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Antibiotics Susceptibility Profile of Bacteria Contaminants Isolated from Door Handles in a Tertiary Institution in Kaduna, Nigeria

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Abstract

Unclean hands serve as a medium for the propagation of microorganisms from place to place and from person to person(s). This study evaluated the antibiotic susceptibility pattern of pathogenic bacteria contamination of selected door handles in Kaduna State University, as they serve as potential sources of infectious bacteria transfer that are of clinical importance and contributing to morbidity and mortality within the community. A total of 60 samples were randomly collected from 4 Faculties using moist sterile swab sticks. Isolation and identification of the bacteria were carried out using conventional biochemical tests while antibiotics susceptibility test was carried out using modified Kirby-Bauer test. The result showed that all the samples collected from door handles were contaminated with microorganisms with mean total of bacteria viable count (cfu/ml) ranging from 3.3×10^3 to 7.6×10^7 . The highest occurring bacteria isolated on the door handle were *S. aureus* (29%), *E. coli* (25.8%), *Salmonella typhi* (12.9%), *Pseudomonas aeruginosa* (9.7%) *Bacillus spp.* (9.7%), *Klebsiella spp* (6.5%) and *Proteus vulgaris* (6.5%) respectively. The antibiotics susceptibility profile of the identified Gram positive isolates showed that *S. aureus* were significantly susceptible to all the antibiotics tested except beta lactams while *Bacillus spp.* were resistant to only Amoxicillin (100%), Ampiclox (100%) and Erythromycin (67%). Among the Gram negative isolates identified, *E. coli* expressed varying resistant pattern but was susceptible to the fluoroquinolones. *Klebsiella spp.* and *Salmonella typhi* were susceptible to other antibiotics tested but resistant to Amoxicillin (100% and 25%), Gentamycin (50% and 25%), Ciprofloxacin (50% and 25%) and Ofloxacin (50% and 50%) respectively. While *P. vulgaris* was resistant to Pefloxacin (62.5%), Amoxicillin (62.5%), Cotrimoxazole (50%), Sparfloxacin and Streptomycin (37.5%), Chloramphenicol and Amoxicillin-Clavulanate (25%) and Gentamicin (12.5%), but showed 100% susceptibility to Ofloxacin and Ciprofloxacin. *Ps. aeruginosa* was observed to show resistance to Sparfloxacin and Amoxicillin (75%), Amoxicillin-Clavulanate (33%), Ciprofloxacin and Gentamycin (25%) and significant percentage of the isolates had $MARI \geq 0.2$. This study shows that microorganisms that are of clinical importance could be isolated from door handles in the evaluated area.

Keywords: Door handles, bacteria, antibiotics resistance, hygiene, Kaduna

Introduction

Environmental contamination with pathogenic microorganisms which are of clinical importance due to their contribution

to morbidity and mortality are increasing daily as a result of ignorance on the part of the populace (Onaolapo *et al* 2015). Scientific research has shown that commonly

used surfaces such as door handles, computers, mobile phones, telephones, desks and automated teller machine (ATM) are potential sources of infectious bacteria and viruses leading to the spread of illnesses such as flu, diarrhoea, cholera, dysentery, typhoid and others (Reynolds *et al.* 2005). Although microorganisms are found everywhere, bacteria and fungi contaminate the body, our houses, workplaces and the whole environment. Fortunately, among the billions of bacteria, only 1500 can be dangerous to our health, causing different diseases such as pneumonia or skin infection (Eltablawy and Elhinfrawi, 2009). The hands serve as a medium for the propagation of microorganisms from place to place and from person to person. Although it is nearly impossible for the hand to be free of microorganisms, the presence of pathogenic bacteria may lead to chronic or acute illnesses (Oranusiet *al.* 2013). Fomites such as door handles consist of either porous or non-porous surfaces or inanimate objects, such that when contaminated with pathogenic microorganisms can transfer them to a new host thereby serving as vehicles of transmission. The colonisation of inanimate objects by viable pathogenic microorganisms including *Enterobacteriaceae* and Gram positive bacteria have been reported (Akinjogunla *et al.* 2016). This group of *Enterobacteriaceae* is a large group of heterogeneous Gram negative rods whose natural habitat is the intestinal tract of humans and animals but the unhygienic behavior of humans can elicit the dissemination of these bacteria. *Enterobacteriaceae* are facultative anaerobes that ferment a wide range of carbohydrates and it possesses a variety of toxins and virulent factors (Jawetz *et al.* 2010). The family includes many genera like *Escherichia*, *Shigella*, *Salmonella*,

Enterobacteria, *Serratia*, *Proteus* and others. Some enteric organisms such as *E. coli* form part of the normal flora and incidentally causes diseases, while others like *Salmonella* and *Shigella* are regular pathogens. *Escherichia coli*, *Klebsiella spp.* *Citrobacteria* have been found to contaminate various contact surfaces including door handles. These bacteria possess virulence factors that enhance their pathogenicity (Akinjogunla *et al.*, 2014). According to Itah (2004), organisms such as *Staphylococcus aureus*, *Bacillus subtilis* and some Gram negative bacteria such as *Escherichia coli*, *Klebsiella*, *Pseudomonas* species have been reported to contaminate various contact surfaces including chairs, tables, windows, door handles and other common household furniture/items. The presence of these pathogenic bacteria on environmental surfaces poses a potential risk to vulnerable, immunocompromised individuals (WHO, 2006). Therefore, this study evaluated the presence of pathogenic bacteria of clinical importance and their antibiotics susceptibility profile in door handles using Kaduna State University as a case study for other sociocultural environment. The findings from this study would probably demonstrate transferability of bacteria from hands to almost any frequently used surfaces especially door handles.

Materials and Methods

Specimen Collection and Processing: A total of 60 swab samples were randomly collected from 4 Faculties within the main campus of Kaduna State University (KASU) and transported in an ice pack to the Microbiology Laboratory of the Department of Pharmaceutical Microbiology and Biotechnology, KASU. Five samples each were collected from the Restrooms, Classes

and Laboratories. The samples were then suspended in 5ml of sterile MacConkey broth and incubated at 35°C for 24h. The overnight culture were shake vigorously for bacteria viable count.

Viable Count: Serial dilution of samples were carried out by arranging 10 test tubes containing 9ml of distilled water each and labelled 10^{-1} , 10^{-2} , 10^{-3} , 10^{-4} , 10^{-5} , 10^{-6} , 10^{-7} , 10^{-8} and 10^{-9} . Using sterile pipette, 1ml of the sample was transferred aseptically into the first test tube thus making a 10^{-1} dilution, from the 10^{-1} dilution, 1ml was taken after aspirating for 3 to 5 times to ensure thorough mixing into the next test tube to make 10^{-2} dilution. This method was serially repeated to the last tube. Sterile pipette was used to transfer 0.1ml of the diluted sample (10^{-2} to 10^{-3}) into appropriately labeled plates of MacConkey agar. Sterile bent glass rod was used to spread the sample on the media. The plates were then incubated at 37°C for 48 hours. The number of coliforms bacteria isolated was counted and the colony forming

unit per millimeter was calculated. Viable bacteria colonies were identified and isolates were picked using inoculation loop and streaked on nutrient agar slant, and stored in a refrigerator at -4°C for further studies.

Bacteria Isolation and identification: Colonies that grew on nutrient agar plates were Gram stained in accordance with standard Gram staining procedure described by Smith and Hussey (2005) and microscopic examination, catalase, coagulase, urease, indole, triple sugar iron tests were carried out as described by Cheesbrough (2010).

Antibiotic Susceptibility Tests: Antibiotic susceptibility tests of the bacteria were carried out using disc diffusion method as described by Cheesbrough (2010) and results were interpreted according to the method described by Clinical and Laboratory Standard Institute (CLSI) (2016) as shown in Table 1.

Table 1: Antibiotics Tested, their Concentration and Zones of Inhibition

Antibiotic	Zone of Inhibition (mm)		
	Susceptible	Intermediate	Resistant
Ceftriaxone (30 µ/ml)	≥21	14-20	≤13
Cefuroxime (30 µ/ml)	≥18	15-17	≤14
Amoxicillin (30 µ/ml)	≥29	-	≤28
Gentamicin (10 µ/ml)	≥15	13-14	≤12
Ampicillin/Cloxacillin (30 µ/ml)	≥29	-	≤28
Erythromycin (10 µ/ml)	≥23	14-22	≤13
Ciprofloxacin (10 µ/ml)	≥21	16-20	≤15
Streptomycin (30 µ/ml)	≥15	12-14	≤11
Perfloxacin (10 µ/ml)	≥21	16-20	≤15
Co-trimoxazole (30 µ/ml)	≥16	11-15	≤10
Spafloxacin (10 µ/ml)	≥21	16-20	≤15

Determination of Multiple Antibiotic Resistance Index (MARI): Multiple

antibiotic resistance index (MARI) which is calculated as number of antibiotics to which

test isolates displayed resistance to divided by the total number of antibiotic to which the test organism has been evaluated for was adopted for this test (Krumperman, 1983).

Results

Sample collection

Significant percentage (50%) of the swabs sampled harboured bacteria. Door handles in

the Faculties of Sciences, Arts and Pharmacy had the highest bacteria percentage rate 60%, 53.3% and 53.3% respectively while College of Medicine had the least bacteria rate (33.3%). Restrooms were the most contaminated (21.7%), followed by Laboratories (18.3%) while the least were class rooms (10%) (Table 2).

Table 2: Percentage Distribution of Bacteria Contaminants from Door Handles Sampled

S/N	Faculties	Samples	Rest Rooms [n = 20]	Laboratories [n = 20]	Class Rooms [n = 20]	Total (%)
1	Pharmaceutical Sciences	15	4	3	1	8 (53.3)
2	College of Medicine	15	2	2	1	5 (33.3)
3	Arts	15	3	3	2	8 (53.3)
4	Sciences	15	4	3	2	9 (60)
Total		60	13 (21.7)	11 (18.3)	6 (10)	30 (50)

The mean total of bacteria viable count (cfu/ml) ranged from 3.5x10⁵ cfu/ml to 9.9x10⁶ cfu/ml within the Faculties

evaluated. The highest total viable count was 7.6x10⁷ cfu/ml while 3.3x10³ cfu/ml was the least observed (Table 3).

Table 3: Mean of Total Bacteria Viable Count (cfu/ml) from Door handles

Samples	Pharmaceutical Sciences	College of Medicine	Arts	Sciences
A	4.8x10 ³	4.2x10 ⁴	3.2x10 ⁶	2.8x10 ⁶
B	7.1x10 ⁶	1.5x10 ⁶	1.5x10 ⁴	3.7x10 ⁵
C	4.8x10 ⁴	3.0x10 ⁵	1.6x10 ⁴	9.9x10 ⁵
D	2.4x10 ⁴	3.2x10 ⁴	7.6x10 ⁷	2.8x10 ⁴
E	2.1x10 ⁶	1.9x10 ⁵	1.6x10 ⁴	2.9x10 ⁴
F	5.2x10 ⁶		2.1x10 ⁵	2.3x10 ⁷
G	6.8x10 ⁶		2.6x10 ⁵	3.3x10 ³
H	3.2x10 ⁶		1.2x10 ⁵	2.9x10 ⁵
I				2.2x10 ⁴
Mean	3.6 x 10⁶	3.5 x 10⁵	9.9 x 10⁶	3.1 x 10⁶

Isolation and identification of bacteria isolates

S. aureus (29%) was the highest prevalent bacteria isolated from door handles in the environment sampled followed by *E. coli*

(25.8%), *Salmonella typhi* (12.9), *Bacillus spp.* (9.7), *Pseudomonas aeruginosa* (9.7) while the least isolated bacteria were *Klebsiella spp.* (6.5%) and *Proteus vulgaris* (6.5%) respectively. Gram negative bacteria

(61.3%) were the most isolated compared to Gram positive bacteria (38.7%) (Table 4).

Table 4: Percentage Occurrence of Bacteria Isolated from Door Handles

Organisms	Faculties				Total (%)
	Pharmaceutical Sciences	College of Arts Medicine	Arts	Sciences	
<i>Klebsiella spp.</i>	1	0	1	0	2 (6.5)
<i>E. coli</i>	2	1	2	3	8 (25.8)
<i>Salmonella typhi</i>	1	1	1	1	4 (12.9)
<i>Proteus vulgaris</i>	0	0	1	1	2 (6.5)
<i>Ps. aeruginosa</i>	0	1	1	1	3 (9.7)
<i>S. aureus</i>	3	1	3	2	9 (29)
<i>Bacillus spp.</i>	1	1	0	1	3 (9.7)
Total (%)	8 (28.3%)	6 (20%)	9 (30%)	9 (30%)	31(100)

Key: -Ve = negative, +Ve = positive

Gram -Ve (61.3%)
Gram +Ve (38.7%)

Antibiotics susceptibility profile of gram positive isolates

S. aureus isolated were significantly ($\geq 67\%$) susceptible to all the antibiotics tested except to betalactams (amoxicillin and amoxicillin/cloxacillin) with 100% and 78% resistance respectively (Figure 1).

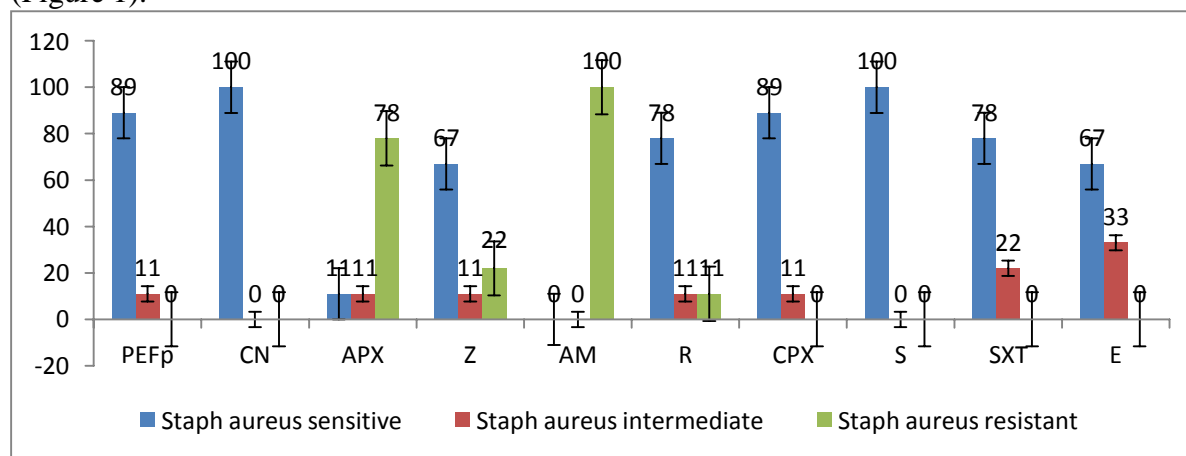


Figure 1: Antibiotics Susceptibility Profile of *S. aureus* Isolated from Door Handle

Key: SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamycin, PEFp = Perfloxacin, S= Streptomycin, APX= Ampicillin-cloxacillin, Z = Cefuroxime, R = Ceftriaxone, E = Erythromycin

Bacillus spp. were also resistant to amoxicillin (100%), amoxicillin/cloxacillin (100%), erythromycin (67%) but susceptible to all other antibiotics tested (Figure 2).

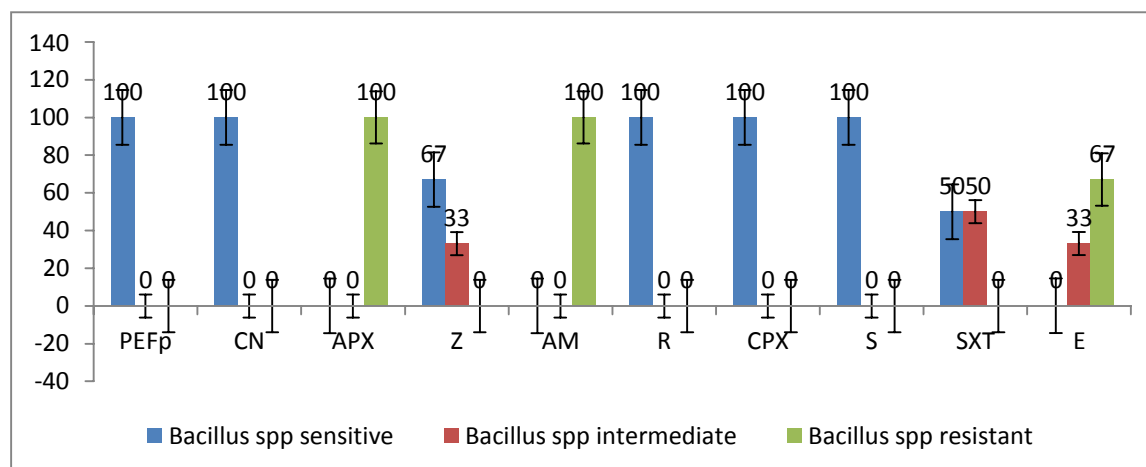


Figure 2: Antibiotics Susceptibility Profile of *Bacillus* spp. Isolated from Door Handle

Key: SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamycin, PEFp = Perfloxacin, S= Streptomycin, APX= Ampicillin-cloxacillin, Z = Cefuroxime, R = Ceftriaxone, E = Erythromycin

S. aureus was observed to express more resistance to the antibiotics tested than *Bacillus spp.* *S. aureus* was observed to express resistance to 4 antibiotics while *Bacillus spp.* was resistant to 3 antibiotics (Table 5).

Table 5: Comparative evaluation of Percentage Antibiotics Resistance of Gram Positive Bacteria Isolated from Door Handles Sampled

Bacteria	Percentage Antibiotics Resistance									
	PEF	CPX	CN	S	SXT	E	APX	CXM	AM	CTX
<i>S. aureus</i>	0	0	0	0	0	0	77.7	77.7	100	11.1
<i>Bacillus spp.</i>	0	0	0	0	0	66.7	100	0	100	0

Key: SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamycin, PEF = Perfloxacin, S= Streptomycin, APX= Ampicillin/cloxacillin, CXM = Cefuroxime, CTX = Ceftriaxone, E = Erythromycin.

The Gram positive isolates were observed to show a tailored resistant pattern only to betalactams, 33.3% of the isolates had multiple antibiotics resistant index (MARI) \geq

0.3 while none of the isolates were multidrug resistant (Table 6). There was no multidrug resistance isolate among Gram positive bacteria isolated from door handle.

Table 6: Determination of Resistant Pattern, Multiple Antibiotics Resistance Index (MARI) and Classification of Resistance among Gram Positive Bacteria Isolated from Door Handle

Isolate	Code	Resistant Pattern	MARI	CR
<i>S. aureus</i>	FPS	APX, AM	0.2	NMDR
	FPS	APX, Z, AM, R	0.4	NMDR
	FPS	APX, AM	0.2	NMDR
	CM	APX, AM	0.2	NMDR
	FA	APX, AM	0.2	NMDR
	FA	APX, AM	0.2	NMDR
	FA	APX, Z, AM	0.3	NMDR
	FS	AM	0.1	NMDR
	FS	AM	0.1	NMDR
	<i>Bacillus spp.</i>	FPS	APX, AM	0.2
CM		APX, AM, E	0.3	NMDR
FS		APX, AM,E	0.3	NMDR

Key: FPS = Faculty of Pharmaceutical Sciences, FS = Faculty of Sciences, CM = College of Medicine, FA = Faculty of Arts, SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, Z = Cefuroxime, R = Ceftriaxone, APX= Ampicillin/cloxacillin, E= Erythromycin, CR = classification of resistance, NMDR = not multidrug resistant

E. coli was significantly ($\geq 75\%$) susceptible to quinolones [Ofloxacin (87.5%), ciprofloxacin (75%)], Augmentin (75%), Chloramphenicol (50%) and Gentamicin (50%). They were observed to show high resistant to Pefloxacin (62.5%), Amoxicillin (62.5%), Cotrimoxazole (50%), Sparfloxacin (37.5%) and Streptomycin (37.5%) (Figure 3).

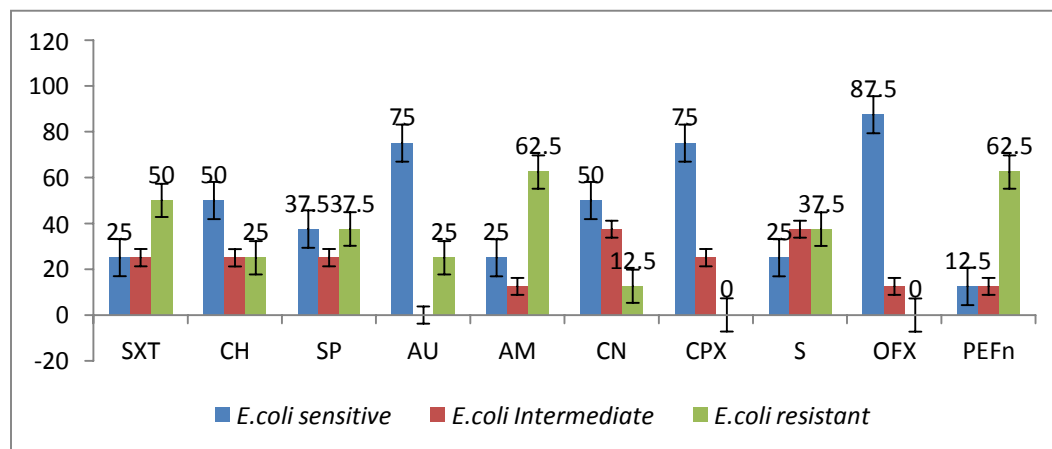


Figure 3: Antibiotics Susceptibility Profile of *E. coli* Isolated from Door Handle

Key: SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamycin, PEFn = Perfloxacin, S= Streptomycin, APX= Ampicillin/cloxacillin, CXM = Cefuroxime, CTX = Ceftriaxone, CH = Chloramphenicol, SP = Sparfloxacin, AU = Augmentin, OFX = Ofloxacin

P. vulgaris was significantly (100%) susceptible to Augmentin (100%), Chloramphenicol (100%), Sparfloxacin (100%), Streptomycin (100%). They were observed to show high resistant to

Amoxicillin (100%), ciprofloxacin (100%), mildly resistant to Ofloxacin (50%), Gentamicin (50%) and Cotrimoxazole (50%) while Pefloxacin was observed to show 100% intermediate resistance (Figure 4).

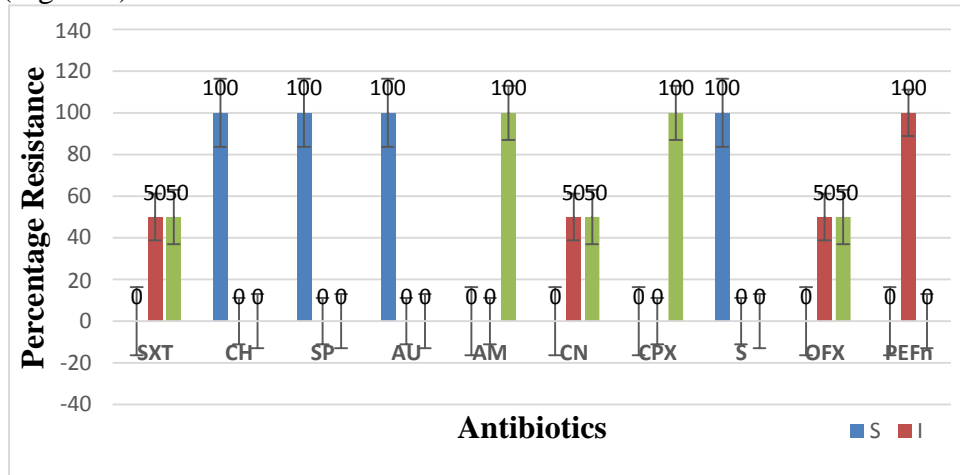


Figure 4: Percentage Antibiotics Susceptibility Profile of *P. vulgaris* Isolated from Door Handle

Key: SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamicin, PEFn = Pefloxacin, S= Streptomycin, APX= Ampicillin/cloxacillin, CXM = Cefuroxime, CTX = Ceftriaxone, CH = Chloramphenicol, SP = Sparfloxacin, AU = Augmentin, OFX = Ofloxacin

Klebsiella spp. Were highly susceptible to not commonly prescribed quinolone [Sparfloxacin (100%) and Pefloxacin (100%)], but mildly resistant to Ciprofloxacin (50%) and Ofloxacin (50%). Mild susceptibility were observed against Cotrimoxazole (50%), Chloramphenicol (50%), Augmentin (50%), Gentamicin (50%) and Streptomycin (50%) (Figure 5).

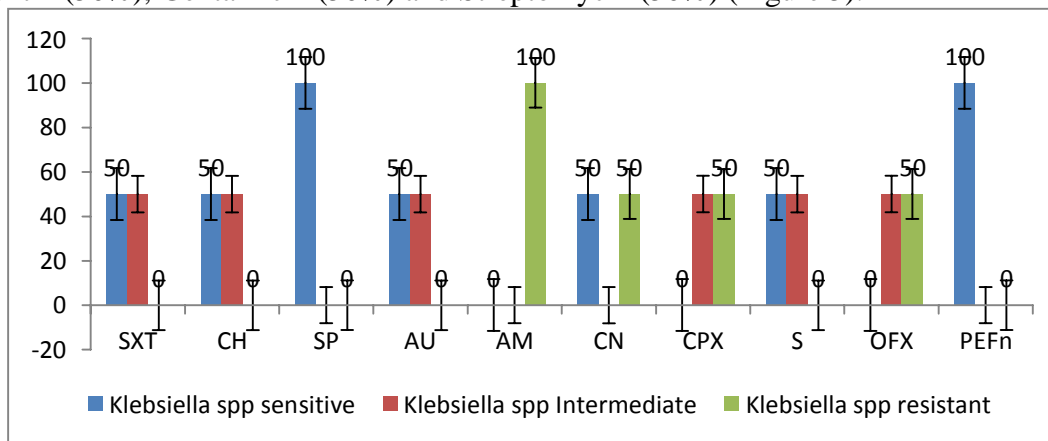


Figure 5: Percentage Antibiotics Susceptibility Profile of *Klebsiella spp.* Isolated from Door Handle

Key: SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamicin, PEFn = Pefloxacin, S= Streptomycin, APX= Ampicillin/cloxacillin, CXM = Cefuroxime, CTX = Ceftriaxone, CH = Chloramphenicol, SP = Sparfloxacin, AU = Augmentin, OFX = Ofloxacin

Salmonella typhi was observed to show high susceptibility to Perfloxacin (100%), Streptomycin (100%), cotrimoxazole (75%), chloramphenicol (75%), Augmentin (75%), Sparfloxacin (75%) mildly susceptible to Gentamicin (50%), Ciprofloxacin (50%), Amoxicillin (50%). Resistance was only significantly observed against Ofloxacin at 50%.

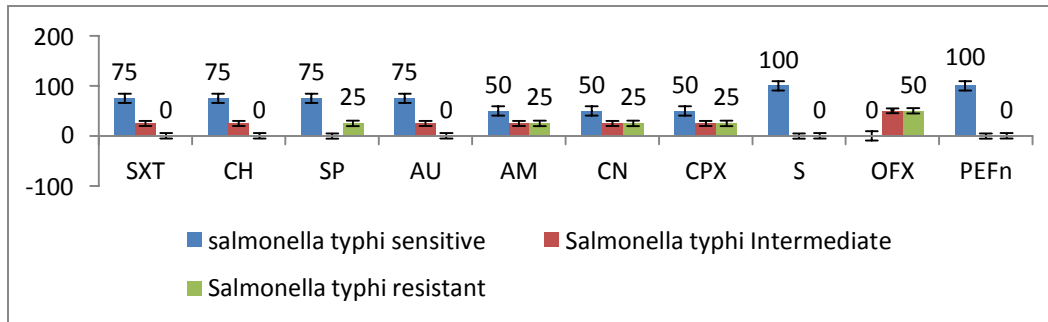


Figure 6: Percentage Antibiotics Susceptibility Profile of *S. typhi* Isolated from Door Handle
Key: SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamicin, PEFn = Perfloxacin, S= Streptomycin, APX= Ampicillin/cloxacillin, CXM = Cefuroxime, CTX = Ceftriaxone, CH = Chloramphenicol, SP = Sparfloxacin, AU = Augmentin, OFX = Ofloxacin

Pseudomonas aeruginosa was susceptible to Perfloxacin (100%), Cotrimoxazole (75%), Gentamicin (75%), Ciprofloxacin (75%) and Ofloxacin (75%). Highly resistant to Streptomycin (75%) and Chloramphenicol (75%) while significant intermediate sensitivity was observed against Sparfloxacin (75%) and Amoxicillin (75%) (Figure 7)

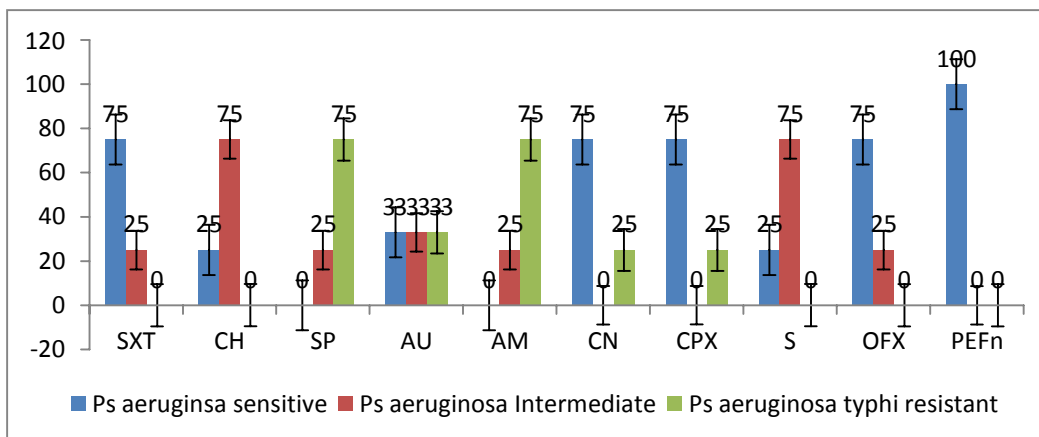


Figure 7: Percentage Antibiotics Susceptibility Profile of *Ps. aeruginosa* Isolated from Door Handle

Key: SXT = Co-trimoxazole, CH = Chloramphenicol, SP = Sparfloxacin, AU = Augmentin, AM= Amoxicillin, CN = Gentamicin, CPX= Ciprofloxacin, CPX = Cefpodosime, S= Streptomycin, OFX = Ofloxacin, PEFn = Perfloxacin

Among the Gram negative bacteria identified *E. coli* was observed to express more resistance across the antibiotics tested followed by *Ps. aeruginosa*, *Proteus vulgaris*, *Klebsiella* spp. while the least susceptible was *Salmonella typhi* (Table 7)

Table 7: Comparative Evaluation of the Percentage Antibiotics Resistant Profile of Gram Negative Bacteria Isolated from Door Handles Samples

Bacteria (No. of isolates)	Percentage Antibiotics Resistance									
	SXT	CH	SP	AU	AM	CN	CPX	S	OFX	PEF
<i>E. coli</i> (8)	50	25	37.5	25	62.5	12.5	37.5	37.5	0	62.5
<i>Klebsiella</i> spp. (2)	0	0	0	0	100	50	50	0	50	0
<i>Salmonella typhi</i> (4)	0	0	25	0	25	25	25	0	25	0
<i>P. aeruginosa</i> (3)	0	0	66.7	33.3	66.7	33.3	33.3	0	0	0
<i>Proteus vulgaris</i> (2)	50	0	0	0	50	50	50	0	50	0

Key: SXT = Co-trimoxazole, CH = Chloramphenicol, SP = Sparfloxacin, AU = Augmentin, AM = Amoxicillin, CN = Gentamycin, CPX = Ciprofloxacin, CPX = Cefpodosime, S = Streptomycin, OFX = Ofloxacin, PEFn = Perfloxacin

The Gram negative isolates had varying resistance pattern, of which 52.6% had MARI \geq 0.3 while 47.4% were multidrug resistant. *Proteus vulgaris* (100%) had more multidrug resistant isolates followed by *E. coli* (75%), *Klebsiella* spp. (50%) while *Ps. aeruginosa* (0%) and *Salmonella typhi* (0%) had no multidrug resistant isolate.

Table 8: Determination of Resistant Pattern, Multiple Antibiotics Resistance Index (MARI) and Classification of Resistance among Gram Negative Bacteria Isolated from Door Handle.

Isolate	Code	Resistant Pattern	NART	MARI	CAR
<i>E. coli</i>	FPS	SXT, SP, AM, CN, S, P	6	0.6	MDR
	FPS	AU, AM, S, P	4	0.4	MDR
	CM	SP, AM, S, P	4	0.4	MDR
	FA	CH, SP, AU	3	0.3	MDR
	FA	CH, AM, P	3	0.3	MDR
	FS	SXT, AM, P	3	0.3	MDR
	FS	SXT	1	0.1	NMDR
	FS	SXT	1	0.1	NMDR
<i>Proteus vulgaris</i>	FA	AM, CN, CPX, OFX	4	0.4	MDR
	FS	SXT, AM, CPX	3	0.3	MDR
<i>Klebsiella spp.</i>	FPS	AM, CN, CPX	3	0.3	MDR
	FA	AM, OFX	2	0.2	NMDR
<i>Salmonella typhi</i>	FPS	CPX		0.1	NMDR
	CM	AM	1	0.1	NMDR
	FA	CN, OFX	2	0.1	NMDR
	FS	SP	1	0.1	NMDR
<i>Pseudomonas aeruginosa</i>	CM	SP, AM	2	0.2	NMDR
	FA	SXT, AU, AM, CPX	3	0.3	NMDR
	FS	SP, CN	2	0.2	NMDR

Key: FPS = Faculty of Pharmaceutical Sciences, CM = College of Medicine, FA = Faculty of Arts, FS = Faculty of Sciences, SXT = Co-trimoxazole, CPX= Ciprofloxacin, AM= Amoxicillin, CN = Gentamycin, P = Perfloxacin, S= Streptomycin, APX= Ampicillin/cloxacillin, CXM = Cefuroxime, CTX = Ceftriaxone, CH = Chloramphenicol, SP = Sparfloxacin, AU = Augmentin, OFX = Ofloxacin, NMDR = Not multidrug resistant, MDR = Multidrug resistant, NART = Number of antibiotics resistant to, MARI = Multiple antibiotics resistant index, CAR = Classification of resistant.

Discussion

Door handles are a significant reservoir of microorganisms. This study revealed a high levels of bacterial contaminants on door handles with a considerable numbers of Gram positive and Gram negative bacteria. However, Gram negative bacteria were predominant compared to Gram positive

ones. Most bacteria in the skin flora are Gram positive, which would account for their predominance on door handles. The study showed a significant difference in this regard. The high prevalence of bacteria isolated in this study is in agreement with the report of Nworie *et al.* (2012) in Abakaliki; Onaolapo *et al.* (2015) and, Otter and French (2009)

who all reported varying percentages of both Gram positive and Gram negative bacteria on door handles and these bacteria are of public health importance. The variation in the contamination level observed in this study may not be unconnected with differences in hygiene and sanitary conditions in the environment.

In this study, the level of contamination was higher in restrooms and laboratories, as compared to classrooms. The Faculty of Science was seen to have a higher level of contamination for door handles compared to other Faculties. The lower level of contamination in College of Medicine and classrooms could be attributed to the fact that they are not being used as frequently as other places studied. This is in agreement with the finding of Nworie *et al.* (2012) who reported that the levels of contamination varied depending on the traffic, exposure and environment. In this study, the most frequently isolated bacteria pathogen was *Staphylococcus aureus*, which may be due to the fact that it is a major component of the normal flora of the skin and nostrils. This probably explains its high prevalence as a contaminant, as it can easily be discharged by several human activities. This observation is in agreement with the findings of other researchers (Brooks *et al.* 2007; Nworie *et al.* 2012). The microorganisms isolated from the door handles in the study were *S. aureus*, *Bacillus spp.*, *Proteus vulgaris*, *E. coli*, *Salmonella typhi* and *Klebsiella spp.* However, the reports from Lynn *et al.* (2013) showed isolated microorganisms as *Staphylococcus spp.*, *Klebsiella spp.*, *E. coli* and *Proteus spp.* but from toilet door handles at secondary schools in Bokkos L.G.A, Plateau State. Chris *et al.* (2002) reported the presence of the bacteria isolates such as *S. aureus* and *E. coli* from the bathroom of

students at the University of Miami, USA. Each of these organisms has been implicated either as a major contaminant or as the most pathogenic bacteria recovered. The fact that bacteria of the Enterobacteriaceae were regularly found on different door handles may indicate fecal contamination of the hands as the origin. Isolation of *Bacillus spp.* in this research and its predominance could be explained by the fact that *Bacillus spp.* are ubiquitous in nature with their spores able to resist environmental changes, withstand dry heat and certain chemical disinfectants for moderate periods. This is also in agreement with the research carried out by Brooks *et al.* (2007) who reported that *Bacillus spp.* were found to be among the predominant organism that were isolated from door handles. From the findings in this study, it was observed that most of the isolates obtained were susceptible to most commonly used antibiotics with varying resistant patterns and multidrug resistance percentages. These findings are in agreement with the research carried out by Adewoyin *et al.* (2013) who reported that antibiotic resistant microorganisms contaminate environmental surfaces such as toilet and most of the isolates obtained in their study were susceptible to commonly used antibiotics except in some cases.

Among the Gram negative bacteria identified, *E. coli* was observed to express more resistance across the antibiotics tested followed by *Ps. aeruginosa*, *Proteus vulgaris*, *Klebsiella spp.* while the least susceptible was *Salmonella typhi*. This could be attributed to the fact that in most reports *E. coli* has been documented to be a significant reservoir of genes coding for resistance to several antimicrobial drugs and therefore is a useful indicator for resistance in bacterial communities (Katakweba *et al.* 2018). The Gram negative isolates had varying resistant

patterns, of which 52.6% had multiple antibiotic resistance index (MARI) ≥ 0.3 while 47.4% were multidrug resistant. *Proteus vulgaris* (100%) had more multidrug resistant isolates followed by *E. coli* (75%), *Klebsiella* spp. (50%) while *Ps. aeruginosa* (0%) and *Salmonella typhi* (0%) had no multidrug resistant isolate. The differences in resistance profiles in the environment studied clearly reflect the differences in the antibiotic resistant selection pressure in the investigated sites (Stephen and Kennedy, 2018). The multidrug resistant characteristic expressed by *P. vulgaris* could be attributed to the fact that *P. vulgaris* produces a chromosomally encoded beta-lactamase, referred to as the cefuroxime-hydrolyzing beta-lactamase (cefuroximase or CumA), which hydrolyzes cephalosporins (Datz *et al.* 1994). The enzyme can be induced by ampicillin, amoxicillin and first generation cephalosporins, weakly induced by carboxypenicillins, ureidopenicillins, cefotaxime and ceftriaxone, and inhibited by clavulanate. More so, studies have shown that strains of *P. vulgaris* that have a mutation in the regulatory genes of this beta-lactamase produce high levels of the enzyme and are resistant to penicillins, cefuroxime, ceftriaxone and cefotaxime (Chelsie and Harry, 2002). According to Igwe *et al.* (2014), isolation of bacteria with high MARI as observed in this study indicates that the isolates were previously exposed to these antibiotics tested.

This study established that door handles through human dispersal could serve as lethal weapon for the transfer of contaminant microorganism of public health importance with multidrug resistance characteristics. Thus, bacteria are mostly isolated from restroom and other areas with high population influx. Hence, it is recommended

that high level of hygiene through frequent washing of hands using soap and hand sanitizer become part of our daily lifestyle, especially with the advent of covid-19, which has shown the possibility of community infection and reinfection through person to person contact and hand dispersal. More so, frequent surveillance is strongly recommended to ensure periodic documentation of pathogenic bacteria which could be transferred in environment.

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