Scientia Africana, Vol. 23 (No. 3), August, 2024. Pp 379-394
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ASSESSMENT OF MICROBIAL CONTAMINATION ON GENERATOR SURFACES: A CASE STUDY AT THE UNIVERSITY OF PORT HARCOURT, NIGERIA

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Received: 03-07-2024
Accepted: 01-08-2024

https://dx.doi.org/10.4314/sa.v23i3.34
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Journal Homepage: http://www.scientia-african.uniportjournal.info
Publisher: *Faculty of Science, University of Port Harcourt.*

ABSTRACT

Microorganisms pervade the atmosphere, with inert surfaces serving as secondary repositories for the transmission of bacteria and fungi, posing public health concerns. This study aimed to assess the microbial burden on top surfaces and handles of specific generators at the University of Port Harcourt. Total Heterotrophic Bacteria counts ranged from 5.0 to 8.13 log CFU/ml, with the highest count observed on the handle of a generator at Ematex and the lowest on the top of a generator at the SSLT building. Total Fungi counts ranged from 5.0 to 6.45 log CFU/ml, with the highest count on the handle of a generator at English House and the lowest on the handle of a generator at Ofrima and the top of a generator at SSLT. Identified organisms include Staphylococcus spp, Enterococcus spp., Klebsiella spp., Bacillus spp., Salmonella spp., Pseudomonas spp., Escherichia coli, as well as Aspergillius spp., Penicillium spp., Chysosporium spp., Fussarium spp., Muccur spp., and Candida spp. Microorganisms on generator handles exceeded those on the top, and the microbial profiles of handles were similar across the generator sets. Improved personal hygiene and regular handwashing is advised to mitigate bacterial presence on hands, which can be transferred from generator surfaces and handles.

Keywords: Bacteria; Bioaerosols; Fungi; Generator surfaces; Public health; Secondary reservoirs

INTRODUCTION

Microorganisms in the atmosphere (bioaerosols) are diverse and dynamic components of Earth's ecosystems, influencing weather, climate, nutrient cycling, and human health in various ways (Shen and Yao, 2023). Dominant among these organisms are bacteria and fungi, which are ubiquitous microorganisms found in various environments, including material surfaces.

Their presence on surfaces can have significant implications across different domains, including healthcare (Frey-Klett et al., 2011). The public health implications of certain bacteria and fungi, include skin infections, respiratory infections, bacteremia, wound infections, gastroenteritis, opportunistic diseases, and allergies (Gnat et al., 2021). Examples include *Staphylococcus aureus*, *Escherichia coli*, and *Candida albicans*. Bacteria and fungi can form biofilms on surfaces, which are communities of microorganisms encased in a matrix of extracellular polymeric substances. Biofilms can be resistant to antibiotics and disinfectants, making them difficult to eradicate and posing a threat in medical settings (Wolfmeier et al., 2018). Surfaces contaminated with pathogenic bacteria and fungi can serve as reservoirs for the spread of infectious diseases through direct contact or via contaminated objects and food (Jablonska-Trypuc et al., 2022). Thus, bacteria and fungi on outdoor material surfaces have a lot of implications.

In the intricate ecosystem of microbial transmission, the journey from animated sources to inanimate environmental reservoirs holds significant implications for public health (Halpin et al., 2021). Microorganisms, propelled by various vectors, can find a niche in inanimate settings, potentially transforming them into secondary reservoirs ripe for proliferation. Understanding this dynamic interplay between animate and inanimate realms is crucial for assessing the risk posed by these reservoirs to human health. Inanimate things are ubiquitous fixtures in many environments which serve as conduits for the transmission and accumulation of microorganisms. Study of microbial loads have implicated a spectrum of microbial diversity, ranging from common inhabitants like *Staphylococcus* spp. and *Escherichiacoli* to fungal counterparts such as *Aspergillus* spp. and *Penicillium* spp. As a common inanimate object in building and homes, generator can serve as microbial burden, with quantity discrimination in the handles and surfaces. Despite the recognized role of surfaces in microbial transmission, research on microbial contamination of generator surfaces is limited, particularly within academic institutions like the University of Port Harcourt. Understanding the microbial profile of these surfaces is crucial for assessing health risks and developing appropriate prevention strategies.

To this end, this study aims to isolate and characterize microorganisms on the surfaces and handles of selected generators at the University of Port Harcourt. By identifying potential pathogens and assessing microbial loads, we seek to inform infection prevention strategies and contribute to a safer campus environment.

METHODOLOGY

Study Area

The research took place at the University of Port Harcourt (4.89786 N, 6.90194 E) in Nigeria, where samples were gathered from various industrial power generating sets located at English House, Ofrima, School of Science Laboratory Technology (SSLT), Animal and Environmental Biology (AEB), Niger Delta Development Commission hostel (NDDC), Ematex, Old Humanities, Park, Mandella block C, and old convocation Arena (Arena) within the university premises.

Sampling Method

Twenty (20) samples in total were gathered from industrial generator sets, with ten collected from the handles and another ten from the tops of the generators using sterile swab sticks moistened with sterile normal saline. These samples were subsequently transported to the laboratory for analysis. Upon arrival at the Microbiology laboratory, the swab sticks were inoculated in sterile Nutrient broth and then incubated for 24 hours.

Total Viable Cell Counts

The fundamental principle of this approach is to determine the total count of viable cells present in the analyzed samples, as outlined by Lundholm (1982). The spread plate technique

Scientia Africana, Vol. 23 (No. 3), August, 2024. Pp 379-394
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was employed for this purpose. MacCartney bottles containing 9 ml of normal saline (0.09 % w/v NaCl) were grouped in sets of three and appropriately labeled as 1:10, 1:100, and 1:1000. A 1 ml aliquot of the broth samples was aseptically transferred into the MacCartney bottle labeled as 1:10. Subsequently, a series of three ten-fold serial dilutions were performed across the remaining bottles, ranging from 1:100 to 1:1000. To inoculate the diluted samples onto agar plates (Nutrient agar, MacConkey agar, Centrimide agar, Sabouraud Dextrose agar, Mannitol Salt Agar), 0.1 ml of the diluted samples from each concentration (1:10, 1:100, and 1:1000) were aseptically transferred and spread evenly using a sterile bent glass rod. Plates were appropriately labeled according to the dilutions and the process was duplicated. Following inoculation, the plates were inverted and then incubated at 37 °C for 24 hours. After the designated incubation period, the plates were examined, and the results were recorded. This procedure was repeated for the remaining samples. The presence of colonies on the agar plates indicated viable cells, and the total viable cell count was determined using a bacterial colony counter.

Isolation of Microorganisms

The isolates from the samples were streaked onto various pre-prepared media, including Nutrient Agar, MacConkey Agar, Mannitol Salt Agar, Centrimide Agar, and Sabouraud Dextrose Agar. These media, along with those exposed for 20 minutes (Stanley &Inuope, 2021) during sample collection, were then placed in the incubator for 24-48 hours. Specifically, Sabouraud Dextrose Agar was incubated at room temperature to encourage fungal growth. Following incubation, microbial growth was isolated and subjected to morphological identification and biochemical characterization. Positive cultures were identified based on their distinct appearance on the respective media, Gram staining, and confirmation through standard biochemical reactions (Franco-Duarte, et al., 2019; Roy, et al., 2023; Talaiekhozani, 2022)

Gram Staining

This technique is a differential method utilized for bacterial identification based on their characteristics as either Gram-positive or Gram-negative organisms, determined by their ability to retain a specific stain within their cell walls. The isolated organisms from the plates were spread onto a clean glass slide using a loopful of water and an inoculum, then allowed to air dry and heat fixed. Following this, the prepared smear underwent a series of staining steps: it was flooded with 1% crystal violet dye for 1 minute, excess stain rinsed off with distilled water, flooded with Lugol's iodine for 1 minute, rinsed again with distilled water, then flooded with 98% alcohol for 30 seconds, quickly rinsed with distilled water, and finally stained with Safranin red for 1 minute before being rinsed with distilled water. After air drying the smears briefly, a drop of oil immersion was added, and they were observed under a light microscope. This entire process was repeated for the filtrate, supernatant, and the entire sample of each plant sample (Franco-Duarte, et al., 2019; Roy, et al., 2023; Talaiekhozani, 2022)

Biochemical Test

The obtained test isolates underwent a series of biochemical tests, which encompassed the following:

Catalase Test

This test serves to distinguish bacteria based on their ability to produce the catalase enzyme. The enzyme's role is to neutralize hydrogen peroxide generated by superoxide dismutase, breaking it down into water and oxygen gas according to the equation: $2H_2O_2 \rightarrow$ (catalase) $2H_2O + O_2$. In this procedure, a drop of 3% hydrogen peroxide was placed on a clean, grease-free microscope slide. Using a flamed and cooled wire loop, a colony of each isolated microorganism was emulsified in the drop of reagent. The presence or absence of gas bubbles was then observed. The appearance of

gas bubbles indicated a positive result, while their absence indicated a negative result, as described by Reiner (2010).

Oxidase Test

This test is employed to detect microorganisms harboring the cytochrome oxidase enzyme, crucial in the oxygen transport chain. It serves to differentiate between oxidase-negative Enterobacteriaceae and oxidase-positive Pseudomonadaceae. In this procedure, a colony of the organism was spread onto a piece of Whatman (No. 1) filter paper previously saturated with oxidase reagent, comprising a 1% solution of N, N, N, N-tetramethyl-p-phenylene-diamine dihydrochloride in purified water. This was facilitated using a clean, grease-free glass slide that had been flame-sterilized and cooled. The presence or absence of a purple coloration within a 10-second interval was then observed (Franco-Duarte, et al., 2019; Roy, et al., 2023; Talaiekhozani, 2022)

Citrate Test

This test is employed to distinguish Enterobacteriaceae based on their ability to utilize citrate as the sole carbon source. Simmon's citrate agar was liquefied with agitation and distributed into test tubes. Following autoclaving, the tubes were allowed to cool and solidify into slants before inoculation with a pure culture using a wire loop. Incubation at 37°C for 24 hours ensued, during which a color shift from green to blue was monitored (Franco-Duarte, et al., 2019; Roy, et al., 2023; Talaiekhozani, 2022)

Indole Test

This test illustrates the capability of specific bacteria to break down the amino acid tryptophan into indole, which gathers in the medium. The indole production test holds significance in Enterobacteriae identification. In this procedure, a colony from the pure culture of each isolated bacterium was suspended in peptone water and then incubated at 37°C for 24 hours. Subsequently, 2-3 drops of Kovac's reagent were introduced. A color change in the top layer from pale yellow to red in the ring indicated a positive result (Franco-Duarte, et al., 2019; Roy, et al., 2023; Talaiekhozani, 2022)

Urease Test

Urea Agar, formulated by Christensen in 1946, was designed for discerning enteric bacilli. The urease test serves to ascertain an organism's capacity to hydrolyze urea by producing the enzyme urease. Urea results from the decarboxylation of amino acids. Hydrolyzing urea generates ammonia and CO_2. Ammonia formation raises the medium's pH, evident through phenol red's color shift from light orange at pH 6.8 to magenta (pink) at pH 8.1. Rapid urease-positive organisms turn the entire medium pink within 24 hours. To conduct the test, a streak was made on the surface of a urea agar slant using a portion of the well-isolated colony of the test organism. The tube cap was left loosely open, and incubation occurred at 35°-37°C in ambient air for 48 hours. Examination for the development of a pink color ensued.

Triple Sugar Iron Test

The triple sugar-iron agar (TSI) test is crafted to distinguish among various groups or genera of the Enterobacteriaceae, all of which are ~~G~~am-negative bacilli capable of fermenting glucose with acid production. Additionally, it aims to discern them from other ~~G~~am-negative intestinal bacilli. This differentiation hinges on discrepancies in carbohydrate fermentation patterns and hydrogen sulfide production among the different groups of intestinal organisms. Carbohydrate fermentation is denoted by gas presence and a noticeable color alteration of the pH indicator, phenol red. The formation of hydrogen sulfide in the medium manifests as a black precipitate that darkens the medium in the butt of the tube. To perform the test, a sterilized straight inoculation loop is employed to touch the top of the isolated colony and subsequently inoculated into the TSI Agar. This is achieved by initially stabbing through the center of the medium to the tube's bottom, followed by streaking on the

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surface of the agar slant. The tube cap is left loosely, and incubation takes place at 35°C in ambient air for 18 to 24 hours (Franco-Duarte, et al., 2019; Roy, et al., 2023; Talaiekhozani, 2022)

Motility test:

Half-strength nutrient agar was prepared and poured in a test tube, and the test organism was inoculated into the semi-solid broth using an inoculating needle via a stab technique. The broth was then incubated at 37°C for 18–24 hours. Afterwards, it was observed for signs of motility, such as haze or cloudiness indicating movement, and spread of growth away from the inoculation site.

Methyl Red-Voges-Proskauer (MR-VP) Test:

This test differentiates between organisms that utilize glucose via mixed-acid fermentation and those that utilize the 2,3-butanediol fermentation pathway.

The Voges-Proskauer (VP) test detects acetoin production, a precursor of 2,3-butanediol, produced during the 2,3-butanediol fermentation pathway.

Procedure:

i) MR-VP broths were prepared and inoculated with the test organism in each tube.

ii) The tubes were incubated at 37°C for 48 hours.

iii) After incubation, the culture suspension was divided into new sterile test tubes.

iv) To one half of each tube, a few drops of methyl red were added, and the color change was observed.

v) To the other half, 30% α-naphthol was added followed by 40% potassium hydroxide. Color changes were observed in both halves.

Identification of Microbial Isolation

The microbial isolate was evaluated for its morphology, biochemical traits, and Gram stain results.

Microscopy for Fungi

Wet preparations were prepared by placing the swabs in a mount of 10% potassium hydroxide (KOH) on a glass slide, covered with a cover slip. Subsequently, the slide was examined under a microscope using a x40 objective to detect the presence of hyphae and arthrospores (Ponka & Baddar, 2014).

Identification of Fungi

Identification of isolates was based on gross morphology, microscopy. For fungal identification, a mash of hypha of the test organism were made on slides containing Lacto phenol cotton blue, covered with a cover slip and observed in X 40 microscope (Ponka & Baddar, 2014).

RESULT

Total Heterotrophic Bacteria count and Total Fungi count of organism isolated from generators in the University of Port Harcourt

The assessment included the evaluation of Total Heterotrophic Bacteria count and Total Fungi count of organisms isolated from generators located across various sites within the University of Port Harcourt. The Total Heterotrophic Bacteria count ranged from 5.0 log CFU/ml to 8.13 log CFU/ml, with the highest count observed on the Handle of the generator at Ematex, and the lowest on the Top of the generator at SSLT building.

For Total Fungi count, the range was from 5.0 log CFU/ml to 6.45 log CFU/ml. The highest count was recorded on the Handle of the generator at English house, while the lowest was observed on the Handle of the generator at Ofrima and the Top of the generator at SSLT.

Among the generator handles, the total bacteria count varied from 6.85 log CFU/ml to 8.13 log CFU/ml, with the highest count found

on the Handle of the generator at Ematex and the lowest at SSLT building. The total fungi count ranged from 5.0 log CFU/ml to 6.45 log CFU/ml, with the highest count recorded on the generator at English house and the lowest on the Handle of the generator at Ofrima.

Concerning generator tops, the total bacteria count ranged from 5.0 log CFU/ml to 8.07 log CFU/ml, with the highest count observed on the generator at Mandella block C and the lowest at SSLT building. The total fungi count varied from 5.0 log CFU/ml to 6.45 log CFU/ml, with the highest count seen on the generator at Old Humanities and the lowest on the Top of the generator at SSLT. These findings are summarized in Table 1 below.

Biochemical and Morphological Characterization of Bacteria Isolated

Biochemical assays were employed to identify bacteria isolated from generators located across various sites within the University of Port Harcourt. The outcomes of these assays are presented in Table 2.

Table 1. Total Heterotrophic Bacteria count and Total Fungi count of organism isolated from generators in the University of Port Harcourt

Sample code		Total Heterotrophic Bacteria			Total Fungi count		
		Count	CFU/ml	LogCFU/ml	Count	CFU/ml	LogCFU/ml
English House	Handle	70	$7.0x10^6$	6.85	28	$2.8x10^6$	6.45
	Top	3	$3.0x10^5$	5.48	2	$2.0x10^5$	5.30
Ofrima	Handle	13	$1.3x10^6$	6.11	1	$1.0x10^5$	5.00
	Top	10	$1.0x10^6$	6.00	-		
SSLT	Handle	7	$7.0x10^6$	6.85	3	$3.0x10^5$	5.48
	Top	1	$1.0x10^5$	6.00	1	$1.0x10^5$	5.00
AEB	Handle	31	$3.1x10^6$	6.49	8	$8.0x10^5$	5.90
	Top	12	$1.2x10^5$	6.08	3	$3.0x10^5$	5.48
NDDC	Handle	94	$9.4x10^6$	6.97			
	Top	61	$6.1x10^6$	6.79	2	$2.0x10^5$	5.30
Ematex	Handle	135	$1.35x10^8$	8.13	5	$5.0x10^5$	5.70
	Top	74	$7.4x10^6$	6.87	3	$3.0x10^5$	5.48
Old Humanities	Handle	68	$6.8x10^6$	6.83	4	$4.0x10^5$	5.60
	Top	76	$7.6x10^6$	6.88	5	$5.0x10^5$	5.70
Park	Handle	84	$8.4x10^6$	6.92	6	$6.0x10^5$	5.78
	Top	84	$8.4x10^6$	6.92	3	$3.0x10^5$	5.48
Mandella block C	Handle	64	$6.4x10^6$	6.81	5	$5.0x10^5$	5.70
	Top	118	$1.18x10^8$	8.07	4	$4.0x10^5$	5.60
Arena	Handle	11	$1.1x10^6$	6.04	2	$2.0x10^5$	5.30
	Top	-			2	$2.0x10^5$	5.30

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Table 2: Biochemical and Morphological Characterization of Bacteria Isolated from generators in the University of Port Harcourt

Samples	Catalase	Citrate	Coagulase	Oxidase	Indole	Urease	Motility	Lactose	Glucose	Sucrose	MR	VP	TSIA				Elevation	Edge	Shape	Surfaces	Pigmentation	Cell shape	Gram reaction	Probable isolate
													Butt	Slant	H_2S	Gas								
English	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
House	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
Handle	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt h	Crm	Rod	-	*Salmonella sp*
Top	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
	-	-	-	+	-	-	-	-	-	-	-	-	Y	R	-	-	Rsd	Ent	Rnd	Smt	Bgn	Rod	-	*Pseudomonas* sp
	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt h	Crm	Rod	-	*Salmonella sp*
Ofrima	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
Handle	-	-	-	+	-	-	-	-	-	-	-	-	Y	R	-	-	Rsd	Ent	Rnd	Smt th	Bgn	Rod	-	*Pseudomonas* sp
	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt h	Crm	Rod	-	*Salmonella sp*
Top	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
SSLT	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
Handle	-	-	-	+	-	-	-	-	-	-	-	-	Y	R	-	-	Rsd	Ent	Rnd	Smt	Bgn	Rod	-	*Pseudomonas* sp
	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt	Crm	Rod	-	*Salmonella sp*
Top	-	-	-	-	-	+	+	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt	Crm	Rod	-	*Salmonella sp*
AEB	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
Handle	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
	-	-	-	+	-	-	-	-	-	-	-	-	Y	R	-	-	Rsd	Ent	Rnd	Smt	Bgn	Rod	-	*Pseudomonas* sp
	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt	Crm	Rod	-	*Salmonella sp*
	-	-	-	-	-	+	+	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
Top	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt	Crm	Rod	-	*Salmonella sp*
	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
NDDC	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
Handle	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
	-	-	-	-	-	+	+	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
Top	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
Ematex	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
Handle	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
Top	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
Old	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
Human	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
Ities	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
Top	-	+	-	+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
Park	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
Handle	-	-	-	-	-	+	+	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
Top	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp
	-	-	-	-	-	+	+	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
	-	-	-	-	+	-	-	+	+	+	+	-	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Crm	Rod	-	*Escherichia coli*
Mandel	-	+		+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
Block	+	-	-	-	-	-	-	-	-	-	+	-	Y	R	+	-	Rsd	Ent	Rnd	Smt	Crm	Rod	-	*Salmonella sp*
Handle	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
	-	-	-	-	+	-	-	+	+	+	+	-	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Crm	Rod	-	*Escherichia coli*
Top	-	+		+	-	+	-	+	+	+	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Mcd	Crm	Rod	-	*Klebsiella* sp
	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt	Crm	Cci	+	*Staphylococcus* sp
	-	-	-	-	-	+	+	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rods	+	*Enterococcus* sp
Arena	-	-	-	-	-	+	-	-	-	-	-	+	Y	Y	-	-	Rsd	Ent	Rnd	Smt	Ylw	Rod	+	*Enterococcus* sp
Handle	+	-	+	-	-	+	-	+	+	+	+	+	Y	Y	-	+	Rsd	Ent	Rnd	Smt h	Crm	Cci	+	*Staphylococcus* sp
Top	-	-	-	+	-	+	-	-	-	-	-	+	Y	Y	-	-	Flt	Ent	Rnd	Smt	Wht	Rod	+	*Bacillus* sp

Keys [+]Positive; [-]Negative;[Y]Yellow; [R]Red// [Rsd]Raised;[Flt]Flat;
[Ent]Entire;[Rnd]Round;[Mcd]Mucoid;[Smt]Smoot;[Crm]Cream;[Ylw]Yellow;[Wht]White;[Bgn]Blue-green;[Rds]Rod;[Cci]Cocci

Percentage Occurrence of Organism Isolated

The isolated bacteria consist of Staphylococcus spp., *Enterococcus* spp., *Klebsiella* spp., *Bacillus* spp., *Salmonella* spp., *Pseudomonas* spp., and *Escherichia coli*. Among these, *Staphylococcus* spp. had the highest occurrence rate at 21.54%, followed by *Enterococcus* spp. and *Klebsiella* spp. at 20.00% each, and *Bacillus* spp. at 16.92%. *Salmonella* spp. accounted for 10.77%, *Pseudomonas* spp. for 7.69%, and *Escherichia* coli for 3.08%. This distribution is illustrated in Fig. 1.

Regarding fungi, *Aspergillus* spp. dominated with a prevalence of 41.94%, followed by *Candida* spp. at 35.48%. *Penicillium* spp. exhibited a prevalence of 22.58%, while *Chysosporium* spp., *Fussarium* spp., and *Mucor* each showed a prevalence of 2.94%. This is depicted in Fig. 2.

The organisms isolated from the handle of the generator encompassed *Staphylococcus* spp., *Enterococcus* spp., *Klebsiella* spp., *Bacillus* spp., *Salmonella* spp., *Pseudomonas* spp., and *Escherichia* coli. *Klebsiella* spp. was the most prevalent at 22.22%, followed by *Staphylococcus* spp. and *Enterococcus* spp. at 19.44% each, and *Bacillus* spp. at 16.67%. *Salmonella* spp. represented 11.11%, *Pseudomonas* spp. 8.33%, and *Escherichia* coli 2.78%. Fig. 3 illustrates this distribution.

Concerning fungi, *Aspergillus* spp. and *Candida* spp. were most prevalent, each at 35.00%, followed by *Penicillium* spp. at 15.00%. *Chysosporium* spp., *Fussarium* spp., and *Mucor* each exhibited a prevalence of 5.0%. This data is presented in Fig. 4.

From the top of the generator, *Staphylococcus* spp., *Enterococcus* spp., *Klebsiella* spp., *Bacillus* spp., *Salmonella* spp., *Pseudomonas* spp., and *Escherichia coli* were isolated, with *Staphylococcus* spp. having the highest prevalence at 24.14%. *Enterococcus* spp. and *Bacillus* spp. showed a prevalence of 20.69% each, *Klebsiella* spp. 17.24%, *Salmonella* spp. 10.34%, and *Pseudomonas* spp. and *Escherichia* coli had the lowest prevalence at 3.45%. This is illustrated in Fig. 5.

Regarding fungi, Aspergillus spp. had the highest prevalence at 42.86%, while Penicillium spp. and Candida spp. had a prevalence of 28.57% each, as depicted in Fig. 6

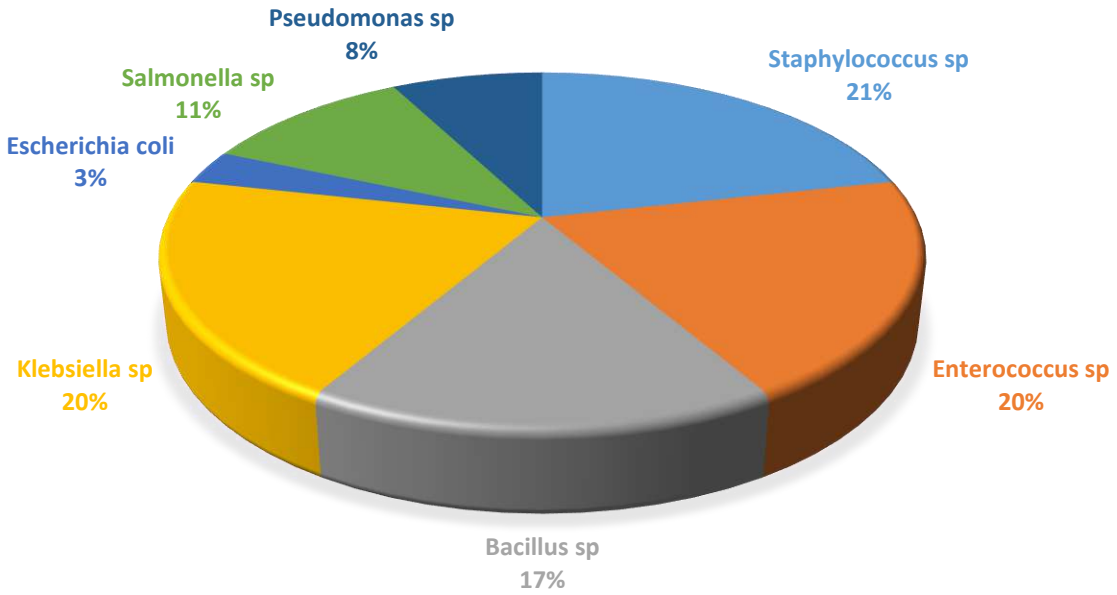

Fig. 1. Percentage occurrence of bacteria isolated from generators in the University of Port Harcourt

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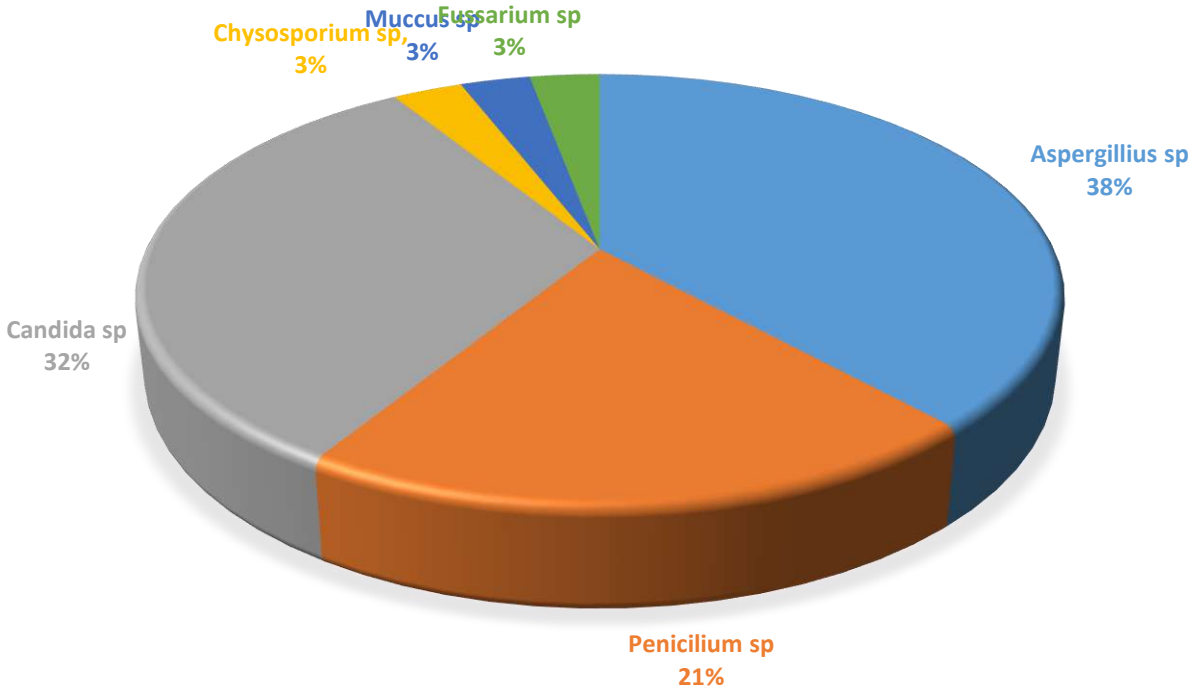

Fig. 2 Percentage occurrence of fungi isolated from generators in the University of Port Harcourt

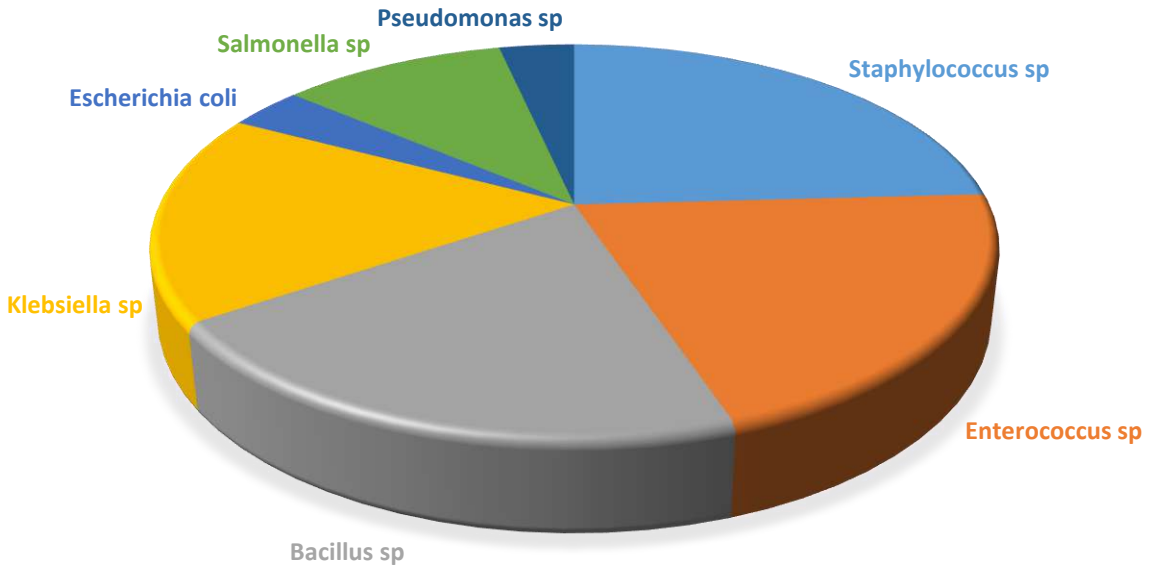

Fig. 3. Percentage occurrence of Bacteria isolated from Top of generator in the University of Port Harcourt

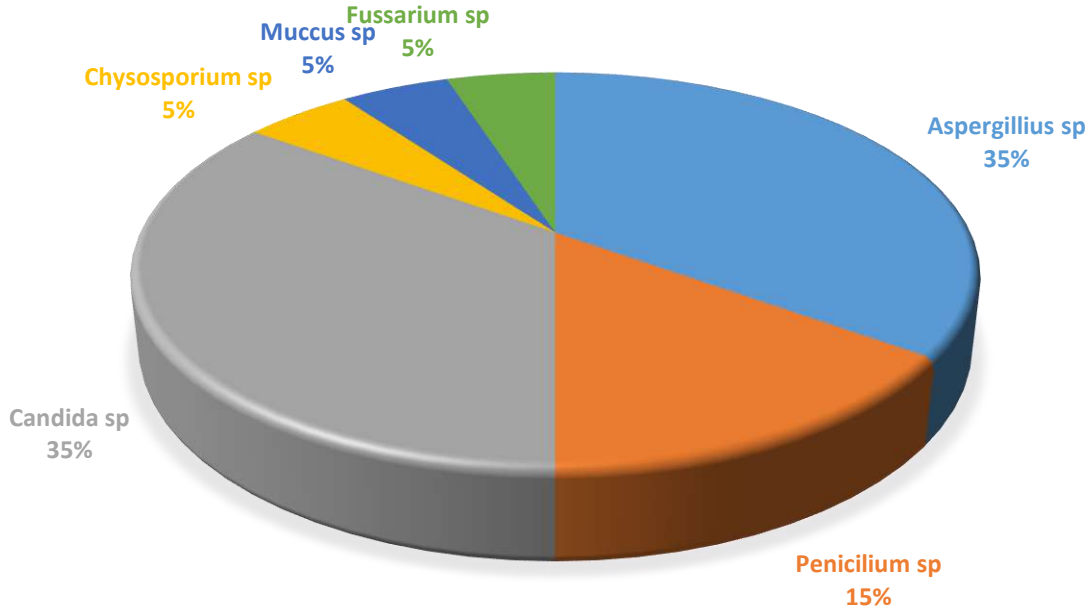

Fig. 4. Percentage occurrence of Fungi isolated from generator handles found in different locations in the University of Port Harcourt

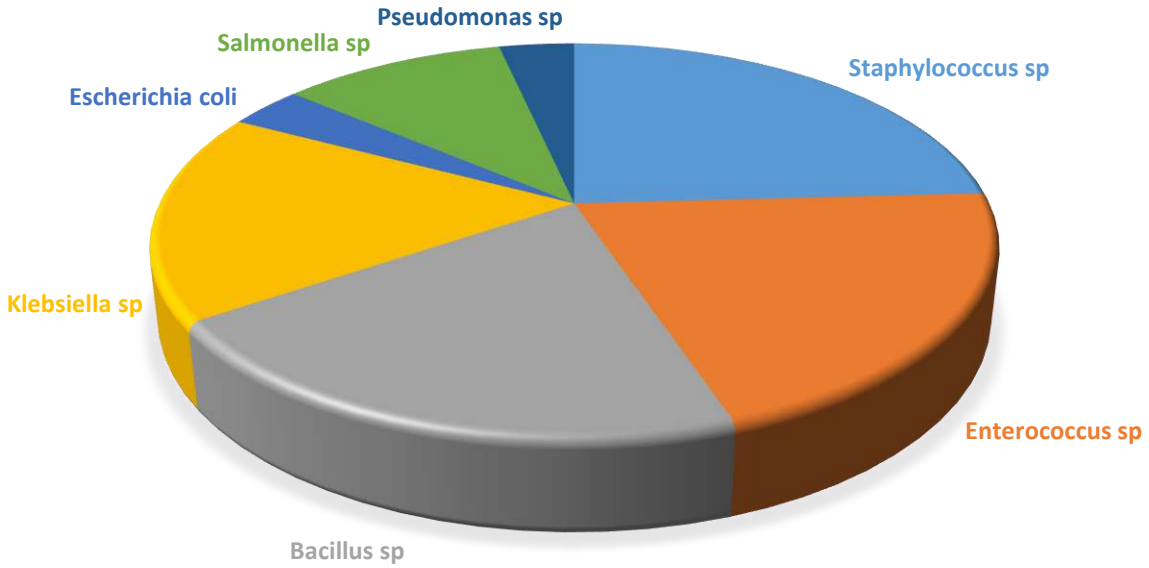

Fig. 5. Percentage occurrence of Bacteria isolated from Top of generator in the University of Port Harcourt

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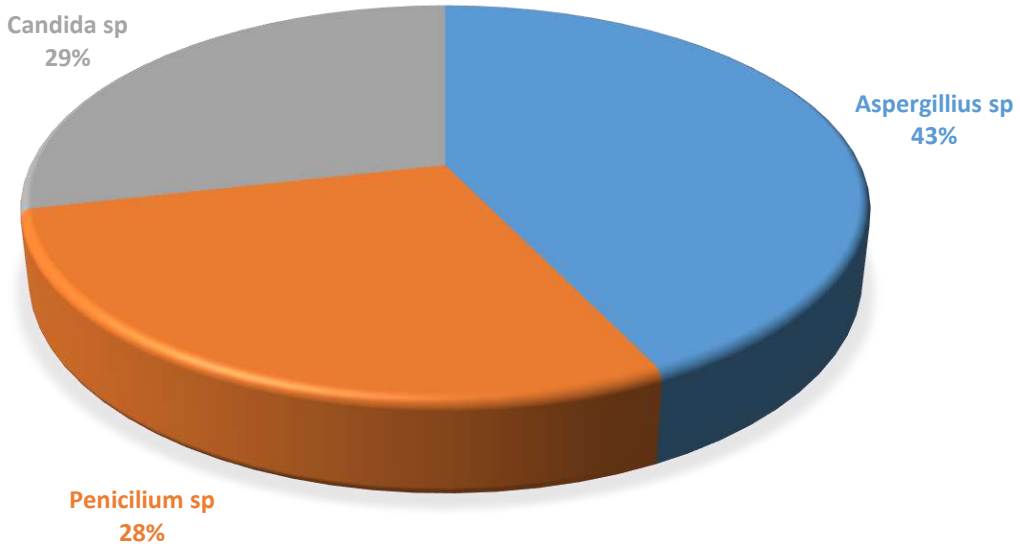

Fig. 6. Percentage occurrence of Bacteria isolated from Top of Generator in the University of Port Harcourt

DISCUSSION

Determination of microbial loads on commonly used materials and equipment is a common trend in public health-related investigation. Knowledge on bacterial and fungi colonization of power generator is limited, thus this investigation dwelt on the isolation of bacteria and fungi on generator surfaces in the University of Port Harcourt, using standard techniques. Results obtained shows that *Staphylococcus* sp. (bacteria) and *Aspergillus* sp (Fungi) dominated the bacterial and fungi genera identified.

Staphylococcus sp., the most frequently isolated bacterium in this study, may be attributed to aerosols transmitted from human bodies and other inanimate objects, as *S. aureus* commonly resides in human nostrils (Laux et al., 2019). This genus has been isolated and identified on numerous inanimate objects (Domon et al., 2016; Rathore et al., 2022) and by extension methicillin-resistant *Staphylococcus aureus* (Lin et al., 2017). Though, report of *Staphylococcus* and other bacteria and fungi is hard to find on generator surfaces, Marques et al. (2007) isolated this genus on the surfaces of steel metal. Like inanimate object, *Staphylococcus* are also found on the surfaces of animal skins, including humans (Schofer et al., 2011). Skin colonization of *Staphylococcus* play the role of commensalism and enjoys wide publication (Noble, 1998; Coates et al., 2014; Brown and Horswill) ~~H~~However, Ghalehnoo (2018) reported skin (structure) infection caused by *Staphylococcus*. *Staphylococcus*-implicated aerosols, gets to the nose and cause respiratory infection especially in immunocompromised individuals. Food in contact of contaminated surfaces can cause foodborne diseases and food poisoning (Nair et al., 2014). Notably, it is the only species found in humans that produces the enzyme coagulase, leading to the designation of other species as coagulase-negative Staphylococci. *Staphylococcus* can also cause soft tissue infections, pneumonia, sepsis, gastroenteritis, and other gastrointestinal symptoms through the ingress of its toxins into the body (Chiranth, 2018). The infection caused by these microorganisms, becomes complex and complicated due to poor hygiene practices (Navab-Daneshmand et al., 2018). From the

foregoing, it is evident that contact with contaminated surfaces, poor hygiene practice and elicitation of survival metabolites and toxins increase the chances of public health diseases. These factors had promoted the cause of gastrointestinal tract infection, opportunistic infections and waterborne diseases by *Escherichia* (Auta and Paul, 2020), urinary tract infections, (particularly among immunocompromised individuals) by *Klebsiella* spp., meningitis, endocarditis, septic arthritis, septic shock, and bacteremia by *Micrococcus* spp. (Roche and Smyth, 2005; Cundell, 2018), coughing, wheezing, chest pain, shortness of breath, as well as allergic reactions such as asthma exacerbations, allergic bronchopulmonary aspergillosis, invasive aspergillosis, and aspergilloma by *Aspergillus* spp. (Bazaz and Denning, 2019; Li et al., 2019), foodborne illnesses and lung infections by *Penicillium* spp. (Navale et al., 2021), liver and kidney damage alongside carcinogenic effects by *Fusarium* (Awuchi et al., 2022).

The identification of bacteria genera and fungal species underscores the diversity of microbial communities within generator environments, necessitating further exploration of their potential health impacts, particularly for individuals with compromised immune systems. In such circumstances, different microbial interaction may ensue, which include, synergism, commensalism, mutualism and parasitism (Zheng et al., 2020). This condition may cause multiple infection in an individual, particularly if immunocompromised. Another condition to consider is the after effect of heavy metal ion from the metal surfaces arising from metal-microbes interaction. Traditionally, microbes cause metal surface modification, influence redox reaction, corrosion inhibition and corrosion (Victoria et al., 2021). Imo et al. (2018) reported the adsorption competence of *Aspergillus versicolor* that colonized a metal surface, which ultimately became deformed. Reaction of *Staphylococcusepidermidis* on metal surface reflected on metal surface oxidation and dissolution (Gabriel et al., 1994). In turn microbe are inhibited or become resistant to metal inhibition (Chandrangsu et al., 2017). In these variety of interaction and effect, it is right to guess that the physiological attributes of the microorganisms might be affected. These changes may be seen in altered metabolic activity, adaptation to metal-rich environment, gene expression in response to metal resistance and stress response, and accumulation of metal ions (Hoostal et al., 2008; Sharma and Kumar, 2021; Winge et al., 1998; Wang et al., 2024). These new attributes imposed by the metal surfaces, might introduce novel impact on humans which may be positive or negative. The possible implication of these physiologically altered microbes create avenue for indebt research in public health microbiology.

The results of this study offer valuable insights into the intricate dynamics of microbial colonization on generator surfaces and handles within the University of Port Harcourt. The prevalence and diversity of microorganisms detected highlight the significance of these energy sources as potential reservoirs for pathogenic organisms, posing a notable concern for public health. One of the key observations from this research is the disparity in microbial load between generator surfaces and handles. The higher microbial burden observed on handles compared to top surfaces underscores the critical role of touchpoints in facilitating microbial dissemination. Such findings emphasize the importance of targeted hygiene interventions, focusing not only on overall surface cleanliness but also on specific areas prone to high microbial accumulation, such as handles.

CONCLUSION

This work was carried out to determine the bacterial and fungal load on generator in the University of Port Harcourt. The bacteria and fungi isolated from the top and handles of commercially used generators showed that they were contaminated. The bacteria and fungi isolated from the handles and tops of the generator sets were similar, however their prevalence rate was slightly different. The

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organisms include: *Staphylococcus* spp., *Enterococcus* spp., *Klebsiella* spp., *Bacillus* spp., *Salmonella* spp., *Pseudomonas* spp. and *Escherichia coli*. Fungi isolated are *Aspergillius* spp., *Penicillium* spp., *Chysosporium* spp., *Fussarium* spp., *Muccur*, and *Candida* spp. Thesemicroorganisms obtained were similar to those obtained by Viani *et al*. (2020), who demonstrated that bioaerosols and humans contributed to the high microbial load, proving that humans are a vector for the transport of bioaerosols. In response to these findings, promoting effective hygiene practices emerges as a crucial strategy for mitigating the risk of microbial transmission from generator surfaces to human hands. Encouraging regular handwashing among individuals who come into contact with generators can significantly reduce the likelihood of microbial transfer and subsequent contamination. Additionally, implementing routine cleaning and disinfection protocols for generator surfaces and handles can help minimize microbial colonization and contribute to creating a safer environment for all occupants.

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