratia odorifera* | 0 | 3 | 0 | 0 | 0 | 0 | 3 |
| *Serratia liquefaciens* | 0 | 2 | 0 | 0 | 0 | 0 | 2 |
| *Serratia rubidaea* | 0 | 0 | 0 | 0 | 8 | 0 | 8 |
| *Serratia marcescens* | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| *Enterobacter aerogenes* | 1 | 2 | 0 | 0 | 0 | 0 | 3 |
| *Streptococcus pneumoniae* | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| **Total** | **40** | **52** | **1** | **3** | **470** | **11** | **577** |

Surfaces appeared to be a major source of contamination, accounting for a total of 470 isolates, while human samples represented a smaller proportion but included clinically significant pathogens such as Staphylococcus aureus (16 isolates) and Pseudomonas aeruginosa (9 isolates). These results highlight a high level of surface contamination and a diversity of isolated pathogens, emphasizing the need for strengthened infection control measures (**Table 2**).

## 4. Discussion

Our results confirm that the hemodialysis unit represents a highly conducive environment for the transmission of opportunistic microorganisms. The surface positivity rate of 98.8% exceeded proportions reported in other dialysis or hospital isolation settings, where frequently touched surfaces (door handles, tables, bed headboards) are recognized as major vectors of healthcare-associated infections [10] [11].

The predominance of *Burkholderia cepacia* (64.8 % of all isolates) is particularly alarming. Members of the *Burkholderia cepacia* complex are non-fermenting Gram-negative bacilli able to form chlorine- and quaternary-ammonium-resistant biofilms, and have repeatedly caused dialysis-related outbreaks through contamination of reverse-osmosis (RO) water, dialysate loops, dressings, or catheter exit sites [12] [13]. Their massive and repeated recovery from benches, machine consoles, and drain ports in our unit suggests 1) a persistent reservoir within the hydraulic circuit or carbon filters, and/or 2) cross-transmission via staff hands or inadequately disinfected shared equipment (blood-pressure cuffs, stethoscopes). To determine whether this reflects a single clonal strain or successive introductions, we plan to genotype representative isolates by recA sequencing or multilocus sequence typing (MLST)—and, if resources permit, whole-genome sequencing—while comparing them with isolates from water, dialysate, and any clinical infections. These data will guide targeted remediation measures such as shock disinfection or replacement of suspect pipework, reinforcement of hand-hygiene compliance, and stricter reprocessing of reusable accessories.

Among patients, the high frequency of fermentative Gram-negative bacilli—*Escherichia coli*, *Klebsiella pneumoniae*, and *Proteus mirabilis*—isolated from urine and blood cultures is consistent with observations from multicenter studies, where *K. pneumoniae* was the most common agent of hemodialysis-associated bloodstream infections [14] [15]. The concomitant isolation of Pseudomonas aeruginosa and Acinetobacter baumannii highlights the risk of infections with multidrug-resistant non-fermentative bacilli in this immunocompromised population.

The simultaneous detection of Staphylococcus aureus among patients and on surfaces suggests potential cross-transmission between skin colonization and environmental contamination, whereas coagulase-negative staphylococci (*S. cohnii, S. xylosus*) were almost exclusively environmental, reflecting their strong affinity for inert surface biofilms.

These findings call for strengthened prevention strategies: systematic disinfection of high-touch surfaces, regular audits of water and dialysate quality, active screening of patients colonized by *Burkholderia cepacia* or *S. aureus*, and a re-evaluation of cleaning protocols according to CDC guidelines for specialized units, including dialysis facilities [16]. Implementing continuous microbiological surveillance would allow for early detection of contamination and adjustment of control measures to reduce infectious burden and improve patient safety. In summary, the high level of contamination by *Burkholderia cepacia* and other non-fermenting Gram-negative bacilli requires, within the dialysis unit, the implementation of weekly environmental monitoring of water, dialysate, and critical surfaces, a revision of disinfection protocols using agents active against biofilms, and systematic antibiotic susceptibility testing to guide therapy and feed a national resistance registry. At the public-health level, these findings argue for the formal integration of dialysis centers into Cameroon's national infection prevention program, the creation of a sentinel laboratory network capable of genotyping epidemic strains, and the development of Cameroonian guidelines on water quality, invasive-device management, and maintenance of hydraulic circuits, with the ultimate goal of sustainably improving the safety of patients with renal failure.

## 5. Conclusion

The hemodialysis unit showed extensive contamination: almost all surfaces and the majority of patient samples harbored bacteria, dominated by *Burkholderia cepacia* in the environment and by fermentative Gram-negative bacilli (notably *E. coli and K. pneumoniae*) in patients, while Staphylococcus aureus circulated between the two. These findings highlight a high risk of cross-transmission and bloodstream infections, emphasizing the urgent need to strengthen targeted disinfection practices, microbiological surveillance, and staff training to reduce the infectious burden and prevent the emergence of resistant strains.

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## Ethical Approval and Consent to Participate

The study received administrative authorisation and ethical approval from the General Hospital of Douala. Written informed consent to participate in this study was provided by the legal guardians/next of kin of the participants.

## Availability of Data and Equipment

The original data supporting the conclusions of this article will be made available by the authors without undue reservation.

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The authors state that the research was conducted in the absence of any external funding.

## Authors' Contributions

ENLPJ designed the experimental approach and the writing plan. ENLPJ and NNE recruited the participants and conducted the laboratory analyses. ENLPJ performed the statistical analysis and prepared all the figures. ENLPJ drafted the manuscript. ENLPJ, NNA, and FMEHD reviewed the manuscript. All the authors made substantial, direct, and intellectual contributions to the work and approved it for publication.

## Conflicts of Interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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