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Bacteriological assessment and antibiotic susceptibility patterns of bacteria isolated from hospital door handles in Port Harcourt, Nigeria

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ABSTRACT

Hospital door handles are frequently touched by healthcare workers, patients, and visitors, making them potential reservoirs for the transmission of infectious agents. This study aimed to isolate and identify bacteria from door handles in selected hospitals in Port Harcourt and to determine their antibiotic susceptibility patterns. Swab samples were collected from door handles in office, reception, and ward areas using sterile swabs moistened with normal saline. The samples were transported to the Microbiology Laboratory for analysis within 1-2 hours of collection. Isolation and identification of bacterial isolates were carried out using standard microbiological procedures, including morphological examination and biochemical tests. Antibiotic susceptibility testing was performed using standard laboratory methods. Data obtained were statistically analyzed, with significance set at $p < 0.05$. Bacterial counts ranged from $2.30 \pm 0.14 \times 10^5$ to $5.81 \pm 0.28 \times 10^5$ CFU/cm² in reception areas, $1.20 \pm 0.12 \times 10^5$ to $6.66 \pm 0.21 \times 10^5$ CFU/cm² in ward areas, and $3.58 \pm 0.70 \times 10^4$ to $1.62 \pm 0.21 \times 10^5$ CFU/cm² in office areas, with significant differences observed among locations. Eight bacterial genera were identified: *Staphylococcus* (15%), *Bacillus* (14%), *Pseudomonas* (14%), *Escherichia coli* (14%), *Streptococcus* (14%), *Klebsiella* (11%), *Proteus* (11%), and *Alcaligenes* (7%). Gram-negative isolates showed high resistance to Ceporex, Ceftriaxone, Cefuroxime, Augmentin (100%), Streptomycin, and Gentamicin, while Gram-positive isolates were highly resistant to Azithromycin, Amoxicillin, Erythromycin, Ceftazidime, and Streptomycin (100%). Hospital door handles in Port Harcourt harbor significant levels of potentially pathogenic and antibiotic-resistant bacteria, emphasizing their role in the transmission of nosocomial infections. Strengthening hand hygiene practices and providing hand sanitizer dispensers near doorways are strongly recommended.

Keywords: Hospital door handles, bacterial contamination, antibiotic susceptibility, nosocomial infections, antimicrobial resistance, healthcare-associated pathogens.

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INTRODUCTION

The transmission of infectious diseases through hand contact remains a major public health concern due to frequent interaction with contaminated fomites such as door handles. These surfaces can harbor bacterial and parasitic pathogens that are implicated in disease transmission and outbreak occurrence (Miller and Diep, 2020; Noskin et al., 2021). Globally, diarrhoeal diseases account for over 1.7 million deaths annually, while respiratory infections cause approximately 1.5 million deaths, many of which may result from indirect contact with contaminated surfaces (Ogg, 2018).

Studies have identified Gram-positive bacteria such as *Staphylococcus aureus* and Gram-negative organisms including *Escherichia coli*, *Klebsiella* spp., and *Pseudomonas* spp. on frequently touched surfaces such as chairs, tables, windows, and door handles (Rusin et

al., 2022). The presence of these pathogens poses a significant threat, particularly to immunocompromised individuals (Pankey and Sabath, 2024). Hard, non-porous surfaces like door handles facilitate high bacterial transfer rates to human hands. Consequently, considerable emphasis has been placed on hand hygiene practices, including the use of hand sanitizers and disinfectant wipes (Stout et al., 2020). Wipes containing higher ethanol concentrations demonstrate enhanced antimicrobial activity and can mechanically remove endospores.

Despite widespread awareness, compliance with hand hygiene remains suboptimal; studies suggest that up to 60% of adults fail to wash their hands when necessary (Itah and Ben, 2004). Misconceptions that microbes are confined to laboratories and hospitals further contribute to risky behaviors when touching everyday surfaces (Stout et al., 2020). Indeed, approximately 80% of infections are transmitted through hand contact with contaminated hands or objects (Tagoe et al., 2021).

Experimental evidence supports the rapid spread of contamination via contact surfaces. Using an invisible fluorescent tracer, Miller and Diep (2020) demonstrated that artificial contamination of public surfaces was transferred to 86% of exposed individuals, with 82% subsequently carrying the tracer to their homes or personal belongings. Many microorganisms can survive for extended periods on non-porous materials such as countertops, telephones, and door handles, with some remaining infectious at very low doses (Kawo et al., 2020; Pinner et al., 2019). Enterococci, for example, can persist under dry conditions on fabrics commonly used in healthcare environments, increasing the likelihood of pathogen transfer after contact with contaminated objects (Kluytmans et al., 2017).

Hospital door handles are frequently contaminated with diverse microorganisms, including bacteria and fungi, making them potential sources of nosocomial infections. Poor hand hygiene among healthcare workers and visitors further amplifies the risk of cross-contamination (Hiddron et al., 2018). Although hand hygiene is recognized as a critical infection control measure, adherence to recommended protocols is often inconsistent (Allegranzi, 2021). Visitors may also introduce external pathogens into healthcare facilities, increasing the microbial burden on shared surfaces (CDC, 2019).

Nevertheless, scientific data on microbial contamination of environmental surfaces, particularly within healthcare settings in developing regions, remain limited (Gao et al., 2020; Heinitz et al., 2020). Hospital environments, especially high-contact surfaces such as door handles, can serve as reservoirs for pathogenic microorganisms. In many healthcare facilities in Port Harcourt, Nigeria, routine surveillance of microbial contamination on these surfaces is inadequate, and information regarding the antibiotic resistance patterns of isolated bacteria is scarce.

The growing prevalence of antibiotic-resistant bacteria presents a critical challenge to public health, particularly in clinical settings where vulnerable patients face increased risk. Insufficient knowledge of bacterial profiles and their susceptibility patterns may compromise infection prevention strategies, resulting in higher rates of hospital-acquired infections, prolonged hospital stays, and increased healthcare costs.

Therefore, this study aimed to determine the prevalence of bacterial contaminants on door handles in selected hospitals in Port Harcourt and to evaluate the antibiotic susceptibility patterns of the isolates, thereby providing data to support improved infection control practices.

MATERIALS AND METHODS

Study area

The study was conducted in selected hospitals within Port Harcourt, Rivers State, Nigeria. Port Harcourt is a major urban center in the Niger Delta region, characterized by a tropical climate with high humidity and significant rainfall, conditions that can promote the survival and transmission of microorganisms on environmental surfaces.

Four hospitals, coded as H1, H2, H3, and H4, were included in the study to ensure spatial representation across the study area. The geographic coordinates of the facilities were recorded using a Global Positioning System (GPS) device. Hospital H1 is located at latitude 4.798518°N and longitude 6.984882°E. Hospital H2 is situated at latitude 4.796346°N and longitude 6.990996°E, while Hospital H3 lies at latitude 4.793831°N and longitude 6.995668°E. Hospital H4 is positioned at latitude 4.798518°N and longitude 6.984882°E.

These hospitals experience high patient turnover and frequent human traffic, increasing the likelihood of microbial contamination on high-contact surfaces such as door handles. The inclusion of multiple hospitals provided a broader assessment of bacterial contamination and antibiotic resistance patterns within healthcare environments in Port Harcourt.

Sample collection

Swab samples were collected from door handles in offices, reception areas, and wards of selected hospitals in Port Harcourt, Rivers State. Each sample was obtained using a sterile swab stick pre-moistened with sterile normal saline. After swabbing the surfaces of the door handles, the swabs were placed in sterile containers containing normal saline, which served as the transport medium.

The surface area of each sampled door handle was measured to enable accurate estimation of bacterial load per unit area. All samples were appropriately labeled and coded before being transported to the Microbiology Laboratory within 1–2 hours of collection to prevent changes in microbial viability or overgrowth.

Bacteriological analysis of samples

Sterilization of equipment and media

All glassware used in this study was thoroughly washed with detergent, rinsed with clean water, and properly dried before use. Culture media were sterilized in an autoclave at 121°C for 15 minutes to ensure aseptic conditions. Normal saline (0.85 g sodium chloride in 100 mL distilled water) was prepared and used as the diluent in accordance with standard microbiological procedures (Cheesbrough, 2006).

Serial dilution

Serial dilutions were performed using the standard method described by Kpormon and Douglas (2018). One milliliter of each swab sample suspension was aseptically transferred into 9 mL of sterile normal saline and thoroughly mixed to obtain a ten-fold dilution. Subsequent serial dilutions were prepared by transferring 1 mL of the previous dilution into fresh diluent up to 10^{-2}, following established procedures (Prescott et al., 2005).

Inoculation, incubation, and enumeration

Total Heterotrophic Bacteria (THB)

An aliquot of 0.1 mL from the 10^{-2} dilution was inoculated in duplicate onto nutrient agar plates using the spread plate technique for the isolation and enumeration of total heterotrophic bacteria, as described by Prescott et al. (2005). The inoculated plates were incubated at 37°C for 24 hours. After incubation, visible colonies were counted, and the mean values were calculated and expressed as colony-forming units per square centimeter (CFU/cm²) using the method adopted by Salo et al. (2000).

Formula for CFU/cm²:

$$\text{CFU/mL} = \frac{Number\ of\ colonies}{Dilution \times volume\ plated} \quad \text{(Equation 1)}$$

$$\text{CFU/cm}^2 = \frac{A \times B}{C} \quad \text{(Equation 2)}$$

Where:
A = CFU/mL
B = Surface area
C = Volume of diluent used (5 mL)

Purification of isolates

Following incubation, distinct colonies exhibiting different cultural and morphological characteristics were carefully selected and sub-cultured onto freshly prepared nutrient agar plates to obtain pure cultures. Purification was achieved through repeated streaking using a sterile inoculating loop until discrete colonies were observed (Obire et al., 2003).

Identification of bacterial isolates

Pure bacterial isolates were identified using standard microbiological procedures as described by Cheesbrough (2006). Preliminary characterization was based on colony morphology and Gram staining. This was followed by a series of biochemical tests, including oxidase, catalase, indole, methyl red, Voges–Proskauer, citrate utilization, starch hydrolysis, coagulase, and carbohydrate fermentation tests. Identification of isolates was confirmed by comparing the results with reference standards in *Bergey's Manual of Determinative Bacteriology* (Holt et al., 1994).

Gram staining was conducted on 24-hour cultures to differentiate Gram-positive bacteria, which appeared purple, from Gram-negative bacteria, which appeared pink to red, while also revealing cellular morphology. The oxidase test was used to detect the presence of cytochrome oxidase through a rapid purple color change, whereas the catalase test identified the breakdown of hydrogen peroxide by the production of bubbles.

The methyl red test determined mixed-acid fermentation, indicated by a red coloration after the addition of the indicator, while the indole test evaluated tryptophan degradation using Kovac's reagent, with a red ring signifying a positive reaction. The Voges–Proskauer test was performed to detect acetoin production, evidenced by a pink to red color after reagent addition.

Citrate utilization was assessed using Simmons citrate agar, where a blue coloration indicated a positive result and green indicated a negative result. Sugar fermentation tests were carried out using phenol red broth with Durham tubes; a yellow color indicated acid production, while gas formation was confirmed by the presence of bubbles in the Durham tubes (Shields and Cathcart, 2010; Peekate, 2022).

Antibiotic susceptibility testing

Antibiotic susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton

agar (MHA), following the guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2017). Standardized bacterial inocula were prepared and evenly spread on MHA plates, after which antibiotic-impregnated discs were aseptically applied.

Bacterial suspensions were standardized to match the 0.5 McFarland turbidity standard to ensure uniform inoculum density. Commercially prepared antibiotic-impregnated disks containing Ceporex, Ceftriaxone, Streptomycin, Ofloxacin, Cefuroxime, Augmentin, Pefloxacin, Ceftazidime, Gentamicin, and Ciprofloxacin were aseptically placed on the surface of the inoculated agar plates, ensuring even distribution. Each disk was positioned approximately 15 mm from the edge of the plate and gently pressed with sterile forceps to ensure proper contact with the agar surface.

The plates were incubated in an inverted position under aerobic conditions at 35°C for 16-18 hours. Following incubation, the plates were examined for confluent or near-confluent bacterial growth. The diameters of the zones of inhibition around each antibiotic disk were measured in millimeters using a ruler on the underside of the plate and recorded. Results were interpreted as susceptible, intermediate, or resistant according to CLSI (2017) standards.

Data analysis

The frequency of bacterial isolates and their antibiotic susceptibility patterns were recorded and analyzed using descriptive statistics with SPSS version 24. Results were presented in tables and charts. Resistance rates were calculated and compared among bacterial species.

RESULTS

Bacteriological counts

The bacteriological evaluation of swabbed door handles from selected hospitals in Port Harcourt revealed varying levels of microbial contamination across sampling locations. Reception door handles recorded the highest bacterial populations in three of the four hospitals, except for Hospital 3, where ward door handles showed higher counts than other locations.

Bacterial counts for reception door handles ranged from $2.30 \pm 0.14 \times 10^5$ to $5.81 \pm 0.28 \times 10^5$ CFU/cm². Ward door handles recorded counts between $1.20 \pm 0.12 \times 10^5$ and $6.66 \pm 0.21 \times 10^5$ CFU/cm², while office door handles showed comparatively lower counts, ranging from $3.58 \pm 0.70 \times 10^4$ to $1.62 \pm 0.21 \times 10^5$ CFU/cm², as presented in Figure 1.

Statistical analysis indicated significant differences (p = 0.05) in bacteriological populations among reception, ward, and office door handles. The mean total heterotrophic bacterial counts were 4.92 $\log_{10}$ CFU/cm² for office door handles, 5.51 $\log_{10}$ CFU/cm² for ward door handles, and 5.61 $\log_{10}$ CFU/cm² for reception door handles (Figure 2).

Figure 3 shows the distribution of bacterial species isolated across the three sampled points in the selected hospitals. The data revealed that *Staphylococcus*, *Bacillus*, and *Pseudomonas* were predominant and were isolated from all three sampling points (reception, ward, and office door handles). In contrast, *Alcaligenes* and *Proteus* species were not isolated from office door handles across the four hospitals.

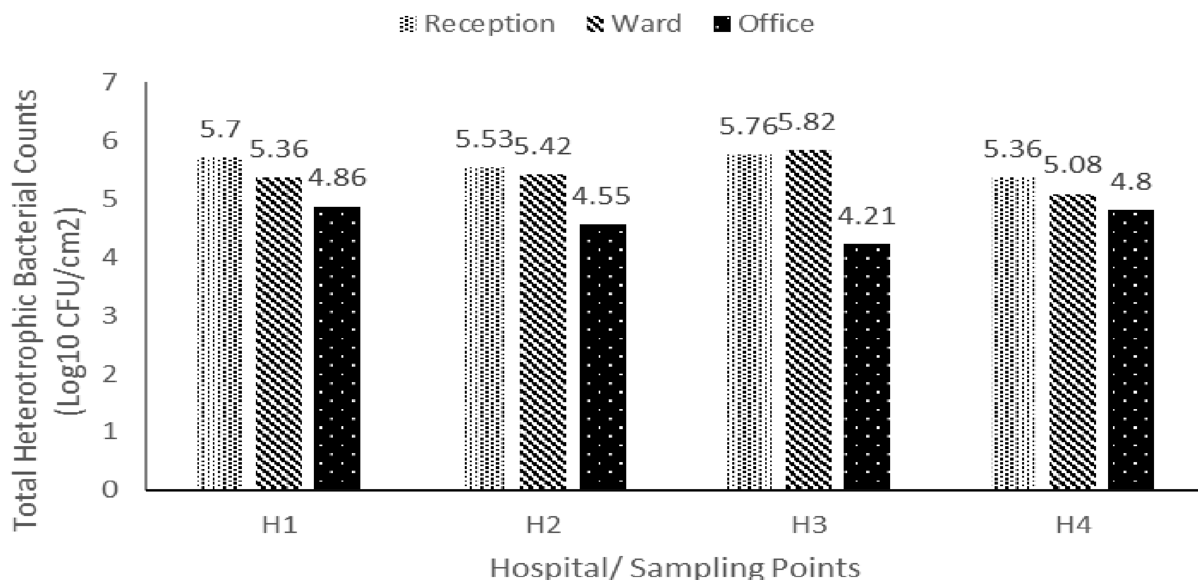

Figure 1. Bacteriological counts expressed in Log_{10} colony forming Unit per centimeter square.

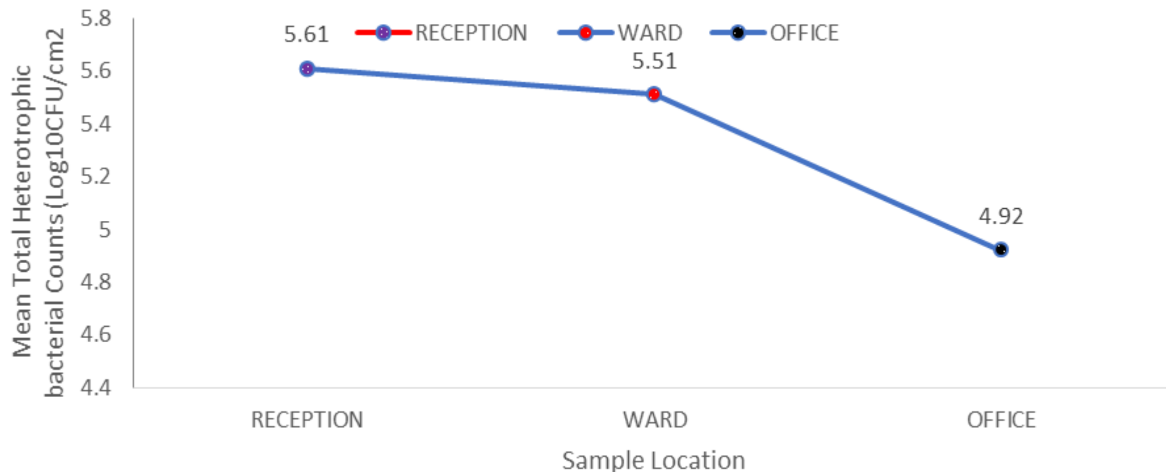

Figure 2. Mean Bacteriological counts expressed in Log_{10} colony forming Unit per centimeter square.

Figure 3. Distribution of the bacterial species isolated across the three sampled points of selected hospitals.

The bacterial species identified and their percentage prevalence were as follows: *Staphylococcus* (15%), *Bacillus* (14%), *Pseudomonas* (14%), *Escherichia coli* (14%), *Streptococcus* (14%), *Klebsiella* (11%), *Proteus* (11%), and *Alcaligenes* (7%), as presented in Figure 4.

Bacteriological analysis also revealed the presence of both Gram-positive and Gram-negative bacteria with varying antibiotic resistance patterns. *Bacillus* species (N = 12) showed high resistance to rifampicin, ceftazidime, streptomycin, and azithromycin (83.4%), as well as amoxicillin (83.4%), but were fully susceptible to ciprofloxacin (100%) and largely susceptible to levofloxacin (83.3%), as shown in Table 1.

Staphylococcus species (N = 12) exhibited high resistance to amoxicillin (83.4%), erythromycin (66.7%), and rifampicin (66.7%), while remaining fully susceptible to ciprofloxacin and levofloxacin (100%) (Table 2). *Streptococcus* species (N = 9) were completely resistant (100%) to azithromycin, amoxicillin, erythromycin, ceftazidime, and streptomycin, but showed high susceptibility to ciprofloxacin (100%), levofloxacin (100%), and cefuroxime (89%) (Table 3).

Among Gram-negative bacteria, *Pseudomonas* species (N = 12) were highly resistant to ceftriaxone (83.4%) and gentamicin (83.3%) but fully susceptible to streptomycin and ofloxacin (100%), with moderate susceptibility to pefloxacin (58.3%) (Table 4). *Alcaligenes* species (N = 4) demonstrated complete resistance to ceporex and augmentin (100%) but were fully susceptible to streptomycin, ofloxacin, pefloxacin, ceftazidime, and ciprofloxacin (100%), with moderate susceptibility to cefuroxime (75%) and gentamicin (75%) (Table 5).

Escherichia coli (N = 11) showed complete resistance to ceporex and gentamicin (100%) and high resistance to ceftriaxone (93%) and ciprofloxacin (93%), while ofloxacin and ceftazidime were fully effective (100%), and pefloxacin showed high susceptibility (90.9%) (Table 6). *Proteus* species (N = 6) were resistant to ceporex, ceftriaxone, cefuroxime, augmentin, and gentamicin (100%) but completely susceptible to streptomycin,

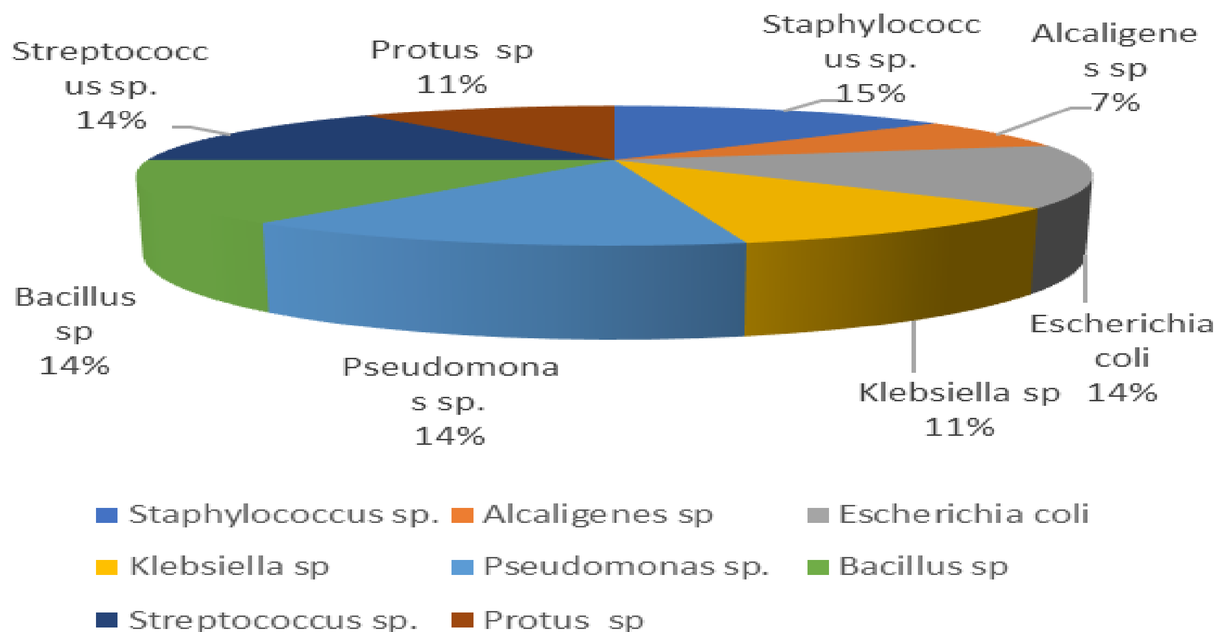

Figure 4. Percentage occurrence of the bacterial species isolated.

Table 1. Antibiotic sensitivity of *Bacillus* species (N = 12).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
AZM	30µg	10 (83.4)	2 (16.6)	0 (0)
AMX	30µg	10 (83.4)	1 (8.3)	1 (8.3)
CPX	10µg	0 (0)	0 (0)	12 (100)
E	5µg	8 (66.7)	0 (0)	4 (33.3)
LEV	5µg	2 (16.7)	0 (0)	10 (83.3)
CN	30µg	0 (0)	12 (100)	0 (0)
CEF	30µg	7 (58.3)	4 (33.3)	1 (8.4)
RD	30µg	12 (100)	0 (0)	0 (0)
CTZ	30µg	12 (100)	0 (0)	0 (0)
S	30µg	12 (100)	0 (0)	0 (0)

Key: AZM = Azithromycin, AMX = Amoxil, CPX = Ciprofloxacin, E = Erythromycin, LEV = Levofloxacin, CN = Gentamicin, CEF = Cefuroxime, RD = Rifampicin, CTZ = Ceftazidime, S = Streptomycin.

Table 2. Antibiotic sensitivity of *Staphylococcus* species (N = 12).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
AZM	30µg	5 (41.7)	4 (33.3)	3 (25)
AMX	30µg	10 (83.4)	1 (8.3)	1 (8.3)
CPX	10µg	0 (0)	0 (0)	12 (100)
E	5µg	8 (66.7)	0 (0)	4 (33.3)
LEV	5µg	0 (0)	0 (0)	12 (100)
CN	30µg	0 (0)	12 (100)	0 (0)
CEF	30µg	7 (58.3)	4 (33.3)	1 (8.4)
RD	30µg	8 (66.7)	4 (33.3)	0 (0)
CTZ	30µg	10 (83.3)	0 (0)	2 (16.7)
S	30µg	8 (66.7)	4 (33.3)	0 (0)

Key: AZM = Azithromycin, AMX = Amoxil, CPX = Ciprofloxacin, E = Erythromycin, LEV = Levofloxacin, CN = Gentamicin, CEF = Cefuroxime, RD = Rifampicin, CTZ = Ceftazidime, S = Streptomycin.

Table 3. Antibiotic sensitivity of *Streptococcus* species (N = 9).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
AZM	30µg	9 (100)	0 (0)	0 (0)
AMX	30µg	9 (100)	0 (0)	0 (0)
CPX	10µg	0 (0)	0 (0)	9 (100)
E	5µg	9 (100)	0 (0)	0 (0)
LEV	5µg	0 (0)	0 (0)	9 (100)
CN	30µg	8 (89)	1 (11)	0 (0)
CEF	30µg	0 (0)	1 (11)	8 (89)
RD	30µg	7 (78)	2 (22)	0 (0)
CTZ	30µg	9 (100)	0 (0)	0 (0)
S	30µg	9 (100)	0 (0)	0 (0)

Key: AZM = Azithromycin, AMX = Amoxil, CPX = Ciprofloxacin, E = Erythromycin, LEV = Levofloxacin, CN = Gentamicin, CEF = Cefuroxime, RD = Rifampicin, CTZ = Ceftazidime, S = Streptomycin.

Table 4. Antibiotic sensitivity of *Pseudomonas* species (N = 12).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
CEP	30µg	5 (41.7)	4 (33.3)	3 (25)
TRX	30µg	10 (83.4)	1 (8.3)	1 (8.3)
S	10µg	0 (0)	0 (0)	12 (100)
CEF	5µg	8 (66.7)	0 (0)	4 (33.3)
OFX	10µg	0 (0)	0 (0)	12 (100)
AU	30µg	0 (0)	12 (100)	0 (0)
PEF	30µg	1 (8.4)	4 (33.3)	7 (58.3)
CTZ	30µg	8 (66.7)	4 (33.3)	0 (0)
CN	30µg	10 (83.3)	0 (0)	2 (16.7)
CPX	30µg	8 (66.7)	4 (33.3)	0 (0)

Key: CEP = Ceporex, TRX = Ceftriaxone, S = Streptomycin, OFX = Ofloxacin, CEF = Cefuroxime, AU = Augmentin, PEF = Pefloxacin, CTZ = Ceftazidime, CN = Gentamicin, CPX = Ciprofloxacin.

Table 5. Antibiotic sensitivity of *Alcaligenes* species (N = 4).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
CEP	30µg	4 (100)	0 (0)	0 (0)
TRX	30µg	0 (0)	2 (50)	2 (50)
S	10µg	0 (0)	0 (0)	4 (100)
CEF	5µg	1 (25)	0 (0)	3 (75)
OFX	5µg	0 (0)	0 (0)	4 (100)
AU	30µg	4 (100)	0 (0)	0 (0)
PEF	30µg	0 (0)	0 (0)	4 (100)
CTZ	30µg	0 (0)	0 (0)	4 (100)
CN	30µg	0 (0)	1 (25)	3 (75)
CPX	30µg	0 (0)	0 (0)	4 (100)

Key: CEP = Ceporex, TRX = Ceftriaxone, S = Streptomycin, OFX = Ofloxacin, CEF = Cefuroxime, AU = Augmentin, PEF = Pefloxacin, CTZ = Ceftazidime, CN = Gentamicin, CPX = Ciprofloxacin.

ofloxacin, pefloxacin, and ceftazidime (100%) (Table 7).

Finally, *Klebsiella* species (N = 8) exhibited complete resistance to ceftriaxone, cefuroxime, augmentin, and ciprofloxacin (100%), with high resistance to gentamicin (87.5%), while remaining fully susceptible to ofloxacin and ceftazidime (100%) and moderately susceptible to streptomycin and pefloxacin (75%) (Table 8).

DISCUSSION

In hospital settings, identifying bacteria on frequently touched surfaces such as door handles and assessing their antibiotic resistance patterns are essential for preventing hospital-acquired infections (HAIs) and limiting the spread of drug-resistant strains (Fasugba et al.,

Table 6. Antibiotic sensitivity of *Escherichia coli* (N = 11).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
CEP	30µg	11 (100)	0 (0)	0 (0)
TRX	30µg	10 (93)	1 (7)	0 (0)
S	10µg	1 (9.1)	1 (9.1)	9 (81.2)
CEF	5µg	0 (0)	3 (27.3)	8 (72.7)
OFX	5µg	0 (0)	0 (0)	11 (100)
AU	30µg	7 (63.6)	4 (36.4)	0 (0)
PEF	30µg	0 (0)	1 (9.1)	10 (90.9)
CTZ	30µg	0 (0)	0 (0)	11 (100)
CN	30µg	11 (100)	0 (0)	0 (0)
CPX	30µg	10 (93)	1 (7)	0 (0)

Key: CEP = Ceporex, TRX = Ceftriaxone, S = Streptomycin, OFX = Ofloxacin, CEF = Cefuroxime, AU = Augmentin, PEF = Pefloxacin, CTZ = Ceftazidime, CN = Gentamicin, CPX = Ciprofloxacin.

Table 7. Antibiotic sensitivity of *Proteus* species (N = 6).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
CEP	30µg	6 (100)	0 (0)	0 (0)
TRX	30µg	6 (100)	0 (0)	0 (0)
S	10µg	0 (0)	0 (0)	6 (100)
CEF	5µg	6 (100)	0 (0)	0 (0)
OFX	5µg	0 (0)	0 (0)	6 (100)
AU	30µg	6 (100)	0 (0)	0 (0)
PEF	30µg	0 (0)	0 (0)	6 (100)
CTZ	30µg	0 (0)	0 (0)	6 (100)
CN	30µg	6 (100)	0 (0)	0 (0)
CPX	30µg	6 (100)	0 (0)	0 (0)

Key: CEP = Ceporex, TRX = Ceftriaxone, S = Streptomycin, OFX = Ofloxacin, CEF = Cefuroxime, AU = Augmentin, PEF = Pefloxacin, CTZ = Ceftazidime, CN = Gentamicin, CPX = Ciprofloxacin.

Table 8. Antibiotic sensitivity of *Klebsiella* species (N = 8).

Antibiotics	Concentrations	R (%)	I (%)	S (%)
CEP	30µg	7 (87.5)	1 (12.5)	0 (0)
TRX	30µg	8 (100)	0 (0)	0 (0)
S	10µg	0 (0)	2 (25)	6 (75)
CEF	5µg	8 (100)	0 (0)	0 (0)
OFX	5µg	0 (0)	0 (0)	8 (100)
AU	30µg	8 (100)	0 (0)	0 (0)
PEF	30µg	0 (0)	2 (25)	6 (75)
CTZ	30µg	0 (0)	0 (0)	8 (100)
CN	30µg	7 (87.5)	1 (12.5)	0 (0)
CPX	30µg	8 (100)	0 (0)	0 (0)

Key: CEP = Ceporex, TRX = Ceftriaxone, S = Streptomycin, OFX = Ofloxacin, CEF = Cefuroxime, AU = Augmentin, PEF = Pefloxacin, CTZ = Ceftazidime, CN = Gentamicin, CPX = Ciprofloxacin.

2021). HAIs remain a global public health challenge, as they complicate patient care and increase healthcare costs.

This study revealed high levels of bacterial contamination on hospital door handles, with counts varying by location. Reception door handles had the highest bacterial counts, followed by ward and office door handles. This pattern likely reflects frequent use, poor hand hygiene practices, overcrowding, and limited infection control monitoring. These findings are consistent with Dawodu et al. (2021), who reported similarly high bacterial loads on public door handles.

Gram-positive bacteria were more prevalent than Gram-negative bacteria, aligning with previous studies

showing that Gram-positive organisms dominate surface microbiota (Birru et al., 2021; Dawodu et al., 2021). Their predominance may be attributed to their natural presence on human skin and mucous membranes, which facilitates transmission through hand contact and contaminated objects (Abraham et al., 2000).

A total of 71 bacterial isolates representing eight species were recovered from the door handles. These included *Staphylococcus* (15%), *Bacillus* (14%), *Pseudomonas* (14%), *Escherichia coli* (14%), *Streptococcus* (14%), *Klebsiella* (11%), *Proteus* (11%), and *Alcaligenes* (7%). These findings are consistent with previous studies in Africa, which have identified *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Klebsiella*, and *E. coli* as common hospital contaminants (Yallew et al., 2019; Itah et al., 2021). The high prevalence of *Staphylococcus aureus* may be due to its normal colonization of the skin and respiratory tract and its ability to spread through sneezing, talking, and direct contact with moist skin (Itah et al., 2021).

Antibiotic susceptibility testing revealed high levels of resistance among the isolates. Gram-negative bacteria were largely resistant to Ceporex, Ceftriaxone, Streptomycin, Cefuroxime, Augmentin, and Gentamicin, while Gram-positive bacteria showed high resistance to Azithromycin, Amoxicillin, Erythromycin, Ceftazidime, and Streptomycin. These findings are consistent with previous reports of widespread multidrug resistance among hospital-associated bacteria (Breijyeh et al., 2021).

The results suggest that many commonly used antibiotics may no longer be effective against these isolates. This resistance is likely driven by factors such as the overuse and misuse of antibiotics, poor prescription practices, and their widespread application in both human medicine and livestock production (Maryam et al., 2020).

Overall, hospital door handles serve as reservoirs for potentially pathogenic and multidrug-resistant bacteria, underscoring the need for improved hygiene practices, regular disinfection of high-touch surfaces, and continuous monitoring of bacterial contamination and antibiotic resistance patterns.

CONCLUSION

Hospital door handles in Port Harcourt are contaminated with both Gram-positive and Gram-negative bacteria, many of which exhibit resistance to commonly used antibiotics. Reception door handles recorded the highest bacterial counts, likely due to frequent contact and inadequate hygiene practices.

The predominant bacterial species identified include *Staphylococcus*, *Bacillus*, *Pseudomonas*, *Escherichia coli*, *Streptococcus*, *Klebsiella*, *Proteus*, and *Alcaligenes*. These findings highlight the role of door handles as potential sources for the transmission of infections and multidrug-resistant bacteria. Regular cleaning and disinfection of high-touch surfaces, strict adherence to hand hygiene practices by healthcare workers and visitors, and routine monitoring of antibiotic resistance patterns are essential measures to reduce the spread of infections in hospital settings.

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