



Rethinking Contextual Waste Management Policies to Mitigate the Risk of Antimicrobial Resistant Infections in Healthcare Settings: Evidence from Selected Hospitals in West Cameroon

**Willite Ngankou Tchapda ^a, Josué Simo Louokdom ^a,
Patrick Mbopi Yamen ^a, O'Neal Dorsel Youté ^{b,c},
Jean Jacques Tchouani Kouemo ^d,
Roméo-Gabin Tchotcheu Seugnou ^a,
Michelle Cleone Taffo ^a,
Leonel Browndon Tchatchouang Tchiasso ^e,
Emmanuel Haddison Sako ^f
and Pierre René Fotsing Kwetche ^{a,g*}**

^a School of Pharmacy, Higher Institute of Health Sciences, Université des Montagnes, Cameroon.

^b Military Health Research Center, Cameroon.

^c Research Working Group, African Youth AMR Alliance Task Force, Cameroon.

^d 2nd Joint Military Hospital, Douala, Cameroon.

^e Dare to Dream for Africa, France.

^f District Hospital of Bangangté, Cameroon.

^g Laboratory of Microbiology, Université des Montagnes Teaching Hospital, Cameroon.

Authors' contributions

This work was carried out in collaboration among all authors. Authors WNT, JSL, PMY, ODY, PRFK conceptualized the study and performed the methodology. Authors JSL, PRFK did data validation and supervision. Author WNT helped in project administration. Authors WNT, MCT, RGTS investigated the work. Authors ODY, LBTT did data curation and formal analysis. Authors WNT, PRFK, EHS searched for resources. Author ODY did data visualization. Authors WNT, ODY wrote the original draft. Authors

*Corresponding author: Email: prfotsingk@gmail.com;

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ABSTRACT

Background: In large numbers of low- and middle-income countries, hospital waste management policies are conducted below the minimum standards due to resource scarcity. In these areas, accumulated wastes often represent potent sources of microbial populations that may evolve as health threats to humans', animals' and environmental health, further exacerbating poverty. Data from accumulated waste and/or its surrounding environment can therefore help to redefine, reorient and optimize waste management policies for the healthcare setting users' safety.

Objective: The aim of this cross-sectional study was to investigate the type, the diversity, the load and the drug susceptibility trends of bacteria populations that grow in the vicinity of solid waste accumulation sites in four healthcare facilities of the Ndé division, West Cameroon.

Methods: Soil and air specimens were collected for bacterial screening at varying distances from the solid waste accumulation sites. Culture, isolation, identification, enumeration and susceptibility tests on bacteria isolates were performed according to standard protocols.

Results: Relevant findings revealed diversified populations made up of 53 bacterial groups including *Staphylococcus* spp. (50.94%), Gram-positive rods (26.42%), *Acinetobacter* spp. (11.32%), *Klebsiella* spp. (7.55%), *Serratia* spp. and *Pseudomonas* spp. (1.89% each). In terms of their loads, Gram-negative rods loads were higher than those observed with other morphological types. Further details indicated higher loads and diversities in soil specimens collected in the vicinity of solid waste accumulation sites. These trends in loads and diversity were particularly obvious in one of the four target healthcare institutions. The susceptibility tests revealed multidrug resistance, with the highest rates recorded against beta-lactam antibiotics. The most effective drugs consisted of Gentamicin, Clindamycin, Erythromycin, and Trimethoprim/Sulfamethoxazole.

Conclusion: These findings are indications that exposed human populations are at risk of contracting resistant bacteria, with a higher likelihood in the vicinity of accumulated wastes in all settings. Accordingly, contextual implementation of hospital hygiene policies in line with biosafety and biosecurity was suggested as a priority to meet the expectations of the 1st, 3rd and 4th United Nations Sustainable Development Goals.

Keywords: Bacterial diversity; resistance; waste accumulation sites; hospital solid wastes; health.

1. INTRODUCTION

Hospital waste globally refers to the waste generated by activities in healthcare facilities. They are produced in patient care units, medical biology laboratories, medical imaging departments, hospital pharmacies, laundry premises, catering and administration units.

From these origins, 85% of wastes are general (non-hazardous) that can be assimilated to household wastes while 15% are hazardous (often toxic and lethal). Hazardous wastes consist of sharp, infectious, pathological, pharmaceutical, cytotoxic, chemical and radioactive pollutants (Janik-Karpinska *et al.*, 2023; Takunda & Steven, 2023).

During wastes management, hazardous wastes must be separated from other wastes because of the significant or potential threat they pose to the environment and the health of living entities. However, in large numbers of low- and middle-income countries' hospitals, hazardous waste items that are not often separated from the non-hazardous, ones cause functional gaps which conflict with standard waste management procedures (Mangizvo & Chinamasa, 2008; Coker *et al.*, 2009; Janik-Karpinska *et al.*, 2023; Takunda & Steven, 2023). In some instances, these wastes are stored and eventually treated in the vicinity of the patient's caretaking premises (Saad, 2013; Adelodun *et al.*, 2021; Takunda & Steven, 2023). When post-accumulation treatments are poorly conducted, all derivatives become serious threats to human, animal and environmental health (Owusu, 2010; Mattiello *et al.*, 2013; Ziraba *et al.*, 2016). In fact, the accumulated wastes represent risk factors for the build-up of toxic and recalcitrant chemical compounds in soils beneath and around their accumulation sites; then, likely to disrupt the local ecological system equilibrium (Nannoni *et al.*, 2015; Vongdala *et al.*, 2018; Esmaeili Nasrabadi *et al.*, 2024).

Moreover, these accumulated wastes represent potent reservoirs for professional and opportunistic pathogenic microorganisms that could interact with their human hosts and cause ranges of damages with regard to their virulence and the exposed host defense potentials or vulnerability. They are also regarded as sources for selection and dissemination of antibiotic resistance phenotypes and genotypes in local bacterial populations that may spread into the surrounding human communities (Hocquet *et al.*, 2016; Anand *et al.*, 2021; Chamkal *et al.*, 2022; Chowdhury & Uddin, 2022). With the risk of environmental spread and according to certain authors, the risk of hospital-acquired resistant infections is high in both indoor patients and amongst people in communities (Hossain *et al.*, 2013; McEwen & Collignon, 2018).

Managing this risk and preventing infections are integral parts of the global hospital hygiene endeavors that aim at meeting the challenges of the 1st, 3rd and 4th Sustainable Development Goals (SDGs) by 2030. Any management and prevention initiatives could only be carried out effectively if the units in charge of hospital hygiene have related relevant pieces of information. In this frame, the aim of the present

study was to provide pieces of information (type, load and drug susceptibility) concerning the bacterial populations that are present in the environment of solid waste accumulation sites within four healthcare institutions in the West region of Cameroon. More specifically, this investigation aimed at identifying and quantifying potential harmful bacteria from soil and ambient air in the solid waste accumulation sites vicinities, and addressing isolates' susceptibility to common conventional antibacterial agents. Upon completions, overall findings highlighted the need for redefining, reorienting and optimizing waste management policies in these and other healthcare facilities in West Cameroon to ensure a better biosafety/biosecurity tandem for hospital users, in line with the above three SDGs concerned with poverty alleviation, healthcare provision and quality education, respectively. These goals are critical with the increased global life expectancy and projected related healthcare challenges like resistant opportunistic infections then, and the overall human welfare.

2. MATERIAL AND METHODS

2.1 Study Design and Ethical/Administrative Considerations

This cross-sectional study was conducted from January 10th through May 15th, 2024 in four healthcare facilities in the West region of Cameroon. Specimen collection was performed in the vicinity of solid waste accumulation sites at the "Université des Montagnes" Teaching Hospital (UdMTH), the Bangangté District Hospital (BangDH), the Bangwa Protestant Hospital (BPH) and the Bandjoun District Hospital (BandDH). Laboratory screening of the specimens was carried out at the UdMTH Laboratory of Microbiology.

Before field work initiation, all ethical and administrative requirements were fulfilled. Namely, they were the ethical clearance N° 2024/091/UdM/PR/CEAQ obtained from the Université des Montagnes Ethics and Quality Assurance Committee, the research authorizations N° 2024/005/CUM/ADMN_GENE, 022/A/MINSANTE/DRSPO/HDB/BGTE and 2024/227/UdM/PR/DECANAT-ISSS/MED, respectively provided by the UdMTH, the BangDH, and Université des Montagnes (UdM) Higher Institute of Health Sciences. The directors of BandDH and BPH, respectively also consented with signed and stamped letters

validating project implementation within their institutions.

2.2 Sample Collection

2.2.1 Solid waste accumulation sites

For the investigation purposes, all samplings were carried out around accessible and used solid waste accumulation sites (SWAS). These SWAS included the pits, the incinerators and the temporary storage sites of infectious solid wastes.

2.2.2 Sampling

The specimens (surface soil and ambient air around the SWAS) were collected according to Kom Fotso *et al.* (2024). Briefly, about 50 g of surface soil was collected aseptically with a sterile spatula at 1 meter (sampling location A) and 30 meters (sampling location B) from the SWAS, then transferred into sterile pots.

In parallel, airborne bacteria were trapped by passive contact (direct contact with the circulating ambient air) on uncovered Petri dishes containing Mannitol Salt, Cetremide and MacConkey agars provided by Liofilchem®. These culture media were chosen for their role in the selective growth of prominent healthcare-associated infections due to bacterial etiologies. These culture media were exposed for 30 min at 1 meter (sampling location A) and 30 meters (sampling location B) from each SWAS.

After collections, soil samples and exposed culture media in Petri dishes (for airborne bacteria) were immediately conveyed to the laboratory in refrigerated containers (4-8°C) for microbial identification and susceptibility testing according to standard procedures.

2.3 Sample Analysis

Previous and standard protocols (Denis *et al.*, 2011; Kom Fotso *et al.*, 2024) were used during this step. *Staphylococcus aureus* ATCC 29213 and *Escherichia coli* ATCC 25922 were used as reference bacterial strains for quality control throughout the process.

At the laboratory, the culture of soil specimens was performed according to the Kom Fotso *et al.* (2024) workflows on appropriate culture media. For airborne bacteria, previously exposed agar plates were immediately incubated. Subsequent

to bacterial growth after 24 h incubation at 37°C, macroscopic examination and enumeration were followed according to the same workflows (Kom Fotso *et al.*, 2024) with soil surface specimens. With airborne bacteria, however, slight modifications were observed in expressing their loads. More precisely in this investigation, airborne bacterial loads were expressed as colony-forming unit (CFU)/60 mm diameter Petri dish/30 min.

Thereafter, microscopy characterization (Gram stain) and biochemical identification tests followed. The catalase test was used for Gram-positive cocci. The tests for oxidase, carbohydrates (mannitol, lactose, glucose) fermentation, motility, urea hydrolysis, indole and tryptophanase production, and citrate metabolism tests were used for Gram-negative rods. The identification of Gram-positive rods was limited to macroscopy and microscopy.

For all bacteria, a pure subculture was conducted at 37°C for 24 h on nutrient agar for susceptibility tests.

2.4 Antibiotic Susceptibility Test

This step was carried out according to the 2023 recommendations of the "Comité de l'Antibiogramme de la Société Française de Microbiologie" (CASFM, 2023). For the clinical categorization of GPR with Penicillin G (10 U) and Ceftazidime (30 µg) testing, the 2013 recommendation of CASFM (2013) was observed. A total of 16 antibacterial agents were then used on 24 h-fresh colonies grown on nutrient agar. Namely, they were Penicillin G (10 U), Oxacillin (1 µg), Amoxicillin (20 µg) (Amoxicillin (25 µg) for GPR), Amoxicillin/Clavulanic Acid (20/10 µg), Ticarcillin (75 µg), Cefoxitin (30 µg), Ceftazidime (30 µg), Ceftriaxone (30 µg), Imipenem (10 µg), Aztreonam (30 µg), Gentamicin (10 µg), Clindamycin (2 µg), Erythromycin (15 µg), Levofloxacin (5 µg), Tetracycline (30 µg), and Trimethoprim/sulfamethoxazole (1.25/23.75 µg).

2.5 Data Analysis

The target variables were the diversity of bacteria types, their loads and the associated clinical categories (susceptible, susceptible at high dose and resistant). Data were recorded and processed with tools from Microsoft Excel 2016. Clinical categories are presented as frequencies in the present paper.

To elude institutions' identity, letters, "W", "X", "Y" and "Z" were used in the result and discussion sections to refer to target healthcare institutions.

3. RESULTS

3.1 Bacterial Diversities and Loads

From the specimens collected in the SWAS areas, 53 bacterial groups were recovered. Out of these, Gram-positive bacteria literally overwhelmed the isolation rates over Gram-negative. In decreasing rates, they were *Staphylococcus* spp. (50.94%), Gram-positive rods (26.41%), *Acinetobacter* spp. (11.32%), *Klebsiella* spp. (7.55%), *Serratia* spp. and *Pseudomonas* spp. (1.89% each).

In further details, bacterial diversities and loads (Table 1) were highest around the 'Y' SWAS with the overall diversities and bacterial loads highest in all soil specimens. Also invariably, the highest diversities and bacterial loads were observed near SWAS in all settings. *Staphylococcus* dominated the diversity trends, while the highest bacterial loads were recorded with Gram-negative rods.

3.2 Bacteria Susceptibility Profile

Susceptibility testing carried out on isolates revealed multidrug resistance (Table 2a and 2b), with the highest rates observed for beta-lactam antibiotics. Gentamicin and the Trimethoprim/Sulfamethoxazole combination proved most effective in general, but for the tests on Gram-positive bacteria, Clindamycin and Erythromycin were added to the list of these effective agents.

4. DISCUSSION

Hospital waste environments are reservoirs of microbes and genes transfer-enabling environments in which cross- and co-selection of antibiotic resistance are predictable events (Hossain et al., 2013; Hocquet et al., 2016; McEwen & Collignon, 2018; Anand et al., 2021; Chamkal et al., 2022; Chowdhury & Uddin, 2022). Foremost exposed to these environmental adulterations, the ecological systems within and surrounding these areas are risky for human and others living entities (Owusu, 2010; Mattiello et al., 2013; Nannoni et al., 2015; Ziraba et al., 2016; Vongdala et al., 2018; Esmaeili Nasrabadi et al., 2024), especially for those with

compromised immune systems like many in healthcare institutions.

The present study conducted in four healthcare institutions of West Cameroon revealed that surface soil and airborne bacteria around SWAS were highly diversified, overwhelmed, however by *Staphylococcus* that represented half of the diversity rates recorded, while Gram-positive and Gram-negative rods each accounted for almost a quarter. This dominance of *Staphylococcus* previously reported in the soil and air around the UdmTH solid waste accumulation sites (Kom Fotso et al., 2024) is most likely in connection with the bacterial cell organization and the non-stringency feature of members from the *Staphylococcus* genus (de Vries & Shade, 2013; Kom Fotso et al., 2024), consistent with their role as relevant group of bacteria that could effectively be used in hospital hygiene assessment (Fotsing Kwetche et al., 2020; Menteng Tchuenté et al., 2023; Kom Fotso et al., 2024; Youté et al., 2024).

In contrast to bacterial diversity, GNR loads were found to be higher than those of other bacterial types. This could be justified by the fact that soil surfaces are richer in easily degradable nutrients (organic substances) which strongly contribute to the residual fitness and perpetuation of Gram-negative bacteria. In addition, Gram-negative bacteria which are generally copiotrophic are often dependent on labile carbon supplied by plant litter and other like sources, then abundant in surface soils (Fierera et al., 2003; Fanin et al., 2019; Naylor et al., 2022). In the context of the present investigation, the SWAS were located in areas covered with vegetation, then humid and conducive for Gram-negative bacteria. Reversely, Gram-positive bacteria are oligotrophic and basically predominate in nutrient-poor environments, beyond the above-mentioned cellular organization which allows resistance to environmental stresses like water deficiency. According to previous authors in fact, bacteria like *Actinomycetes* and other Gram-positive bacteria are common in deeper soils, while Gram-negative populations decrease with increasing depths (Fierera et al., 2003; Fanin et al., 2019; Naylor et al., 2022). Otherwise, the type of target specimen may justify the low rates of GPR detection, while deeper soil samples might have provided different values of bacterial diversities and loads. In addition, Kom Fotso et al. observed that this distribution might also reflect the protocol used, as it was not the most effective one for GPR that are actually expected

Table 1. Bacterial diversity and loads in the subjected specimens

Bacteria categories	Solid waste accumulation sites	Sampling locations	W				Z		X				Y					
			Gram-positive rods	<i>Klebsiella</i> spp.	<i>Staphylococcus</i> spp.	<i>Acinetobacter</i> spp.	Gram-positive rods	<i>staphylococcus</i> spp.	<i>Acinetobacter</i> spp.	Gram-positive rods	<i>staphylococcus</i> spp.	<i>Acinetobacter</i> spp.	Gram-positive rods	<i>Klebsiella</i> spp.	<i>Pseudomonas</i> spp.	<i>Serratia</i> spp.	<i>Staphylococcus</i> spp.	
Airborne bacteria (CFU/60 mm diameter Petri dish/30 min)	Pit	A				-	-	1110*	-	660	3600	-	1380	-	-	-	3000	
		B		-		-	-	720*	-	-	2100*	-	60	-	-	-	240	
	Incinerator	A	-	-	1800							-	-	15360	-	-	2160*	
		B	-	-	600							-	-	-	-	-	1380	
	ISW temporary storage site	A	-	-	120										-			
		B	-	-	-													
	Soil bacteria (CFU/g of surface soil)	Pit	A				6420	660*	-	15180	2730*	-	16800	1860*	-	-	-	2520
			B					6000	-	2460	12000	2100	1200	-	12000	-	-	1200*
Incinerator		A	-	1320	2220*							15360	-	-	-	-	5970*	
		B	-	-	240								-	4050*	-	3660	12000	-
ISW temporary storage site		A	4230*	9000	6240										-			
		B	-	-	420													

ISW: Infectious solid wastes; A: Sampling location 1 meter from the waste accumulation site; B: Sampling location 30 meters from the waste accumulation site

* Bacterial loads from CFUs belonging to two distinct colony morphotype (macroscopy)

Table 2a. Bacterial susceptibility profile

Antibiotics	W									Z								
	GNR			GPR			Staphylococcus spp.			GNR			GPR			Staphylococcus spp.		
	R	SHD	S	R	SHD	S	R	SHD	S	R	SHD	S	R	SHD	S	R	SHD	S
Amox./clav. (20/10 µg)	100	0	0	100	0	0	-	-	-	-	-	-	100	0	0	-	-	-
Amoxicillin (20 µg)*	100	0	0	0	0	100	-	-	-	-	-	-	0	0	100	-	-	-
Aztreonam (30 µg)	100	0	0	-	-	-	-	-	-	100	0	0	-	-	-	-	-	-
Cefoxitin (30 µg)	0	0	100	100	0	0	100	0	0	-	-	-	100	0	0	67	0	33
Ceftriaxone (30 µg)	50	50	0	-	-	-	-	-	-	50	0	50	-	-	-	-	-	-
Ceftriaxone (30 µg)	50	0	50	100	0	0	-	-	-	50	50	0	100	0	0	-	-	-
Clindamycin (2 µg)	-	-	-	0	0	100	57	0	43	-	-	-	0	0	100	33	0	67
Erythromycin (15 µg)	-	-	-	0	0	100	14	0	86	-	-	-	0	0	100	33	0	67
Gentamicin (10 µg)	0	0	100	0	0	100	0	0	100	0	0	100	0	0	100	33	0	67
Imipenem (10 µg)	-	-	-	-	-	-	-	-	-	100	0	0	-	-	-	-	-	-
Levofloxacin (5 µg)	0	0	100	0	0	100	0	100	0	0	0	100	0	0	100	33	67	0
Oxacillin (1 µg)	-	-	-	100	0	0	100	0	0	-	-	-	100	0	0	100	0	0
Penicillin G (10 U)	-	-	-	100	0	0	100	0	0	-	-	-	0	100	0	100	0	0
Tetracycline (30 µg)	100	0	0	0	0	100	14	0	86	-	-	-	0	0	100	0	0	100
Ticarcillin (75 µg)	-	-	-	-	-	-	-	-	-	50	0	50	-	-	-	-	-	-
Trim./Sulf. (1.25/23.75 µg)	50	0	50	0	0	100	14	0	86	-	-	-	0	0	100	33	33	33

GNR: Gram negative rods; GPR: Gram positive rods; -: not tested;

R: rate of resistance isolate; SHD: rate of isolate susceptible at high dose; S: rate of susceptible isolate;

Amox./clav.: Amoxicillin/Clavulanic Acid (20/10 µg); Trim./Sulf.: Trimethoprim/sulfamethoxazole (1.25/23.75 µg)

* Amoxicillin (25 µg) for GPR

Table 2b. Bacterial susceptibility profile

Antibiotics	X									Y								
	GNR			GPR			Staphylococcus spp.			GNR			GPR			Staphylococcus spp.		
	R	SHD	S	R	SHD	S	R	SHD	S	R	SHD	S	R	SHD	S	R	SHD	S
Amox./clav. (20/10 µg)	-	-	-	50	50	0	-	-	-	100	0	0	50	50	0	-	-	-
Amoxicillin (20 µg)*	-	-	-	0	50	50	-	-	-	100	0	0	50	50	0	-	-	-
Aztreonam (30 µg)	100	0	0	-	-	-	-	-	-	50	17	33	-	-	-	-	-	-
Cefoxitin (30 µg)	-	-	-	50	50	0	100	0	0	33	0	67	100	0	0	100	0	0
Ceftriaxone (30 µg)	100	0	0	0	0	0	-	-	-	100	0	0	-	-	-	-	-	-
Ceftriaxone (30 µg)	0	100	0	100	0	0	-	-	-	80	0	20	100	0	0	0	0	0
Clindamycin (2 µg)	-	-	-	0	0	100	0	0	100	-	-	-	0	0	100	0	0	100
Erythromycin (15 µg)	-	-	-	0	0	100	0	0	100	-	-	-	0	0	100	0	0	100
Gentamicin (10 µg)	0	0	100	0	0	100	0	0	100	0	0	100	0	0	100	14	0	86
Imipenem (10 µg)	100	0	0	-	-	-	-	-	-	100	0	0	-	-	-	-	-	-
Levofloxacin (5 µg)	0	0	100	0	0	100	0	100	0	0	17	83	0	0	100	0	100	0
Oxacillin (1 µg)	-	-	-	100	0	0	100	0	0	-	-	-	100	0	0	100	0	0
Penicillin G (10 U)	-	-	-	100	0	0	100	0	0	-	-	-	50	0	50	100	0	0
Tetracycline (30 µg)	-	-	-	0	0	100	50	0	50	25	25	50	0	0	100	29	0	71
Ticarcillin (75 µg)	0	0	100	-	-	-	-	-	-	0	67	33	-	-	-	-	-	-
Trim./Sulf. (1.25/23.75 µg)	-	-	-	0	0	100	0	0	100	0	0	100	0	0	100	57	14	29

GNR: Gram negative rods; GPR: Gram positive rods; -: not tested;

R: rate of resistance isolate; SHD: rate of isolate susceptible at high dose; S: rate of susceptible isolate;

Amox./clav.: Amoxicillin/Clavulanic Acid (20/10 µg); Trim./Sulf.: Trimethoprim/sulfamethoxazole (1.25/23.75 µg)

* Amoxicillin (25 µg) for GPR

to grow better on nutrient agar or deMan Rogosa Sharpe agar. Acknowledging therefore that plate count, trypticase soy, nutrient or GPR selective agars could generate different trends, their use will be considered to address this crucial issue during the forthcoming related research initiatives.

In connection with sample types, bacterial diversities and loads were lower in ambient air than in soil samples. These findings (soil *versus* ambient air difference) could be attributable to the accumulative and nutritive characteristics of soil compared to the transporter nature (non-accumulative and non-nutritive) of ambient air.

Observing that bacterial diversities and loads were also higher at sampling locations that were closer to the waste accumulation sites basically reflects the presence of conducive requirements like nutrients in the accumulated wastes (that, in turn, serve as microbial reservoirs) and human (hospital staff) activities at distances (Sumampouw & Risjani, 2014; Anand *et al.*, 2021) and specifically, from the sampling locations A and B. How each of the related factors (soil contamination by antibiotic resistance genes, antibiotic-resistant bacteria and emerging contaminants; increased nutrient richness, variation in abiotic and biotic entities) directly or indirectly impact variations of bacterial populations as observed by previous authors (Sumampouw & Risjani, 2014; Wang *et al.*, 2020; Anand *et al.*, 2021) is yet to be fully elucidated. Similar future projects are, therefore, expected to provide clearer explanations for the fact that the greatest bacterial diversities and loads were observed in the healthcare institution “Y”. At the same time, however, it was observed that the accumulated waste loads were also bigger at the “Y” where the local vegetation on the SWAS area was most abundantly extended. In line with above arguments, these findings from the “Y” could help anticipate the high environmental contamination from the accumulated wastes, the frequent human activities in the vicinities of waste accumulation sites and the high nutrient richness which in turn corroborates the local high bacterial diversity as well as the anticipable higher likelihood of human affections.

Investigations through the bacterial susceptibility to conventional antibacterial agents revealed high rates of antibiotic-resistant isolates, especially with beta-lactam antibiotics. If these bacteria are generally known to be of hospital

origin (from inside hospital premises and spread to the surroundings *via* poor waste disposal or other vehicles), these alarming resistance rates are not surprising. Previous studies (Tchapdie Ngassam *et al.*, 2017; Fotsing Kwetche *et al.*, 2020; Menteng Tchuenté *et al.*, 2023) reported similar trends on the surfaces and in the air circulating in these hospitals. This resistance trend is at first glance, fundamentally attributable to the selection pressure exerted by antibiotics, antiseptics and disinfectants used in caretaking and hospital hygiene; drug derivatives like heavy metals in wastes; but also, other related selection-driving paths in communities. This involves mobile genetic elements responsible for co-selection and/or cross-selection of resistance phenotypes by the famous traditional and fundamental mechanisms (transduction, conjugation or transformation) (McEwen & Collignon, 2018; Anand *et al.*, 2021; Chamkal *et al.*, 2022; Chowdhury & Uddin, 2022) that control horizontal genetic transfer within and across bacteria phylogenetic barriers and eventually disseminate in the “hospital – waste – community” frame (Gould & MacKenzie, 2002; Cantón & Morosini, 2011; Cantón *et al.*, 2013; Wales & Davies, 2015; Hughes & Andersson, 2017), facilitated by inherent gaps in biosecurity. These phenomena are currently known to be amplified by the use of selection drivers in animal farms and crop production, and encouraged by higher demands that accompany increased human populations and welfare needs. If these bacteria are considered to be of environmental origin and to belong to the SWAS area, these resistances might involve the acquisition of mobile genetic elements spread from accumulated wastes (Anand *et al.*, 2021; Chowdhury & Uddin, 2022), a co-selection during the development of tolerance to biocides (Wales & Davies, 2015) in the accumulated wastes and to those used during routine management of the SWAS areas, a co-selection during the tolerance process against heavy metals present in the accumulated wastes (Wales & Davies, 2015; Anand *et al.*, 2021; Chowdhury & Uddin, 2022) or other stressing factors.

Mastering their origins and the pathways they follow represents pressing research challenges with the current One Health paradigm that requires holistic contributions to address all health issues (Cantón *et al.*, 2013; McEwen & Collignon, 2018). These holistic contributions would guide orientations of contextual waste management policies at all locations, and could extend to other healthcare institutions that share

similar environmental variables or be adjusted to suit local realities.

Gentamicin was the most effective drug, followed by Clindamycin and Erythromycin in Gram-positive bacteria. These are advisable broad-spectrum alternatives for potential infections acquired in these hospitals. These antibiotics proved to be effective on some bacterial populations recovered from hospital surfaces and from ambient air of three out of the four target institutions (UdMTH, BangDH, BPH) (Tchapdie Ngassam *et al.*, 2017; Fotsing Kwetche *et al.*, 2020; Menteng Tchuente *et al.*, 2023); as well as in a parallel survey conducted on bacterial population profile in high-risk infectious premises within the same institutions (Taffo *et al.*, 2024).

Relatively, high rates of isolates susceptible to Trimethoprim/Sulfamethoxazole were observed. This finding has become uncommon in human or animal medicine, and resurfaces debate orientations towards the environmental origin of these bacteria. In fact, bacteria recovered from hospital environments in previous studies (Tchapdie Ngassam *et al.*, 2017; Fotsing Kwetche *et al.*, 2020; Menteng Tchuente *et al.*, 2023) and in the above parallel investigation (Taffo *et al.*, 2024) revealed high resistance rates with this drug combination. This contrasting figure also deserves further comparative investigations.

In 2021, Kom Fotso *et al.* (2024) reported high rates of susceptible isolates from the UdMTH with a similar investigation protocol. Rate variation between 2021 and 2024 could be, at first glance in line with bacterial population evolution due to weaknesses in hospital hygiene over time or other factors yet to be properly highlighted. Admitting that the isolates are potential infectious disease etiologies (professional or opportunistic pathogens), and that their loads are above infectious doses (Dancer, 2014), each of these sites would represent a risky place for patients, especially "Y". Otherwise, and based on the present findings, the hygiene policies should be rethought holistically to mitigate the current potentially overlooked healthcare-associated infections risks, though most of the resistant bacterial strains likely disseminate from farms (Simo Louokdom *et al.*, 2018; Yawat Djogang *et al.*, 2018; Fotsing Kwetche *et al.*, 2021; Ngandjui Yonga *et al.*, 2021; Zegang Tchabda *et al.*, 2021; Mbognou *et al.*, 2024). Then, resistance

dissemination from farms should also deserve similar consideration in the overall policy regarding the control of resistant infections which firmly relies on all stakeholders' education. Accordingly, encouraging observance of biosafety and biosecurity rules in these areas of waste accumulation sites and institutions as a whole appears as a priority necessity to meet the 1st, 3rd and 4th Sustainable Development Goals expectations. This improvement could help prevent the selection, and the spread of resistant infectious agents, then mitigate infectious disease rates and related drawbacks in exposed vulnerable populations.

5. CONCLUSION

The present investigation on waste accumulation site bacteria profile revealed that half of it consisted of *Staphylococcus*, while Gram-positive and Gram-negative rods accounted for a quarter each. In terms of bacterial loads, Gram-negative rods loads were greater than those of the other bacterial types. Their diversities and loads were lower in the ambient air than in the soil samples. Highest bacterial diversities and loads were basically observed in the vicinity of solid waste accumulation sites. Investigations through the susceptibility profile revealed high rates of resistant isolates, especially to beta-lactams, while Gentamicin, Clindamycin, Erythromycin and Trimethoprim/Sulfamethoxazole were most effective. Encouraging observance of rules in line with biosafety and biosecurity in contextual hospital hygiene policies emerged as a priority necessity to meet the United Nations' 2030 1st, 3rd and 4th Sustainable Development Goals needs.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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