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Detection and distribution of multi-drug resistant (MDR) bacterial isolates of clinical and public health significance on hospital fomites and hands of healthcare workers in Mubi General Hospital.

Musa Y. Tula[1]* Joel Filgona[2], Richard Elisha[3], Terry L. Thomas[3], Francis O. Iruolaje[4]
Department of Biological Science Technology, Federal Polytechnic Mubi, PMB 035 Mubi, Adamawa State, Nigeria [1], Department of Microbiology, Adamawa State University, Mubi, Adamawa State, Nigeria [2], Department of Biomedical and Pharmaceutical Technology, Federal Polytechnic Mubi, Adamawa State [3], Department of Science Laboratory Technology, Federal Polytechnic Bauchi, Bauchi State [4].
Author for Correspondence*: birtyty@gmail.com/+234918341934/ORCID Number: 0000-0001-8666- 6839. https://dx.doi.org/10.4314/sokjmls.v7i3.6

Abstract

Despite the progress made in technology and clinical science, bacterial contamination of hospital fomites, healthcare workers, and the entire environment with its attendant consequences constitute a major problem in many countries of the world. One hundred (100) samples including surfaces of hospital fomites and the hands of healthcare workers were analyzed for bacterial growth on selective and or differential media and the bacteria obtained were identified by standard procedure. The bacterial isolates were screened for antibiotic susceptibility test by the Kirby-Bauer agar disk diffusion method. Of the 100 samples collected, 77 were from inanimate surfaces while 23 were from the hands of healthcare workers. The predominant inanimate surface swabs collected came from beddings (26%), and the least came from door handles (11.0%). The distribution of samples based on wards showed that 54% of the samples were from female wards, 23% from children's wards, and 20% came from the male ward. Out of 100 samples collected from various sites, bacterial growth was observed in 34(34.0%) specimens while the remaining 66 (66%) had no bacterial growth. A total of 72 bacterial isolates were recovered from the 34 specimens. Overall, *Staphylococcus aureus* (26.0%) was the most common isolate recovered, while the least was *Serratia marcescens* and *Shigella* spp. Of the Gram-negative organisms, *Pseudomonas aeruginosa* was the most predominant specie, whereas *Escherichia coli* which represents 50.0% (15/30), was the predominant Enterobacteriaceae specie encountered. Bacterial isolates were mostly recovered from beddings with 24 isolates, and the least was from sink and door handles with 8 isolates each. Resistance to ampicillin by all the isolates was the highest, but with no statistical difference (P=0.468) with resistance to septrin, and gentamycin. Whereas some isolates were resistant to 9-10 antibiotics, others were resistant to 1-2 antibiotics. From these, the multidrug resistance (MDR) phenotype was shown by 35(66.0%) of these isolates. *Escherichia coli* portrayed 11(73.3%) MDR phenotypes, while *Pseudomonas aeruginosa* exhibited 8(50.0%) MDR phenotypes. Multiple antibiotic resistance (MAR) index of greater than 0.2 was shown by 38(71.7%) bacterial isolates. Of these, 12(31.6%) and 9(23.7%) were from *E. coli* and *P. aeruginosa* respectively. Most of the bacterial isolates that were resistant to at least an antibiotic were commonly isolated from patients' beddings (30.2%), tables (28.3%), and sinks (20.8%). This study, therefore, shows that hands of healthcare workers and inanimate surfaces frequently touched within the hospital environment constitute potential reservoirs for emerging MDR pathogens and may also serve as sources of their transmission.

Keywords: *MDR, hospital fomite, hands, healthcare workers, Mubi, general hospital*

Introduction

Despite the advancement in technology and clinical science, bacterial contamination of hospital fomites, healthcare workers, and the entire environment with its attendant consequences constitute a major problem in many countries of the world (Ayatollahi *et al*., 2017), particularly the resource constraint countries like Nigeria. The contamination of surfaces depends on their characteristics, such as whether they are smooth, porous, or rough, and/or on their state,

such as whether they are dry, wet, new, or old. These bacteria can live for a few days to a very long period on numerous surfaces of hospital fomites (Boer *et al.,* 2016). The surfaces of hospital fomites may act as a reservoir for bacteria and can play important role in the widespread and common transmission of the major pathogens connected to nosocomial infections (NIs) (Caselli *et al*., 2019; Muthoni, 2021).

Nosocomial infection or healthcare-associated infections (HAIs), is an infection derived in the hospital by an individual who was admitted for an ailment other than the acquired infections and is caused by a variety of microorganisms, particularly bacteria (Muthoni, 2021; Jain *et al*., 2021). The sources of the pathogens can be from an infected or colonized patient, hospital fomites, and or healthcare workers (Schulster and Chinn, 2003).

With the introduction of antimicrobial agents into clinical use, many lives were saved and the anguish of millions of people worldwide was reduced (Ayukekbong *et al*., 2017). However, the benefit of such a landmark achievement was short-lived due to the emergence of drug-resistant bacteria. The emergence and spread of these resistant bacteria, especially the ones with multi-drug resistant (MDR) phenotype in the hospital environment constitute a serious public health concern (Magiorakos *et al*., 2012). This is of particular importance in resource-limited countries which would have devastating consequences considering the indigent nature of the healthcare facilities, poor drug quality, limited antibiotic options available, lack of antibiotic stewardship programs, and overall resource constraints observed in such countries.

Data reporting pathogens associated with hospital fomites and healthcare workers in the study area is lacking completely. More so, Mubi general hospital, constitutes a referral healthcare facility for people of the Adamawa-north senatorial zone, comprising 5 local government areas (LGAs), including Hong LGA, which is located in the Adamawa-central senatorial zone, and some LGAs and communities in Borno State, due to its proximity to these areas. Therefore, this study was carried out to determine in Mubi general hospital the distribution of MDR bacteria in hospital fomite and Hands of healthcare workers as a means of epidemiological surveillance for reference purposes.

Materials and methods

Study Area

The study area is Mubi general hospital. Mubi General Hospital is located in Mubi-South LGA of Adamawa State within the coordinates 10°15'54.9"N 13°16'10.0E.

Sample collection

A simple random sampling method was used to collect samples from various surfaces in the hospital wards, Surface swab specimens were collected from predefined surfaces such as tables, door handles, sinks, beddings, and hands of healthcare workers by using cotton swabs moistened with sterile normal saline (Muthoni, 2021).

Sample Processing

Samples obtained randomly from the hands of healthcare workers, hospital fomites were aseptically introduced into sterilized MacConkey agar plates, Mannitol salt agar plates, Salmonella-Shigella agar, and Cetrimide agar plates. The inoculated agar plates were incubated aerobically at 37°C for 24 h. Discrete colonies of the isolates were sub-cultured onto sterile nutrient agar plates. The plates were incubated aerobically at 37°C for 24 h. After the incubation, the pure isolates were transferred aseptically into nutrient agar slants and kept at refrigeration temperature for further use.

Bacteria Identification

After Gram-staining, each bacterial isolate was identified phenotypically on Microgen A kit (Tula *et al*., 2022). However, *Pseudomonas aeruginosa* was identified based on its reaction to the cetrimide agar plate

Antibiotic susceptibility pattern of the bacterial isolates

The antibiotic susceptibility test of the isolates was determined by the disk diffusion test according to the recommendations of the Clinical Laboratory Standard Institute (CLSI, 2017). The antibiotic disk containing the following antibiotics were used: septrin (30µg), ampicillin (30 µg), ciprofloxacin (10

µg), amoxicillin (30 µg), cefuroxime (20 µg), ceftriaxone (25 µg), gentamycin (10 µg), perfloxacin (30 µg), streptomycin (30 µg), and Erythromycin (10 µg). The zone diameter of each antibiotic disc was measured and interpreted using the criteria published by the Clinical Laboratory Standard Institute (CLSI, 2017).

Screening for Multiple Antibiotic Resistant (MAR) index of the isolates

Multiple antibiotic resistant (MAR) index of the isolates was determined using the formula MAR = x/y. Where x is the number of antibiotics to which the test isolate displayed resistance and y is the total number of antibiotics to which the test organisms have been evaluated for sensitivity (Tula *et al.*, 2016).

Ethical consideration

Verbal informed consent was obtained from the healthcare workers of the hospital, and consent was sought and obtained from the management of the hospital.

Statistical analysis

All the data were presented in percentages and were analyzed using analysis of variance (ANOVA). Values were considered significant when the P-values are < 0.05.

Results

Of the 100 samples collected, 77 were from inanimate surfaces while 23 were from staff hands. The predominant inanimate surfaces swabs collected came from beddings (26%), and the least came from door handles (11.0%) as shown in Figure 1. The distribution of samples based on wards showed that 54% of the samples were from female wards, 23% from children's wards, and 20% came from the male ward. From the 4 female wards (wards 3-6) in which samples were collected, the predominant samples came from ward 6 with 26 samples, while the least from ward 5 with 4 samples.

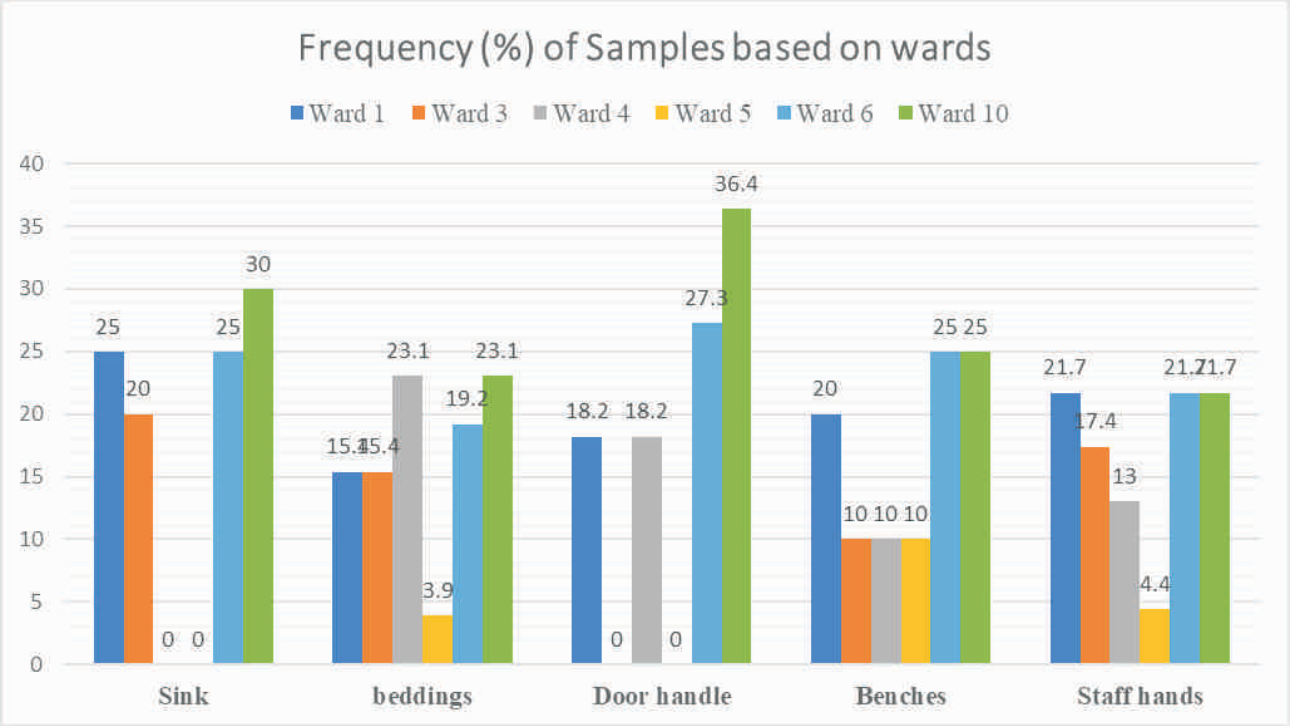

Fig. 1: **Frequency (%) of samples from hospital fomites and hands of healthcare workers**
Legend: Ward 1= Male surgical, Ward 3-6= female, ward 10= children

Out of 100 samples collected from various sites, bacterial growth was observed in 34(34.0%) specimens while the remaining 66 (66%) had no bacterial growth. A total of 72 bacterial isolates were recovered from the 34 specimens due to the presence of mixed bacterial flora isolated from various sites. Of these, Gram-positive consisting of only *Staphylococcus aureus* constitute 36.1%, while Gram-negative organisms constitute 63.9% of the recovered isolates. Of the Gram-negative organisms, *Pseudomonas aeruginosa* was the most predominant species. Whereas Enterobacteriaceae represent 65.2% (30/46) of Gram-negative bacteria species, the Pseudomonadaceae family consisting only of *Pseudomonas aeruginosa* makes up the remaining 34.8% (16/46). Among the Enterobacteriaceae, *Escherichia coli* which represents 50.0% (15/30) was the predominant Enterobacteriaceae recovered, while *Serratia marcescens* and *Shigella* spp. were the least encountered Enterobacteriaceae and constitute 6.7% (2/30) each.

Overall, *Staphylococcus aureus* (26.0%) was the most common isolate recovered, followed by *Pseudomonas aeruginosa* (16.0%), while the least was *Serratia marcescens* and *Shigella* spp. (2.0%) as shown in Table 1.

Based on sites of sampling, bacterial isolates were mostly recovered from beddings with 24(92.3%) isolates, followed by staff tables with 17 (85.0%) isolates and the least was from sinks with 8 (40.0%) isolates. More so, *S. aureus* isolate was the predominantly recovered bacterial species from beddings, staff tables, and hands of healthcare workers. However, *Pseudomonas aeruginosa* was the most detected bacterial species in sinks and door handles (Table 1)

Based on wards, the bacterial isolate was mostly recovered from female ward 3 with 22 isolates, followed by male ward 1 with 17 isolates, and the least was from female ward 5 with 2 isolates. Frequency based on hospital wards showed that *Staphylococcus aureus* was the most detected bacterial species in male ward 1, and female wards 3 and 6, while *Pseudomonas aeruginosa* was the most recovered organism in female wards 4, 5, and children ward 10 (Table 2).

All *Shigella* spp., isolates were resistant to ampicillin, gentamycin, ciprofloxacin, and septrin. Similarly, all the isolates of *Citrobacter diversus* and *Klebsiella pneumoniae* were resistant to gentamycin and septrin. The isolates of *Escherichia coli* (100%), *C. diversus* (75.0%), *Providencia rettgeri* (100%), *Serratia marcescens* (50.0%) and *Staphylococcus aureus* (33.8%) were mostly resistant to ampicillin (Table 3).

The result further showed that resistance to ampicillin by all the isolates was the highest, but with no statistical difference (P=0.468) with resistance to septrin, and gentamycin. More so, resistance to erythromycin was the least, but quite similar to resistance to pefloxacin, cefuroxime, amoxicillin, ceftriaxone, ciprofloxacin, and streptomycin (P=0.300) as shown in Table 2. *Shigella* spp. was the isolate that depicted the highest resistance to the tested antibiotics, but quite not different from the ones portrayed by *E. coli* and *P. rettgeri* (P=0.082). Similarly, *S. aureus* exhibited the least resistance to the tested antibiotics but was quite not different from that showed by *K. pneumoniae* and *Citrobacter diversus* (P=0.056).

The result of the resistance profile of all the isolates was presented in Table 4. The resistance profiles of all the bacterial isolates were distinct and highly variable. From the 72 bacterial isolates recovered from inanimate surfaces and staff hands in the hospital environment, only 53(73.6%) were resistant to at least an antibiotic. Whereas some isolates were resistant to 9-10 antibiotics, others were resistant to 1-2 antibiotics. From these, the multidrug resistance (MDR) phenotype was shown by 35(66.0%) of these isolates. *Escherichia coli* portrayed 15 distinct resistance profiles, with 11(73.3%) MDR phenotypes, while *Pseudomonas aeruginosa* exhibited 13 resistance profiles with 8(50.0%) MDR phenotypes.

The multiple antibiotic resistant (MAR) index of the bacterial isolates varies between 0.1 – 1.0. Multiple antibiotic resistant (MAR) index of greater than 0.2 was shown by 38(71.7%) bacterial isolates. Of these, 12(31.6%) and 9(23.7%) were from *E. coli* and *P. aeruginosa* respectively.

Most of the bacterial isolates that were resistant to at least an antibiotic were commonly isolated from patients' beddings (30.2%), tables (28.3%), and sinks (20.8%) as shown in Table 4.

Table 1: Frequency of Bacterial isolates from Hospital environment samples based on sites

Organisms	Sink (n=20)	Beddings (n=26)	Door Handles (n=11)	Staff tables (20)	Hands of Healthcare workers (23)	Total (n=100)
Escherichia coli	2(10.0)	5(19.2)	0	4(20.0)	4(17.4)	15(15.0)
Klebsiella pneumoniae	0	2(7.7)	0	1(5.0)	0	3(3.0)
Pseudomonas aeruginosa	5(25.0)	4(15.4)	2(18.2)	3(15.0)	2(8.7)	16(16.0)
Citrobacter diversus	0	2(7.7)	1(9.1)	0	1(4.4)	4(4.0)
Shigella spp	0	1(3.8)	0	0	1(4.4)	2(2.0)
Providentia rettgeri	1(5.0)	0	1(9.1)	1(5.0)	1(4.4)	4(4.0)
Serratia marcescens	0	1(3.8)	0	1(5.0)	0	2(2.0)
Staphylococcus aureus	0	9(34.6)	4(36.4)	7(35.0)	6(26.1)	26(26.0)
Total	**8(40.0)**	**24(92.3)**	**8(72.7)**	**17(85.0)**	**15(65.2)**	**72(72.0)**

Table 2: Frequency of bacterial isolates from Hospital environment based on wards

Organisms	Ward 1 (n=20)	Ward 3 (n=14)	Ward 4 (n=13)	Ward 5 (n=4)	Ward 6 (n=23)	Ward 10 (n=26)	Total (n=100)
Escherichia coli	4(20.0)	5(35.7)	2(15.4)	0	4(17.4)	0	15(15.0)
Klebsiella pneumoniae	2(10.0)	1(7.1)	0	0	0	0	3(3.0)
Pseudomonas aeruginosa	0	4(28.6)	3(23.1)	2(50.0)	2(8.7)	5(19.3)	16(16.0)
Citrobacter diversus	1(5.0)	2(14.3)	1(7.7)	0	0	0	4(4.0)
Shigella spp	0	1(7.1)	1(7.7)	0	0	0	2(2.0)
Providentia rettgeri	1(5.0)	0	1(7.7)	0	1(4.3)	1(3.8)	4(4.0)
Serratia marcescens	2(10.0)	0	0	0	0	0	2(2.0)
Staphylococcus aureus	7(35.0)	9(64.3)	0	0	6(26.1)	4(15.4)	26(26.0)
Total	**17(23.6))**	**22(30.6)**	**8(11.1)**	**2(2.8)**	**13(18.1)**	**10(13.9)**	**72(72.0)**

Table 3: Resistance Pattern of Bacterial isolates

Isolate	Freq	PEF[b]	CN[a]	APX[a]	Z[b]	AM[b]	R[b]	CPX[b]	S[b]	SXT[a]	E[b]
E. coli[ab]	15	4(26.7%)	10(66.7%)	15(100%)	7(46.7%)	8(53.3%)	5(33.3%)	1(6.7%)	9(60.0%)	10(66.7%)	4(26.7%)
*Shigella*spp[a]	2	1(50%)	2(100%)	2(100%)	1(50%)	1(50%)	1(50%)	2(100%)	1(50%)	2(100%)	1(50%)
C. diversus[bc]	4	0	4(100%)	3(75%)	0	0	0	0	3(75%)	4 (100%)	0
P. aeruginosa[b]	16	4(25%)	9(56.3%)	12(75.0%)	8(50.0%)	9(56.3%)	5(31.3%)	2(12.5%)	2(12.5%)	7(43.8%)	3(18.8%)
K. pneumoniae[bc]	3	0	3(100%)	2(66.7%)	0	0	0	1(33.3%)	0	3(100%)	0
P. rettgeri[ab]	4	2(50%)	1(25%)	4(100%)	2(50%)	2(50%)	1(25%)	0-	1(25%)	3(75%)	2(50%)
S. aureus[c]	26	2(7.7%)	5(19.2%)	8(33.8%)	1(3.9%)	1(3.9%)	1(3.9%)	0	1(3.9%)	8(33.8%)	0
S. marcescen[b]	2	1(50%)	1(50%)	1(50%)	1(50%)	1(50%)	1(50%)	0	1(50%)	1(50%)	0

Legend: Pef =perfloxacin, CN=gentamycin, APX=ampicillin, Z=cefuroxime, Am=amoxicillin, R=ceftriaxone, CPX=ciprofloxacin, S=streptomycin, SXT=septrin, E=erythromycin. Parameters with the same superscript connote statistically not different (P>0.05)

Table 4: Antibiotic resistance profile and MAR index of bacterial isolates from hands of healthcare workers and fomites of the hospital environment

Isolates	Resistance profile	No of isolate	No of antibiotic	MDR Status	MAR Index	Source
E. coli	sxt, s, am, z, apx, cn, e, pef, r, cpx	1	10	MDR	1.0	Bedding
	sxt, s, am, z, apx, cn, e, pef,r	1	9	MDR	0.9	Table
	sxt, am, z, apx, cn, e, pef, r	1	8	MDR	0.8	Bedding
	sxt, s, am, z, apx, cn, r	1	7	MDR	0.7	Sink
	sxt, s, am, apx, cn, e, r	1	7	MDR	0.7	Sink
	sxt, s, am, z, apx, cn	1	6	MDR	0.6	Table
	sxt, s, cn, apx	1	4	MDR	0.4	Table
	s, am, z, apx	1	4	MDR	0.4	Bedding
	am, z, apx	1	3	-	0.3	Table
	sxt, s, apx	1	3	MDR	0.3	Table
	sxt, apx, cn	1	3	MDR	0.3	Sink
	apx, cn, pef	1	3	MDR	0.3	Bedding
	sxt, apx	1	2	-	0.2-	Table
	s, apx	1	2	-	0.2	HHCW
	apx, cn	1	2	-	0.2	HHCW

P. a eruginosa	am, sxt, s, r, z, apx, cn, pef,e	1	9	MDR	0.9	Sink
	am, apx, z, cn, sxt, s, r, cpx	1	8	MDR	0.8	Bedding
	am, apx, z, cn, sxt, pef, e	1	7	MDR	0.7	Table
	am, pef, cn, apx, z, r, e	1	7	MDR	0.7	Sink
	am, r, z, apx, cn, pef, cpx	1	7	MDR	0.7	DH
	am, apx, z, cn, r, sxt	1	6	MDR	0.6	Sink
	am, apx, z, cn	1	4	MDR	0.4	Sink
	am, z, apx	1	3	-	0.3	Bedding
	apx, cn, sxt	2	3	MDR	0.3	Bedding
	sxt, apx	1	2	-	0.2	HHCW
	Apx	1	1	-	0.1	Table
	Am	1	1	-	0.1	Table
Shigella spp	sxt, e, cn, apx, z, am, r, cpx, s, pef	1	10	MDR	1.0	Bedding
	sxt, cn, cpx, apx	1	4	MDR	0.4	HHCW
K. pneumoniae	sxt, cn, apx, cpx	1	4	MDR	0.4	Table
	sxt,cn,apx	1	3	MDR	0.3	Bedding
	sxt, cn	1	1	-	0.2	Bedding
S. marcescens	sxt, pef, cn, apx, z, am, r, s	1	8	MDR	0.8	Table
P. rettgeri	sxt, s, apx, e, pef, z, am, r,cn	1	9	MDR	0.9	Table
	sxt, apx, e, pef, z, am	1	6	MDR	0.6	HHCW
	apx, sxt	1	2	-	0.2	Sink
	Apx	1	1	-	0.1	Table
C. diversus	sxt, s, cn, apx	2	4	MDR	0.4	Beddings
	sxt,s,cn	1	3	-	0.3	DH
	sxt,cn,apx	1	3	MDR	0.3	HHCW
S. aureus	sxt, e, pef, apx, am, z	1	6	MDR	0.6	HHCW
	pef, cn, apx, r	1	4	MDR	0.4	HHCW
	sxt, s, cn, apx	1	4	MDR	0.4	Table
	sxt,cn,apx	2	3	MDR	0.3	Sink, DH
	sxt,apx	1	2	-	0.2	Bedding
	sxt,cn	1	2	-	0.2	Table
	Apx	2	1	-	0.1	Sink. Bedding
	Sxt	2	1	-	0.1	Bedding, sink

Legend: MDR=Multiple Drug Resistance, MAR=Multiple Antibiotic Resistance, HHCW=hands of healthcare workers, DH=door handle

Discussion

The aerobic culture results revealed that only 34% of fomites surfaces and hands of healthcare workers' samples were found contaminated by various bacterial pathogens. This finding was lower than the report of similar studies in Northern (Aminu *et al*., 2014) and Southern (Ikeh and Isamade, 2011) Nigeria which reported contamination rates of 65.7% and 99.0% respectively. Similarly, the finding of this study was quite lower than the previous study in Ethiopia and Morocco which reported 52.9% (Gelaw *et al*., 2013) and 88.4% (Chaoui *et al*., 2019) growth rate respectively. Away from Africa, similar studies from Taiwan, Iran, and Scotland reflected a contamination rate of 63.5% (Chen *et al*., 2014), 57.0% (Ekrami *et al*., 2011) and 95.7% (Brady *et al*., 2007) respectively in hospital environmental samples, which were higher than the findings of this study. On the other hand, lower contamination rates than the one in this study were previously reported. These include the 20.0% and 17.8% contamination rates reported in South-Eastern Nigeria (Uneke *et al*., 2014) and Iraq (Nasser *et al*., 2013) respectively.

The differences could be attributed to different geographical locations, differences in the use of aseptic techniques, disinfection, and fumigations in the hospital environment. It may also be due to differences and the sensitivity of the method used for the isolation of bacterial species (Meunier *et al*., 2005; Bitew *et al*., 2021).

In this study, most of the bacterial isolates were associated with beddings. The high rate of these organisms contaminating beddings could be due to constant contact with patients and healthcare workers. Reports from previous studies found contamination levels ranging from 10^2 to more than 10^5cfu/10 cm^2 on hospital bedding after one-night use (Malnick *et al*., 2008; Lebreton *et al*., 2017), how much more if the bedding is used by a patient for a week or more. Contamination of hospital bedding could also arise due to whole or broken hospital mattresses. A study conducted in the United State of America reported the failure of terminal cleaning to eliminate bacteria from the surface of the mattress. Another study reported that hospital mattresses are often the most contaminated areas of hospital rooms, especially if they are ruptured, soiled, or contaminated with infected exudates from patients, which if not replaced will contaminate the bedding used on them (Hooker *et al*., 2012). Previous studies have also shown that because hospital pillows and duvets are not frequently changed, they could serve as sources of contamination of hospital beddings (Pinon *et al*., 2013).

The surface contamination of inanimate objects in the indoor of hospital wards as seen in this study depends on many factors among which include inadequate sanitation, infrequent use of quality organic cleaning agents, and lack and or failure of the air treatment system. This is in addition to intrinsic factors that enhance the survival of microorganisms on the surfaces of hospital equipment and fomites; biofilm and spore formation, among others (Chaoui *et al*., 2019).

The higher number of Gram-negative isolates in this study corroborates previous studies (Orji *et al*., 2005; Muthoni, 2021). Contrary to the finding of this study, higher frequencies of Gram-positive than Gram-negative organisms were reported in previous studies (Tesfaye *et al*., 2015; Getachew *et al*., 2018; Bitew *et al*., 2021). Though studies have shown that Gram-positive and Gram-negative bacteria can survive up to months on dry inanimate surfaces in hospitals (Bhatta *et al*., 2018). However, the higher number of Gram-negative bacilli in this study could be because Gram-negative bacteria can remain stable for months on dry surfaces, humid environments, and adverse conditions that other bacteria are unable to tolerate (Moniri & Momen, 2006; Ayatollahi *et al*., 2016).

In contrast to the finding of this study, other similar studies reported the dominance of bacterial species other than *S. aureus*. These include *Providencia rettgeri* (Muthoni, 2021) and Coagulase-negative Staphylococci (CoNS) (Getachew *et al*., 2018; Maina, 2020). However, the preponderance of *S. aureus* over other bacterial isolates in this study corroborates findings from other studies (Hammuel *et al*., 2014; Dégbey *et al*., 2021). The high dominance of *S. aureus* in this study is not surprising because of its' opportunistic and ubiquitous nature. *Staphylococcus aureus* is well known nosocomial pathogen with its ability to survive in a hospital

environment or on surfaces for several days and can be a source of infection in patients as previously noted (Aminu *et al*., 2014; Bhatta *et al*., 2018; Afle *et al*., 2019). Also, the ability of *S. aureus* to form biofilm on inanimate objects prolongs their survival and spread (Bhatta *et al*., 2018).

Furthermore, the dominance of *S. aureus* on the beddings, tables, and staff hands may be probably because they are members of the body flora of both asymptomatic carriers and sick persons. The organism can be spread by the hand, expelled from the respiratory tract, or transmitted by animate or inanimate objects. Their main source(s) of colonization on the fomites might likely be nasal carriage by hospital personnel, likely facilitated by hand-to-mouth or hand-to-nose contact while using these fomites, and/or by poor hand-washing habits (Aminu *et al*., 2014).

The dominance of Enterobacteriaceae among the Gram-negative bacteria (GNB) was in agreement with a previous study (Afle *et al*., 2019). This suggests faecal-oral contamination, and these organisms can give rise to foodborne infections, urinary tract infections, and diarrhea (Al-Harmoosh *et al*., 2019). The isolation of many members of the Enterobacteriaceae may also be due to poor hygienic practices in the wards. Also, a study attributed the presence of enteric bacilli in hospital facilities to visitors who attend to their sick relatives (Orji *et al*., 2005). Infections caused by Gram-negative bacteria are specific because of the efficacy of these bacteria in the acquisition of genes that encode antibiotic resistance mechanisms. In the hospital environment, these pathogens play an important role in the public health impact of healthcare-associated infections (Afle *et al*., 2019).

In the Enterobacteriaceae family, *Escherichia coli* was the most prevalent organism found contaminating fomites and staff hands. This agreed with previous reports from the Benin Republic (Afle *et al*., 2019) and Northern Nigeria (Aminu *et al*., 2014). *Escherichia coli* is a pathogen of healthcare-associated infections that poses problems in hospitals. These include urinary tract infections, septicaemia, pneumonia, neonatal meningitis, peritonitis, and gastroenteritis (Hassan *et al*., 2015; Afle *et al*., 2019).

The isolation of *Pseudomonas aeruginosa* from the sinks confirms the reports of previous studies (Udeze *et al*. 2012; Hammuel *et al*., 2014) that sinks are the most common place in the hospital environment where *P. aeruginosa* are predominantly found. This could be because *P. aeruginosa* is often isolated in a moist environment where they form biofilm. *Pseudomonas aeruginosa* is a very important opportunistic pathogen in hospitals and it's opportunistic ability has been demonstrated in patients with burn wounds and eye infections (Al-Harmoosh *et al*., 2019).

The presence of organisms contaminating hospital fomites could be due to a failure in bio-cleaning and sterilization or disinfection procedures. Furthermore, studies have shown that, despite effective cleaning procedures and the use of disinfectants, pathogenic bacteria are generally found on surfaces and other equipment commonly used in hospitals (Mora *et al*., 2016; Degbey *et al*., 2021).

The high resistance to ampicillin by all the bacterial isolates corroborates reports from previous studies (Alam *et al*., 2013; Hammuel *et al*., 2014; Chaoui *et al*., 2019). The resistance of these bacterial isolates to ampicillin may be a pointer to the fact that these organisms had a β-lactamase enzyme that help to break the β-lactam ring in the antibiotic and rendered it ineffective. After ampicillin, the organisms also portrayed higher and significant resistance to septrin and gentamycin in a manner similar to ampicillin. This finding was similar to an earlier similar study reported in Pakistan (Irshad and Yasmeen, 2019). This suggests that in addition to the presence of Beta-lactamase enzymes, the organisms must have had other resistance enzymes or mechanisms.

Reduced resistance to erythromycin by all the isolates in this study, corroborate the finding of a previous report in Kano, Nigeria (Aminu *et al*., 2014). This suggests that this class of antibiotic was often not prescribed and used in the hospital and may be used as a therapeutic option for infections caused by these organisms. Other antibiotics that the isolates showed reduced resistance similar to and not significantly different from erythromycin include pefloxacin

and ciprofloxacin.

The majority of the isolates showed resistance to one or more antibiotics. More so, multiple-antibiotic resistance (MDR) was detected in at least 60.0% of isolates that were resistant to at least an antibiotic. This was comparable to earlier studies from Ethiopia (Worku *et al*., 2018; Birru *et al*., 2021). This might be the result of excessive use of antibiotics in the treatment of bacterial infections. It is expected that these isolates have received antibiotic pressure in the hospital environment during treatment (Alam *et al*., 2013; Birru *et al*., 2021). Such multiple antibiotic resistances are known to arise by the acquisition of resistance genes through genetic exchange and mutation and physiological mechanisms such as possession of specific proteins and efflux pump (Alam *et al*., 2013). The incidence of variable resistance patterns and distinct resistance profiles portrayed by most bacterial isolates (even within the same species) in this study connote that these bacterial strains might have arisen from distinct clones of the same or different species.

The high MAR index portrayed by isolates of this study was in agreement with a similar previous study in Zaria, Nigeria (Hammuel *et al*., 2014). A MAR index higher than 0.2 identifies organisms that originate from high-risk sources of contamination, where antibiotics are often used. MAR indices less than, or equal to 0.2, identify strains from environments where antibiotics are seldom or never used (Tula *et al*., 2016). A large proportion of organisms detected in the study area had MAR indices higher than 0.2, which implies that a very large proportion of the bacterial isolates in the study area have been exposed to several antibiotics.

Detection of antibiotic resistance organisms in a hospital environment as seen in this study connote higher consumption of antibiotics in the hospital, the discharge of antimicrobial residues, and resistant bacteria. The implication is that patients stand the risk of acquiring infections other than the ones they were admitted with. The consequences include increased antibiotic resistance burden, treatment failure, prolonged hospital stay due to delay in effective treatment options, high hospital costs, and increased morbidity and mortality (Prasad *et al*., 2018). Moreover, the presence of resistant isolates in fomites in a hospital environment serves as a possible reservoir for the transfer of resistant genes into other highly infectious pathogens (Rabbani *et al*., 2017; Irshad and Yasmeen, 2019). Therefore, it is high time to develop and implement policies for periodic surveillance of pathogens and provide proper guidance, on the judicious use of antibiotics.

Conclusion

This study, therefore, concludes that hands of healthcare workers and inanimate surfaces frequently touched or neighboring patients within the hospital environment constitute potential reservoirs for emerging MDR pathogens and also serve as sources of transmission. If adequate measures are not put in place to curtail this menace, the provision of quality health care services will be impaired by the spread of these emerging pathogens. In the light of the above, there is a need to emphasize holistic hand hygiene and decontamination of these sites on a regular basis.

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