

Bacterial Ecology and Antimicrobial Resistance Patterns in the Chemotherapy Ward of CNRAO, Côte d'Ivoire: A Sub-Saharan Experience

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Abstract Background: Cancer patients receiving chemotherapy are highly vulnerable to environmental infections due to treatment-induced immunosuppression, yet bacterial contamination and antibiotic resistance patterns in African oncology facilities remain uncharacterized. We conducted a comprehensive environmental surveillance of a West African chemotherapy unit to identify infection risks threatening these vulnerable patients. **Methods:** We collected 39 environmental samples (36 surfaces, 3 air) from high-touch sites across the chemotherapy unit at Centre National de Radiothérapie et d'Oncologie Médicale Alassane Ouattara (August-October 2024). Bacterial isolates underwent identification using conventional methods and API systems, with antimicrobial susceptibility testing by Kirby-Bauer disk diffusion under EUCAST 2023 guidelines. Extended-spectrum β -lactamase (ESBL) production was confirmed by double-disk synergy testing. **Results:** Surface contamination occurred in 63.9% of samples; air remained sterile. Twenty-nine isolates recovered: *Bacillus* spp. (34.5%), coagulase-negative staphylococci (27.6%), *Pseudomonas aeruginosa* (20.7%), Enterobacteriaceae (17.2%). Water sources harbored *Pseudomonas* and ESBL-producers. Resistance was substantial: 40% Enterobacteriaceae produced ESBLs with fluoroquinolone co-resistance, 14.3% coagulase-negative staphylococci exhibited methicillin/aminoglycoside resistance, all *P. aeruginosa* (6/6) showed intermediate colistin susceptibility. *Bacillus* demonstrated aminopenicillin resistance but carbapenem susceptibility. No carbapenemase-producers detected. **Conclusions:** This chemotherapy unit surveillance reveals concerning environmental contamination with resistant opportunistic pathogens. *Bacillus* predominance and water-associated *Pseudomonas*/ESBL-Enterobacteriaceae colonization highlight unique tropical ecology patterns. Enhanced cleaning protocols, water system management, and antimicrobial stewardship adapted to local resistance are urgently needed. These baseline data inform infection prevention programs protecting vulnerable African cancer patients.

Keywords: Antimicrobial resistance, Environmental surveillance, Healthcare-associated infections, Sub-Saharan Africa, Côte d'Ivoire

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1. Introduction

Healthcare-associated infections present a persistent threat to hospitalized patients worldwide, with particularly devastating consequences in vulnerable populations such as cancer patients undergoing chemotherapy. While wealthy nations report infection rates around 4-5%, resource-limited countries in Africa, Latin America, and Asia face substantially higher burdens reaching 14-18%

[1,2]. These stark disparities reflect not only differences in healthcare infrastructure but also gaps in infection surveillance systems and prevention resources that leave the world's most vulnerable patients inadequately protected.

Within hospitals, the physical environment including bed rails, medical equipment, sinks, and frequently touched surfaces serves as an often-overlooked reservoir for disease-causing bacteria. These environmental niches harbor diverse microbial communities originating from patients, healthcare workers, and visitors, creating complex transmission networks [3]. Though debate

continues regarding the precise role of environmental contamination in causing infections, mounting evidence demonstrates that hospital surfaces act as important stepping stones in spreading dangerous drug-resistant organisms like methicillin-resistant *Staphylococcus aureus* (MRSA) [4,5]. The microbial composition of healthcare facilities fluctuates based on patient populations served, medical procedures performed, antibiotic usage patterns, and cleaning practices employed [6,7]. For patients with weakened immune systems particularly those receiving chemotherapy these environmental bacteria pose extraordinary risks, as even organisms typically considered harmless can cause life-threatening infections when the body's defenses are compromised. Chemotherapy drugs, while targeting cancer cells, simultaneously devastate the immune system [8]. Extended hospitalizations during neutropenic episodes provide ample opportunity for patients to acquire hospital-adapted organisms that have evolved resistance to multiple antibiotics. Despite extensive research examining environmental microbiology in intensive care units, surgical suites, and other high-risk hospital areas [9,10], a critical knowledge gap exists regarding bacterial contamination in oncology chemotherapy units, especially across sub-Saharan Africa. This vast region confronts unique challenges that amplify infection risks [11,12].

The Centre National de Radiothérapie et d'Oncologie Médicale Alassane Ouattara (CNRAO) in Abidjan, Côte d'Ivoire, serves as the country's premier cancer treatment facility, delivering life-saving chemotherapy to patients from across the nation. Very few studies have mapped out the bacteria present and antibiotic resistance patterns in chemotherapy units across West Africa. Our study addresses this major gap by offering a clear microbiological snapshot of an oncology chemotherapy department in sub-Saharan Africa.

This study aimed to (i) characterize bacterial contamination patterns in a chemotherapy unit, (ii) identify species distribution, and (iii) assess antimicrobial resistance profiles of recovered isolates.

2. Methodology

2.1. Study Design and Setting

A cross-sectional environmental surveillance study was conducted from August 15 to October 15, 2024, at the chemotherapy unit of Centre National de Radiothérapie et d'Oncologie Médicale Alassane Ouattara (CNRAO), Abidjan, Côte d'Ivoire. The unit comprises eight infusion bays, individual patient rooms, a treatment room, and physician offices, serving approximately 120 immunocompromised patients monthly.

2.2. Sample Collection

Environmental sampling targeted high-touch surfaces and air quality across four zones: (i) individual patient rooms (n=7 sites: bedside table, bed rail, door handle, mattress, infusion pole, sink, air intake), (ii) infusion bays (n=11 sites: bed rail, lighting fixture, mattress, curtain, sink, infusion pole, oxygen device, medication cart, door

handle, air intake, waste area), (iii) treatment room (n=5 sites: examination bed, mattress, sink, infusion pole, medication cart), and (iv) physician office (n=3 sites: patient chair, door handle, sink). We conducted a one-time cross-sectional survey between chemotherapy sessions to capture a realistic "snapshot" of contamination levels across the high-touch surfaces and air zones. This design is efficient and resource-friendly, allowing us to assess environmental risk without disrupting clinical operations. Regular surface cleaning activities were carried out in the morning before the service opened and after closing. Samples were therefore not taken immediately after the morning cleaning.

Surface samples were collected using sterile cotton swabs pre-moistened with physiological saline, employing the double-swab technique with parallel then perpendicular strokes (23). The areas of the surfaces sampled were standardised to an average of 26 cm². Air sampling utilized passive settle plates (nutrient agar exposed for 20 minutes at 1.2-1.5 m height). Samples were transported to the laboratory within 30 minutes.

2.3. Microbiological Analysis

Swabs underwent enrichment in brain-heart infusion broth at 37°C for 24-48 hours. Enrichment cultures were streaked onto selective media: nutrient agar (total counts), EMB agar (Gram-negatives), Hektoen enteric agar (enteric pathogens), blood agar (fastidious organisms), cefrimide agar (*Pseudomonas*), bile-esculin azide agar (*Enterococcus*), and mannitol salt agar (staphylococci). Plates were incubated at 37°C for 24-72 hours. Pure isolates were obtained by iterative subculture using four-quadrant streaking.

Bacterial identification employed standard methods: Gram staining, catalase and oxidase testing, and biochemical characterization using Leminor miniaturized galleries for Enterobacteriaceae. API 20E and API 20NE systems (bioMérieux, France) provided confirmatory identification. *Staphylococcus* species were differentiated by coagulase and DNase testing. *Bacillus* species were identified by characteristic morphology (3-5 µm rods with square ends).

2.4. Antimicrobial Susceptibility Testing

Antibiotic resistance was determined by Kirby-Bauer disk diffusion on Mueller-Hinton agar following SFM/EUCAST 2023 guidelines (25). Inocula (0.5 McFarland standard) were flooded onto pre-dried plates. Antibiotic panels included:

Enterobacteriaceae (n=14): ampicillin, amoxicillin-clavulanate, mecillinam, cefoxitin, cefotaxime, ceftazidime, cefepime, meropenem, imipenem, gentamicin, amikacin, ciprofloxacin, levofloxacin, fosfomycin.

Non-fermenters (n=11): ampicillin, ticarcillin-clavulanate, ceftazidime, cefepime, imipenem, meropenem, tobramycin, amikacin, ciprofloxacin, levofloxacin, colistin.

Staphylococci (n=10): cefoxitin, gentamicin, tobramycin, kanamycin, erythromycin, tetracycline, fusidic acid, rifampicin, norfloxacin, moxifloxacin.

Bacillus (n=6): ampicillin, amoxicillin-clavulanate,

gentamicin, tetracycline, imipenem, meropenem.

Disks were placed ≥ 15 mm from plate edges and ≥ 30 mm apart. After pre-diffusion, plates were incubated at 37°C for 18-20 hours. Inhibition zones were measured with digital calipers and interpreted per SFM/EUCAST 2023 breakpoints. Quality control employed *Escherichia coli* ATCC 25922, *Staphylococcus aureus* ATCC 25923, and *Pseudomonas aeruginosa* ATCC 27853.

ESBL production was confirmed by double-disk synergy testing with ceftazidime/cefotaxime and amoxicillin-clavulanate (20-25 mm apart). Methicillin resistance was screened using ceftoxitin disks (27). MDR was defined as non-susceptibility to ≥ 1 agent in ≥ 3 antimicrobial categories (28).

2.5. Data Analysis

Data were recorded on standardized forms and analyzed using Microsoft Excel 2016 and Epi Info 7.2.3.1. Descriptive statistics included frequencies and percentages for categorical variables (species distribution, contamination rates, resistance patterns). Results were visualized using tables and diagrams.

2.6. Ethical Considerations

This environmental surveillance was approved by CNRAO administration as part of routine infection control activities. No human subjects or patient samples were involved. Biosafety level 2 protocols were followed per WHO guidelines.

3. Results

3.1. Environmental Contamination Patterns

We systematically examined 39 sites across the Chemotherapy unit over two months, focusing predominantly on physical surfaces (36 samples, 92.3%) with limited air sampling (3 samples, 7.7%). The shared infusion bay, where patients spend hours receiving treatment, contributed nearly one-third of specimens (30.8%). Individual patient rooms, treatment areas, and physician offices accounted for 28.2%, 23.1%, and 17.9% respectively.

Table 1. Distribution of surface Sampling Sites

Sampling site	n	Percentage (%)
Sink and faucet	5	13.9
Entry door handle	5	13.9
Mattress	4	11.1
Infusion pole	4	11.1
Bed rail	4	11.1
Medication cart	3	8.3
Light switch	3	8.3
Oxygen delivery device	2	5.6
Patient chair	2	5.6
Bedside table	2	5.6
Climate control remote	1	2.8
Privacy curtain	1	2.8
Total	36	100

Water sources sinks and faucets and frequently touched door handles each represented 13.9% of surface samples, followed by patient contact surfaces: mattresses, infusion poles, and bed rails (11.1% each) (Table 1) This deliberate sampling strategy targeted surfaces identified as critical transmission points for healthcare-associated pathogens.

3.2. Microbiological Culture Yields

Surface samples yielded positive bacterial cultures in 63.9% of cases (23/36), revealing substantial environmental microbial burden despite routine disinfection protocols. In contrast, all air samples (3/3) remained sterile.

The positive culture rate among surfaces varied by location, with shared infusion areas and water sources demonstrating higher contamination frequency compared to low-touch vertical surfaces.

3.3. Bacterial Diversity and Taxonomic Distribution

Twenty-nine bacterial isolates were recovered from positive cultures, representing diverse taxonomic groups reflective of environmental, skin commensal, and opportunistic pathogen reservoirs. Gram-positive bacilli predominated (34.5%, 10/29), followed by Gram-positive cocci (27.6%, 8/29), non-fermenting Gram-negative bacilli (20.7%, 6/29), and Enterobacteriaceae (17.2%, 5/29).

Table 2. Distribution of Isolated bacterial groups

Isolated bacterial groups	n	Percentage (%)
Enterobacteria	5	17.24
Non-fermentative Gram-negative bacilli	6	20.69
Gram-positive cocci	8	27.59
Gram-positive bacilli	10	34.48
Total	29	100

At the species level, *Bacillus spp.* emerged as the most prevalent organism (34.5%, 10/29), consistent with ubiquitous environmental spore-forming bacilli capable of surviving standard disinfection procedures. Coagulase-negative staphylococci (CoNS) ranked second (24.1%, 7/29). *Pseudomonas aeruginosa*, a notorious opportunistic pathogen in immunocompromised hosts, accounted for 20.7% of isolates (6/29), predominantly recovered from water-associated sites. Enterobacteriaceae comprised *Escherichia coli* (6.9%, 2/29) and *Enterobacter cloacae* (10.3%, 3/29), with *Staphylococcus aureus* detected as a single isolate (3.4%, 1/29). (Table 3)

Table 3. Distribution of bacterial isolates recovered from environmental samples

Bacterial species	Number of isolates	Percentage (%)
<i>Pseudomonas aeruginosa</i>	6	20.7
<i>Staphylococcus aureus</i>	1	3.4
Coagulase-negative Staphylococcus	7	24.1
<i>Enterobacter cloacae</i>	3	10.3
<i>Escherichia coli</i>	2	6.9
<i>Bacillus spp.</i>	10	34.5
Total	29	100

3.4. Antimicrobial Resistance Profile

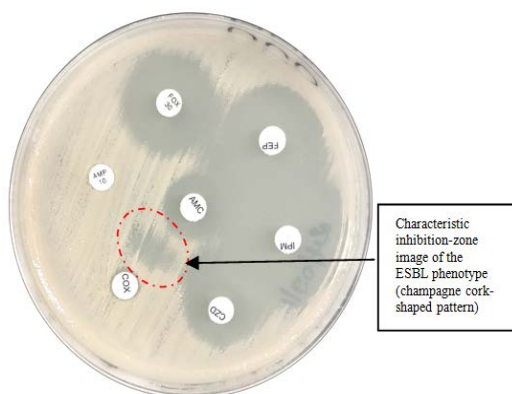
The single *Staphylococcus aureus* isolate demonstrated pan-susceptibility to all tested agents including cefoxitin (methicillin-susceptible, MSSA), aminoglycosides, fluoroquinolones, rifampicin, tetracycline, and fusidic acid. However, macrolide resistance was detected (erythromycin-resistant), suggesting potential inducible clindamycin resistance (MLS_B phenotype).

Among the seven coagulase-negative *Staphylococcus* (CoNS) strains studied, one strain was methicillin-resistant (MR-CoNS) and showed resistance to kanamycin, tobramycin, and gentamicin (KTG phenotype). This strain was isolated from a swab of the Privacy curtain (paravent) of the common chemotherapy room (Table 4).

Table 4. Antimicrobial resistance profile of Coagulase-negative staphylococci (CoNS) strains

Coagulase-negative Staphylococci (CoNS)	Resistance N (%)	Intermediary N (%)	Susceptibility N (%)
NXN (Norfloxacin)	0	0	7 (100)
TMN (Tobramycin)	1 (14.28)	0	6 (85.71)
MXF (Moxifloxacin)	0	0	7 (100)
GMN (Gentamicin)	1 (14.28)	0	6 (85.71)
FOX (Céfoxitine)	1(14.28)	0	6 (85.71)
KMN (Kanamycin)	1(14.28)	0	6(85.71)
FAD (Fusidic Acid)	1(14.28)	0	6(85.71)
TET (Tetracycline)	2(28.57)	0	5(71.43)
RIF (Rifampicin)	0	0	7 (100)
ERY (Erythromycin)	1(14.28)	0	6(85.71)

Of the two *Escherichia coli* isolates obtained, one was an extended-spectrum β -lactamase (ESBL) producer. This strain originated from the specimen collected from the sink in Category Room No. 2 (Figure 1). Among the three *Enterobacter cloacae* strains isolated, one was an extended-spectrum β -lactamase (ESBL) producer associated with resistance to fluoroquinolones (Table 5). This strain was isolated from the sample collected from the infirmity sink. All *Pseudomonas aeruginosa* isolates exhibited intermediate susceptibility to colistin, and one isolate was resistant to ticarcillin + clavulanic acid (TCC) (Table 6)



FEP: Cefepim; **FOX:** Cefoxitin; **AMC:** Amoxicillin-clavulanic Acid; **IPM:** Imipenem; **COX:** Cefotaxime; **AMP:** Ampicillin; **CZD:** Ceftazidim.

Figure 1. ESBL *Escherichia coli* environmental strain

Table 5. Antimicrobial resistance profile of *Enterobacter cloacae* strains

Enterobacter cloacae	Resistance N (%)	Intermediary N (%)	Susceptibility N (%)
GMN (Gentamicin)	1(33,34)	0	2 (66,66)
CIP (Ciprofloxacin)	1 (33,34)	0	2 (66,66)
FOS (Fosfomycin)	0	0	3(100)
AKN (Amikacin)	0	0	3 (100)
LVX (Levofloxacin)	1(33,34)	0	2 (66,66)
MEC (Mécillinam)	0	0	3 (100)
MEM (Meropenem)	0	0	3(100)
AMP (Ampicillin)	3 (100)	0	0
CAZ (Ceftazidim)	1(33,34)	0	2 (66,66)
IPM (Imipenem)	0	0	3 (100)
AMC (Amoxicillin + clavulanic Acid)	3 (100)	0	0
CTX (Cefotaxim)	1 (33,34)	0	2 (66,66%)
FEP (Cefepim)	1 (33,34)	2 (66,66)	0

Table 6. Antimicrobial resistance profile of *Pseudomonas aeruginosa* strains

Pseudomonas aeruginosa	Resistance N (%)	Intermediary N (%)	Susceptibility N (%)
TMN (Tobramycin)	0	0	6 (100)
CIP (Ciprofloxacin)	0	6 (100)	0
AKN (Amikacin)	0	0	6 (100)
LVX (Levofloxacin)	0	6	0
MEM (Meropenem)	0	1 (16,66)	5 (83,34)
CAZ (Ceftazidim)	0	6 (100)	0
IPM (Imipenem)	0	4 (66,66)	2 (33,34)
FEP (Cefepim)	0	6	0
TCC (Ticarcillin + Acid clavulanic)	1 (16,64)	5(83,33)	0
COL (Colistin)	0	6 (100)	0

All *Bacillus* spp. isolates were resistant to amoxicillin-clavulanic acid (AMC) and ampicillin (AMP); conversely, they were all susceptible to gentamicin (GMN) and meropenem (MEM).

Overall, most environmental isolates (89.7 %) belonged to the non-MDR category. ESBL-producing and methicillin-plus-aminoglycoside-resistant strains made up 6.9 % and 3.4 % of isolates, respectively (Table 7)

Table 7. Distribution of environmental isolates by multidrug-resistance phenotype

MDR Phenotype	Number of isolates	Percentage (%)
<i>ESBL-producing strain</i>	2	6.9
Methicillin- and aminoglycoside-resistant (KAN/TOB/GEN) strain	1	3.4
<i>Non-MDR strain</i>	26	89,7
Total	29	100

4. Discussion

This cross-sectional surveillance study provides one of the first comprehensive characterization of the bacterial ecosystem and antimicrobial resistance landscape in a West African chemotherapy unit, revealing substantial environmental contamination with clinically relevant opportunistic pathogens and emerging resistance

phenotypes.

Surface contamination was detected in 63.9% of sampled sites, substantially exceeding rates reported in previous African healthcare facility surveys. Meité et al. documented 46.4% positivity in surgical intensive care units in Côte d'Ivoire [13], while Samira et al. found 40% contamination in Algerian hospital environments [14]. This elevated burden may reflect several converging factors: the open-bay infusion area design facilitating cross-contamination between adjacent patient stations, high patient throughput with frequent surface contact during prolonged chemotherapy sessions, potential gaps in environmental cleaning frequency or technique, and tropical climate conditions favoring microbial survival on fomites.

During neutropenic nadirs, patients lose their primary defense against bacterial invasion, rendering environmental pathogens that pose negligible risk to immunocompetent individuals capable of causing life-threatening bacteremia and sepsis [15]. The documented recovery of *Pseudomonas aeruginosa*, Enterobacteriaceae, and methicillin-resistant staphylococci from high-touch surfaces establishes plausible transmission pathways for healthcare-associated infections in this vulnerable population.

Interestingly, all air samples (3/3) yielded sterile results despite substantial surface contamination. This discordance likely reflects multiple factors: passive settle plate methodology demonstrates limited sensitivity for airborne bacteria compared to active volumetric sampling [16], the sampling duration may have been insufficient to capture transient airborne events, and functional HVAC systems in sampled zones may effectively remove airborne particles.

The predominance of Gram-positive bacilli (34.5%), specifically *Bacillus* spp., represents a notable departure from typical nosocomial ecology where Gram-negative organisms dominate in most high-income country surveillance studies [17]. This finding aligns more closely with environmental microbiology studies from tropical regions where spore-forming bacilli persist despite disinfection protocols. Andrianjafy et al. in Madagascar [18] and Barbosa et al. in Brazil [19] similarly reported *Staphylococcus* spp. predominance in hospital environments, though their studies did not systematically culture *Bacillus*, often dismissed as non-pathogenic environmental contaminants.

Bacillus cereus group organisms cause catheter-associated bloodstream infections, pneumonia, and wound infections in neutropenic patients with case fatality rates approaching 20-30% [20]. Our recovery of *Bacillus* from 34.5% of isolates across diverse surfaces including mattresses, bed rails, and infusion poles suggests widespread environmental colonization requiring enhanced cleaning protocols and potential consideration in empirical antimicrobial regimens.

The substantial recovery of *Pseudomonas aeruginosa* (20.7% of isolates) exclusively from water-associated sites (sinks, oxygen humidifiers) corroborates extensive literature documenting hospital plumbing systems as persistent *Pseudomonas* reservoirs [21]. This Gram-negative opportunist demonstrates remarkable adaptability to oligotrophic aquatic environments, forming robust biofilms within drain pipes and faucet aerators that

continuously seed the healthcare environment [22]. Several nosocomial *Pseudomonas* outbreaks in oncology and transplant units have been traced to contaminated water sources, with whole-genome sequencing confirming patient isolates matched drain genotypes [23].

The detection of methicillin-resistant coagulase-negative staphylococci (MR-CoNS) exhibiting the classic KTG (kanamycin-tobramycin-gentamicin) co-resistance phenotype represents a concerning finding with important clinical and epidemiological implications. This resistance constellation, mediated by *mecA* gene-encoded altered penicillin-binding protein 2a (PBP2a) for methicillin resistance and aminoglycoside-modifying enzymes for KTG resistance, typifies healthcare-adapted staphylococcal clones that emerge under intense antimicrobial selection pressure [24].

While CoNS are traditionally regarded as low-virulence commensals, they represent leading causes of catheter-related bloodstream infections, particularly in patients with long-term central venous access devices ubiquitous in chemotherapy administration [25]. The environmental detection of MR-CoNS on a privacy curtain in the shared infusion bay, a high-touch surface contacted by multiple healthcare workers between patient encounters, suggests healthcare worker hands as probable transmission vectors.

This finding mirrors results from Meité et al. [13] who documented high methicillin resistance prevalence in environmental *Staphylococcus* isolates from Ivorian intensive care units, suggesting endemic circulation of resistant staphylococcal clones in West African healthcare facilities. The single *S. aureus* isolate demonstrated susceptibility to all agents except erythromycin, a more favorable profile than reported from many settings.

The recovery of ESBL-producing *E. coli* and *E. cloacae* (40% ESBL prevalence among Enterobacteriaceae isolates) from patient room and treatment area sinks represents a critical infection control concern. ESBL-producing Enterobacteriaceae have emerged as dominant nosocomial pathogens globally, causing healthcare-associated urinary tract infections, bloodstream infections, and pneumonia with increased mortality compared to susceptible strains [26].

Hospital wastewater systems serve as ecological niches where ESBL-producing bacteria persist despite antimicrobial exposure, with drain biofilms harboring concentrations exceeding 10⁶ CFU/mL [27]. Retrograde splashing during handwashing, aerosolization during sink use, and inadequate hand hygiene after sink contact facilitate transmission from drains to patient care zones. Several documented outbreaks in hematology-oncology units have been terminated only after complete drain removal and replacement [28].

This multidrug-resistant phenotype, often plasmid-mediated and horizontally transferable, severely constrains empirical therapy options for suspected Gram-negative infections. The preservation of carbapenem susceptibility across all Enterobacteriaceae isolates represents an encouraging finding, suggesting carbapenemase-producing organisms have not yet become established in this environment, though continued surveillance remains essential.

Most clinical microbiology laboratories dismiss *Bacillus* as culture contaminants, particularly when isolated from non-sterile sites like environmental surfaces.

However, several factors support their clinical relevance in this chemotherapy setting: ubiquitous recovery across multiple sites and sampling occasions argues against random contamination, their documented capacity to cause invasive infection in neutropenic hosts, and their intrinsic resistance to empirical antibiotics commonly used for febrile neutropenia (β -lactams) creates opportunities for breakthrough infection.

Environmental *Bacillus* control presents unique challenges given spore resistance to standard disinfectants. Quaternary ammonium compounds and alcohol-based products demonstrate minimal sporicidal activity, while hypochlorite solutions at appropriate concentrations remain the most effective environmental control measure [29].

Several methodological factors warrant acknowledgment when interpreting our findings. The choice of swab-based surface sampling, while practical and widely used, demonstrates reduced sensitivity for Gram-positive cocci compared to contact agar plates, potentially underestimating staphylococcal contamination [22]. Conversely, moistened swabs may enhance Gram-negative bacilli recovery, possibly inflating *Pseudomonas* and Enterobacteriaceae detection. Future surveillance incorporating both methodologies would provide more comprehensive environmental characterization.

The single cross-sectional survey design limits our ability to assess temporal contamination dynamics, identify persistent versus transient organisms, or evaluate seasonal variations potentially relevant in tropical settings. Longitudinal surveillance tracking contamination patterns before and after cleaning, across day and night shifts, would strengthen understanding of environmental microbiology in this setting.

Sample size constraints, particularly the limited Enterobacteriaceae recovery ($n=5$), reduce statistical power for resistance prevalence estimation and preclude multivariable analysis of contamination risk factors. Nevertheless, even this modest surveillance revealed clinically significant resistant organisms (ESBL-producers, MR-CoNS) warranting intervention.

The absence of molecular characterization limits our ability to determine whether resistant isolates represent clonal expansion of single strains versus polyclonal diversity, distinguish hospital-adapted versus community-acquired organisms, or identify specific resistance genes. Future studies incorporating genomic epidemiology would illuminate transmission dynamics and inform targeted interventions.

Conclusions

This inaugural environmental surveillance study from a West African chemotherapy unit reveals substantial bacterial contamination with opportunistic pathogens demonstrating concerning resistance patterns including ESBL production, methicillin resistance, and intermediate susceptibility to last-line agents. The predominance of *Bacillus* spp., often dismissed as contaminants but capable of causing invasive infection in immunocompromised hosts, highlights taxonomic patterns potentially unique to tropical healthcare settings. Water sources emerge as critical reservoirs for *Pseudomonas aeruginosa* and

ESBL-producing Enterobacteriaceae, warranting targeted engineering and disinfection interventions.

These baseline data establish the foundation for evidence-based infection prevention programs protecting vulnerable cancer patients and provide a framework for expanded surveillance across African oncology centers. Future research should incorporate longitudinal sampling designs, molecular epidemiology to elucidate transmission dynamics, and intervention studies assessing the impact of enhanced environmental control measures on contamination reduction and ultimately, healthcare-associated infection rates. As cancer incidence rises across sub-Saharan Africa and chemotherapy access expands, ensuring microbiologically safe care environments represents a fundamental component of comprehensive oncology care delivery.

Declaration of Conflicting Interests

The authors declare no potential conflicts of interest in the research, writing, and/or publication of this article.

Authors' Consent

After several readings and corrections of the manuscript, the authors approved the publication of this article.

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