Premier Journal of Engineering and Applied Sciences
Publication of Nigerian Society of Engineers, Ibadan Branch
P J E A S
Vol. 2, No. 3, 2021 ISSN:2734-3170

Characterization of Bacteria from Toilet Door Handles in some Selected Buildings at Obafemi Awolowo University, Ile-Ife, Osun State

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ARTICLE INFO

Received: March, 2021
Accepted: June, 2021
Published: July, 2021

Keywords:
Antibiotic sensitivity
Human pathogens,
Infectious disease
Toilet door handles

ABSTRACT

Fomite is a non-living material capable of transporting infectious organisms, and it is one of the most common ways for bacterial diseases to spread. In this study, characterization of bacteria from door handles of forty public toilets of some selected buildings at Obafemi Awolowo University campus was carried out. The selected toilet door handles were swabbed with sterile, cotton-tipped applicators (swab stick) and moistened with sterile distilled water. Biochemical examination of bacterial isolates and antibiotic sensitivity pattern were evaluated. The result of biochemical examination of bacterial isolates revealed widespread contamination by twelve bacterial species in the following order: Staphylococcus aureus (33.1%), Staphylococcus sp. (19.2%), Klebsiella sp. (13.8%), Bacillus sp. (6.9%), Proteus vulgaris (3.1%), Proteus mirabilis (4.6%), Micrococcus sp. (6.2%), Serratia sp. (3.1%), Salmonella sp. (4.6%), Enterobacter sp. (1.5%), Citrobacter freundii (3.1%) and Streptococcus sp. (0.8%). Results of antibiotic sensitivity pattern showed that 81.25% of the Gram-positive bacteria isolates were susceptible to Cipfloxacin while 87.5% of them were resistant to Chloramphenicol. Gram-negative bacteria isolates were 85.71% susceptible to Ofloxacin and 100% resistant to Augmentin, Ceftriazone and Tetracycline. The bacteria transmitted through toilet door-handles were mostly human pathogens (e.g. Staphylococcus aureus, Klebsiella species, Proteus species and Salmonella species) and opportunistic pathogen (e.g. Staphylococcus species and Citrobacter species). The findings of this study are important for public health and safety since they demonstrate the presence of bacterial pathogens on toilet door handles, which is important in reducing the transmission of infectious disease.

1. INTRODUCTION

Microorganisms live as transient pathogens in fomites or hands in a variety of cases, posing serious health risks as sources of population and hospital-acquired infections (Pittet *et al.*, 1999). The rising frequency of infectious outbreaks of such diseases, as well as the pace at which they spread from one population to another, has become a major public health issue (Galtelli *et al.*, 2006). Apart from people's day-to-day interactions, which is one way disease spreads, the other main cause and spread of population acquired infections is fomites (Li *et al.*, 2009). If fomites come into contact with humans or the natural environment

of pathogenic organisms, they become a significant source of infectious disease transmission (Nworie *et al.*, 2012). Fomites, such as convenience door handles, toilets, toilet seats and faucets, sinks, lockers, benches, and tables, are particularly important in public offices, hospitals, hotels, restaurants, and restrooms (Bright *et al.*, 2010). Toilet and bathroom door handles have been implicated as one of the most likely causes of infection (Reynolds, 2005). Users bring their own microbial flora and other species they have picked up elsewhere into public restrooms and bathrooms, placing them on door handles/knobs on their way in and out (Goldhammer *et al.*, 2006). The probability of disease transmission via fomites, on the other hand, is determined by a number of factors which include: the extent of site contamination and exposure; the amount of pathogen excreted by the host; the possibility of the infectious agent being transferred to a susceptible individual; the virulence of the organism; the immuno-competence of those in contact; and the use of control measures.

Microbes from human secretions such as saliva, skin, urine, and faeces can contaminate toilets (Anjum *et al.*, 2018). Public health is at danger when bacteria from public toilets penetrate human body through hand-to-mouth or hand-to-food contact. Human hands are the most important organs for physical manipulation. The hand is a paired organ that is dominated by the opposite hemisphere of the brain and allows one to do a variety of tasks (Maria and Eliane, 2004). The hand acts as a conduit for the transmission of microorganisms from one location to another and from one human to another. While microbial contamination of the hand is virtually impossible to avoid, the presence of pathogenic bacteria can cause chronic or acute illness. Microorganisms, like body normal flora and transient microbes contacted from the atmosphere, are commonly found on human hands (Lindberg *et al.*, 2004).

Several people have suffered from the so-called bathroom syndrome in the past, and they have avoided using public restrooms to avoid being polluted by the filthy atmosphere. Families, colleges, and health care providers must accept regular hand washing as the first line of protection in preventing the spread of disease that has been ignored. Many people, on the other hand, seem to simply run water over their hands without using soap, and others do not wash their hands at all after using the toilet (Barker and Bloomfield, 2000). The most likely sources of infection have been identified as toilet and bathroom door handles (Reynolds, 2005). Bacteria get into toilets and stay there for a long time, even after flushing and washing with antimicrobial fluids several times (Barker and Jones, 2005).

Bacteria analysis of public bathrooms allows people to understand which restrooms pose the greatest risk of contamination to the general public. A high microbial load of pathogenic microorganisms can be found in drains and toilet tanks. These pathogens enter the public toilet when a healthy or acutely ill person uses the facility and infects it with the pathogen, and a healthy person with weakened immunity comes into contact with the pathogen when using the facility (Barker and Jones, 2005).

Students at Obafemi Awolowo University are susceptible to some bacterial infections and ailments such as urinary tract infections (UTIs) and typhoid owing to inadequate toilets hygiene caused by a water deficit. As a result, the aim of this study was to isolate bacteria from toilet door handles at Obafemi Awolowo University campus, biochemically characterize the isolated bacteria, determine the prevalence of bacteria isolated from toilet door handles, and determine the antibiotic sensitivity pattern of the bacteria isolates. The findings of this study will demonstrate the presence of bacterial pathogens on toilet door handles, which is important in reducing the transmission of infectious disease and will increase awareness of the University administration on the necessity of effective hygiene.

2. METHODOLOGY

Sample Collection

The swab-rinse method of the American Public Health Association, as defined by Reynolds *et al.* (2005) was used to collect samples from the toilet door handles of some selected buildings at Obafemi Awolowo

University, Ile-Ife. Swabs of sterile cotton-tipped applicators (swab stick) moistened with sterile distilled water were used to clean door handles. The samples were taken immediately to the laboratory for analysis.

Culture Technique

Each of the swab sticks were inoculated into 5 ml of sterile nutrient broth in a test tube and incubated overnight. 1 ml was taken from the cultured broths which serve as the stock solution and transferred aseptically into first of the eight test tubes containing 9 ml of sterile distilled water arranged serially for the dilution. The first test tube was also shaken properly after the transfer for adequate mixing of the content. The process is repeated serially until it reaches the last test tube.

Pour Plate Method

An aliquot of 1 ml from 10^{-6} and 10^{-8} dilutions were dispensed into different sterile petri dishes on the bench. The plates were doubled for each of the dilutions. A molten nutrient agar prepared in 250 ml conical flask was allowed to cool to about 45^{o}C and gently poured inside each of the petri dishes and swirled gently to mix properly. After pouring, the molten agar was allowed to set and the plates were then incubated in an inverted position at 37^{o}C for 18-24 hours. At the end of incubation, plates were examined for growth. Bacterial isolates were first differentiated by macroscopic examination of the colony.

Isolation of Pure Culture

The selected colonies were sub cultured on fresh nutrient agar plates by streaking carefully on the medium using a sterile inoculating loop. For each set of streaks made, the inoculating loop was flamed so that distinct colonies of the organism were obtained. The plates were inverted and incubated at 37^{o}C for 24 hours, after which the plates were examined for growth. Uniformity in growth as well as appearance of distinct colonies on the plate indicated pure isolates. After obtaining pure isolates, fresh nutrient agar slants were prepared in MaCartney bottles. After the sterilization, the bottles were arranged such that they lay on their sides so that slants were formed, a colony of each isolates were aseptically transferred onto the slant by streaking it on the slant bottles and then placed in an incubator for 24 hours after which they were kept in the refrigerator at 4^{o}C for further studies.

Identification of Isolates

Bacteria isolates were identified using the Bergey's Manual of Determinative Bacteriology. Preliminary identification of bacterial isolates was performed using colonial and morphological characteristics of the isolates. Bacterial isolates were further characterized for physiological study through biochemical reaction of the bacterial isolates.

Antibiotic Sensitivity Testing

The standard agar disc diffusion method was employed. A distinct colony of each test organism was taken from the stock culture and inoculated into 10 ml sterile water using a sterilized loop. The suspension was then thoroughly mixed. The resulting mixture was then applied to the surface of a dried 9 cm plate of Mueller Hinton agar and spread evenly with a sterile cotton tipped applicator. Antibiotics multidisc were lightly but firmly pressed onto the surface of the plate using sterile forceps. The plates were then refrigerated at 4^{o}C for 30 minutes to ensure adequate diffusion of the antibiotics before been incubated at 37^{o}C for 18-24 hours. The diameter of the zones of inhibition were measured and compared with the standard provided by the manufacturer and consequently interpreted as susceptible, intermediate or resistant.

3. RESULTS AND DISCUSSION

Bacterial Isolates

Bacteria can exist as transient pollutants on inanimate items, particularly high-touch surfaces, where they can cause community-acquired diseases. The role of such surfaces, known as fomites in transmission has been extensively studied (Xiao, 2018). One hundred and thirty (130) bacteria isolates were obtained from forty (40) toilet door handles samples collected in this work, as presented in Table 1. The bacteria found

in this analysis were mostly human flora members. This suggests that humans are responsible for the bulk of bacteria found on toilet door handles. Pathogens can be transmitted through inanimate surfaces from man's hand, feaces, and liquid secretion; these organisms are capable of living on fomite surfaces for lengthy periods of time, albeit this relies on the nature of the fomites, the type of microorganisms, and environmental variables (Lopez *et al*., 2013).

Table 1: Distribution of sampled toilet door handles and their corresponding isolates

Building Complex	Number of Samples	Number of Isolates
BSMT	4	29
BSFT	4	28
SBMT	4	6
SBFT	4	6
WHMT	4	5
WHFT	4	7
FAMT	4	13
FAFT	4	13
FAGMT	4	7
FAGFT	4	16
Total	**40**	**130**

Key: BSMT – Biological Science Male Toilet, **BSFT** – Biological Science Female Toilet
SBMT – Senate Building Male Toilet, **SBFT** – Senate Building Female Toilet
WHMT – White House Male Toilet, **WHFT** – White House Female Toilet
FAMT – Faculty of Arts Male Toilet, **FAFT** – Faculty of Arts Female Toilet
FAGMT – Faculty of Agric Male Toilet, **FAGFT** – Faculty of Agric Female Toilet

The samples collected from door-handles of BSMT (Biological Sciences Male Toilets) showed the highest contamination with a total number of 29 (22.3%) organisms isolated while the lowest contaminated door-handles was found to be WHMT (White House Male Toilets) with 5 (3.85%) organisms isolated. This variation could be as a result of number of toilet users and the nature of work carried out in these buildings coupled with users' hygiene (Olajubu, 2019).

Morphological and Biochemical Characterization

Bacteria were identified based on morphological and biochemical characteristics (Table 2). Gram staining and biochemical test carried out on the bacteria resulted in presumptive identification of the bacteria using Bergey's Manual of Determinative Bacteriology. The biochemical analysis revealed that the studied toilet door handles were contaminated by mainly twelve bacterial species. The bacteria isolated were: *Staphylococcus aureus*, *Staphylococcus* sp., *Klebsiella* sp., *Bacillus* sp., *Proteus vulgaris*, *Proteus mirabilis*, *Micrococcus* sp., *Serratia* sp., *Salmonella* sp., *Enterobacter* sp., *Citrobacter freundii* and *Streptococcus* sp. The significant degree of contamination of the toilet door handles in this investigation agrees with Nworie *et al.* (2012). Furthermore, one of the five most prominent genera represented is Staphylococcus sp, Streptococcus sp, and Bacillus sp (Al-Harmoosh *et al.*, 2018; Alonge *et al.*, 2019).

Prevalence of Bacterial Isolates

The bacterial pathogens recovered from the toilet door handles in this investigation were similar with previous findings (Maori *et al.*, 2013; Odigie *et al.*, 2017), with *Staphylococcus aureus* being the most common (Onwubiko and Chinyeaka, 2015) as shown in Figure 1. *Staphylococcus aureus* was the only bacterial species recovered from all toilet door handles examined, with a prevalence rate of 33.1% while *Streptococcus* sp. as the lowest prevalence rate of 0.8%. The following were the prevalence rates for the other bacterial isolates: *Staphylococcus* sp. (19.2%), *Klebsiella* sp. (13.8%), *Bacillus* sp. (6.9%), *Proteus vulgaris* (3.1%), *Proteus mirabilis* (4.6%), *Micrococcus* sp. (6.2%), *Serratia* sp. (3.1%), *Salmonella* sp. (4.6%), *Enterobacter* sp. (1.5%), and *Citrobacter freundii* (3.1%).

Table 2: Morphological and Biochemical Characterization of the Isolates

Cultural characteristics	Gram's reaction	Biochemical tests														Probable Organism
		Catalase	Citrate	Lactose	Urease	Motility	Indole	Oxidase	Starch Hydrolysis	Spore Formation	Methyl Red	Voges Proskauer	Hydrogen Sulphide	Triple Sugar Iron Slant	Triple Sugar Iron Bottom	Coagulase	Mannitol	
Circular, creamy colonies	-ve rod	+	+	+	NT	-	-	NT	NT	NT	-	+	-	A	A	NT	NT	*Klebsiella* sp.
Circular, creamy colonies	-ve rod	+	-	-	-	+	-	-	-	-	+	-	+	K	A	NT	NT	*Salmonella* sp.
Circular, creamy colonies	+ve rod	+	+	NT	+	-	-	-	NT	-	+	+	NT	NT	NT	+	AG	*Staphylococcus aureus*
Circular, white colonies	-ve rod	+	+	-	+	+	-	-	NT	NT	+	-	+	K	A	NT	NT	*Proteus mirabilis*
Circular, red colonies	-ve rod	NT	NT	+	-	+	-	-	NT	NT	+	-	-	K	A	NT	NT	*Serratia* sp.
Circular, creamy colonies	+ve rod	+	+	NT	+	-	-	-	NT	-	+	+	NT	NT	NT	-	AG	*Staphylococcus* sp.
Circular, white colonies	+ve cocci	+	-	NT	NT	NT	-	+	-	NT	NT	NT	NT	NT	NT	NT	NAG	*Micrococcus* sp.
Circular, creamy colonies	-ve rod	+	+	+	+	NT	-	-	NT	-	+	-	NT	NT	NT	NT	NT	*Citrobacter freundii*
Circular, creamy colonies	-ve rod	+	+	+	+	+	+	-	NT	NT	-	+	-	A	A	NT	NT	*Enterobacter* sp.
Circular, creamy colonies	+ve rod	+	+	-	+	+	NT	NT	-	+	+	+	-	K	A	NT	NT	*Bacillus* sp.
Circular, white colonies	-ve rod	+	-	-	+	+	+	-	NT	NT	+	-	+	K	A	NT	NT	*Proteus vulgaris*
Circular, white colonies	+ve cocci	-	+	+	-	-	-	NT	NT	NT	+	-	-	NT	NT	NT	NT	*Streptococcus* sp.

Key: NT = Not Tested +ve = Positive -ve = Negative A = Acidic K = Alkaline AG = Acid and Gas NAG = No Acid and Gas

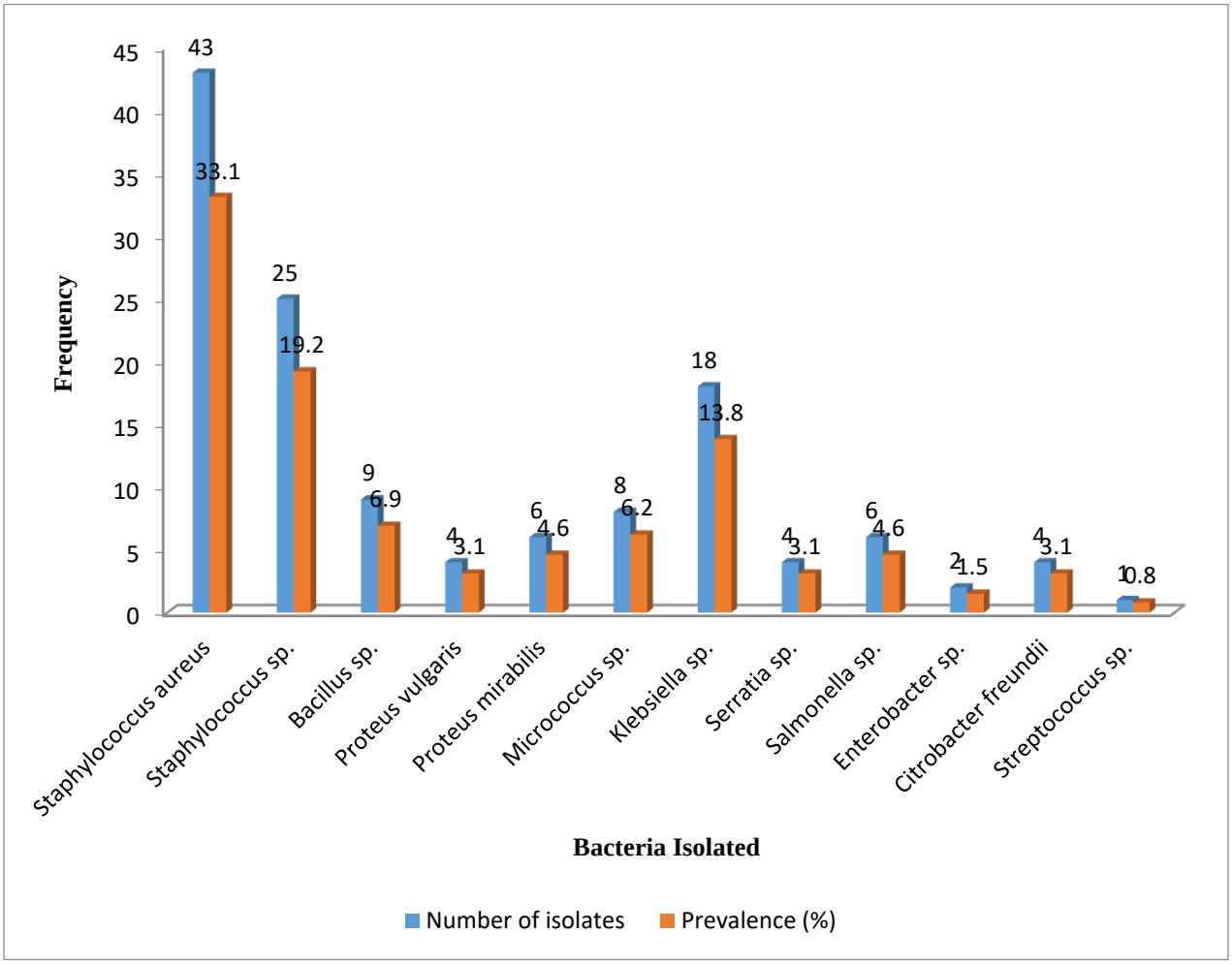

Figure 1: Prevalence of Bacteria Isolated from Toilet Door Handles

The incidence of gram positive bacteria was 66.2% and gram negative bacteria was 33.8% (Figure 2), indicating that the majority of these bacteria were normal flora of the human skin (Rintala *et al.*, 2008). Gram positive bacteria were identified as the main type of organisms in several previous studies on bacteria associated with door handles (Al-Harbi *et al*. 2017; Al-Harmoosh *et al*. 2019). Among the organisms isolated were human pathogens (e.g. *Staphylococcus aureus*, *Klebsiella species*, *Proteus species* and *Salmonella species*) while some were opportunistic pathogen (e.g. *Staphylococcus species* and *Citrobacter freundii)*. These findings were in line with those of Lynn *et al.* (2013) and Opere *et al.* (2013).

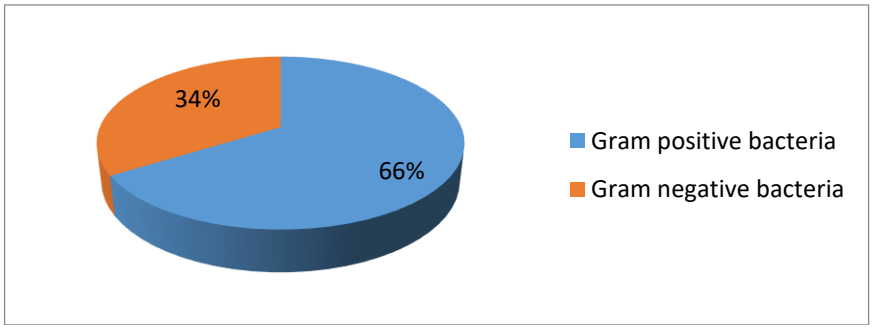

Figure 2: Prevalence of Gram positive and Gram negative bacteria

Contamination with *Staphylococcus sp.* and *Streptococcus sp.* which are skin microbiota, showed that individual handlers had direct touch with the toilet door (Alonge *et al.*, 2017). Presence of *Bacillus* sp. in this study can be explained by the fact that *Bacillus* species are widespread in nature, and their spores can endure environmental changes, dry heat, and certain chemical disinfectants for short periods of time. This is also in line with the findings of Brooks *et al.* (2007), who found *Bacillus* sp. to be the most common organisms on door handles. *Salmonella* sp. are enteric organisms that have been linked to deadly infections such as Shigellosis and Typhoid fever, necessitating immediate attention and the implementation of appropriate hygiene measures. *Klebsiella* sp. can survive for days or even months on surfaces and for a long time on the hands (Prescott *et al.*, 2005), thus as long as it is present on the hands, it will be disseminated to other locations by persons. The presence of Enterobacteraicea among the gram-negative bacteria suggests that the handles were contaminated with faeces, perhaps resulting in food poisoning and urinary tract infections (Wojgani, 2012).

Antibiotic Sensitivity

Sensitivity of isolates to the antibiotics was tested and interpreted using Clinical and Laboratory Institute Standards established for Antimicrobial Susceptibility Testing (CLSI, 2013). Some of the commercial antibiotics examined exhibited strong levels of inhibition against the isolates as shown in Tables 3(a-d), indicating that they could be useful in fighting infection caused by toilet usage. Furthermore, several of the gram negative isolates had multiple antibiotic resistances, which could pose a serious concern to health-care providers because bacteria have been shown to exchange gene-mediated resistance between organisms of the same and different genera. A critical look at the antibiotic sensitivity pattern shows that 81.25% of the Gram-positive bacteria isolates are susceptible to Cipfloxacin while 87.5% of them are resistant to Chloramphenicol. Gram-negative bacteria isolates are 85.71% susceptible to Ofloxacin and 100% resistant to Augmentin, Ceftriazone and Tetracycline. The new study's findings were consistent with Faparusi (2020), which found antibiotic-resistant bacteria strains in public male and female toilets door handles at Federal Polytechnic, Ilaro.

Table 3a: Antibiotic sensitivity testing of gram-positive isolates (zone of inhibition measured in millimeter)

Organisms		**APX**	**CPX**	**GEN**	**OFL**	**AMX**	**STR**	**SXT**	**PFX**	**ERY**	**CHL**
Staphylococcus aureus	Mm1	12(R)	22(S)	13(I)	18(S)	0(R)	15(S)	15(I)	19(S)	0(R)	0(R)
	Bom4	0(R)	19(S)	10(R)	16(S)	0(R)	0(R)	18(S)	19(S)	0(R)	22(S)
	Zm4	11(R)	19(S)	13(I)	24(S)	13(R)	14(I)	15(I)	21(S)	24(S)	0(R)
	Bcf4	0(R)	18(S)	20(S)	15(I)	0(R)	13(I)	0(R)	20(S)	0(R)	0(R)
	Fam22	0(R)	20(S)	15(S)	11(R)	13(R)	16(S)	18(S)	19(S)	0(R)	0(R)
	Sbm42	17(R)	25(S)	14(I)	18(S)	16(I)	8(R)	18(S)	23(S)	18(I)	0(R)
Staphylococcus sp.	Bcm1	0(R)	10(R)	13(I)	11(R)	0(R)	13(I)	10(R)	19(S)	0(R)	0(R)
	Zf1	0(R)	17(S)	12(R)	18(S)	0(R)	0(R)	18(S)	18(S)	0(R)	0(R)
	Faf32	13(R)	24(S)	21(S)	10(R)	21(S)	21(S)	16(S)	23(S)	14(I)	0(R)
	Whm42	0(R)	10(R)	0(R)	10(R)	0(R)	0(R)	22(S)	16(S)	0(R)	0(R)
Bacillus sp.	Whm1	0(R)	20(S)	15(S)	21(S)	20(S)	17(S)	19(S)	20(S)	21(S)	21(S)
	Sbm2	0(R)	16(S)	10(R)	16(S)	18(S)	11(R)	19(S)	16(S)	16(R)	10(R)
	FAgf13	12(R)	19(S)	20(S)	21(S)	17(S)	17(S)	16(S)	19(S)	21(S)	0(R)
Micrococcus sp.	FAgm1	18(S)	21(S)	20(S)	19(S)	12(R)	13(I)	19(S)	17(S)	16(R)	0(R)
	Fam13	16(S)	14(I)	15(S)	14(I)	17(S)	17(S)	16(S)	19(S)	17(I)	0(R)
Streptococcus sp.	Whf41	13(R)	21(S)	18(S)	14(I)	0(R)	19(S)	22(S)	22(S)	16(I)	0(R)

Key: R = Resistant, S = Susceptible, I = Intermediate
APX: Ampiclox (30µg), CPX: Ciprofloxacin (10µg), GEN: Gentamycin (10µg)
OFL: Ofloxacin (5µg), AMX: Amoxicilin (25µg), STR: Streptomycin (10µg)
SXT: Septrin (30µg), PFX: Pefloxacin (10µg), ERY: Erythromycin (5µg)
CHL: Chloramphenicol (30µg)

Table 3b: Antibiotic sensitivity testing of gram-negative isolates (zone of inhibition measured in millimeter)

Organisms		AUG	CRO	NIT	GEN	COT	OFL	AMX	CPX	TET	PFX
Proteus vulgaris	Zm8	0(R)	0(R)	0(R)	10(R)	10(R)	10(R)	10(R)	10(R)	10(R)	19(S)
Proteus mirabilis	Bcm3	0(R)	0(R)	0(R)	11(R)	11(I)	26(S)	10(R)	27(S)	10(R)	18(S)
Klebsiella sp.	Bom3	0(R)	0(R)	0(R)	21(S)	11(1)	25(S)	10(R)	11(R)	10(R)	18(S)
	Mf3	0(R)	0(R)	0(R)	10(R)	10(R)	20(S)	10(R)	20(S)	10(R)	18(S)
	Zf3	0(R)	0(R)	0(R)	16(S)	16(S)	26(S)	14(I)	28(S)	14(R)	23(S)
	Bof2	0(R)	0(R)	0(R)	11(R)	10(R)	20(S)	10(R)	11(R)	10(R)	19(S)
	Faf12	0(R)	0(R)	0(R)	10(R)	17(S)	18(S)	15(R)	10(R)	10(R)	18(S)
Serratia sp.	Zm11	12(R)	10(R)	0(R)	10(R)	0(R)	20(S)	0(R)	22(S)	11(R)	18(S)
	Bcf5	0(R)	0(R)	14(R)	20(S)	11(I)	22(S)	10(R)	17(I)	10(R)	15(I)
Salmonella sp.	Bom1	12(R)	10(R)	17(S)	22(S)	0(R)	20(S)	10(R)	22(S)	11(R)	18(S)
	Zf8	0(R)	0(R)	13(R)	16(S)	11(I)	18(R)	15(R)	10(R)	13(R)	22(S)
Enterobacter sp.	Fam32	0(R)	0(R)	0(R)	20(S)	16(S)	28(S)	11(R)	11(R)	10(R)	19(S)
Citrobacter sp.	Zf5	0(R)	0(R)	0(R)	10(R)	10(R)	18(S)	10(R)	23(S)	10(R)	16(S)
	Faf41	0(R)	0(R)	0(R)	16(S)	16(S)	25(S)	14(I)	25(S)	14(R)	22(S)

Key: R = Resistant S = Susceptible I = Intermediate
AUG: Augmentin (30µg) CRO: Ceftriazone (30µg) NIT: Nitrofurantoin (200µg)
GEN: Gentamycin (10µg) COT: Cotrimoxazole (25µg) OFL: Ofloxacin (5µg)
AMX: Amoxicillin (25µg) CPX: Ciprofloxacin (10µg) TET: Tetracycline (30µg)
PFX: Pefloxacin (5µg)

Table 3c: Percentage of antibiotic susceptibility pattern of gram-positive bacteria isolates

Antibiotics (%)	APX	CPX	GEN	OFL	AMX	STR	SXT	PFX	ERY	CHL
Resistant	81.25	12.5	25.0	25.0	31.25	31.25	12.5	0.00	56.25	87.5
Intermediate	0.00	6.25	25.0	18.75	6.25	25.0	12.5	0.00	25.0	0.00
Sensitivity	18.75	81.25	50.0	56.25	62.5	43.75	75.0	100	18.75	12.5

Key: APX: Ampiclox (30µg) CPX: Ciprofloxacin (10µg) GEN: Gentamycin (10µg)
OFL: Ofloxacin (5µg) AMX: Amoxicilin (25µg) STR: Streptomycin (10µg)
SXT: Septrin (30µg) PFX: Pefloxacin (10µg) ERY: Erythromycin (5µg)
CHL: Chloramphenicol (30µg)

Table 3d: Percentage of antibiotic susceptibility pattern of gram-negative bacteria isolates

Antibiotics (%)	AUG	CRO	NIT	GEN	COT	OFL	AMX	CPX	TET	PFX
Resistant	100	100	92.86	50.0	42.86	14.29	85.71	42.86	100	0.00
Intermediate	0.00	0.00	0.00	0.0	28.57	0.00	14.29	7.14	0.00	7.14
Sensitivity	0.00	0.00	7.14	50.0	28.57	85.71	0.0	78.57	0.00	78.57

Key: AUG: Augmentin (30µg) CRO: Ceftriazone (30µg) NIT: Nitrofurantoin (200µg)
GEN: Gentamycin (10µg) COT: Cotrimoxazole (25µg) OFL: Ofloxacin (5µg)
AMX: Amoxicillin (25µg) CPX: Ciprofloxacin (10µg) TET: Tetracycline (30µg)
PFX: Pefloxacin (5µg)

4. CONCLUSIONS

The analysis of isolated bacteria from toilet door handles indicated high level of bacterial contamination, which could be a source of pathogenic disease transmission to humans via contaminated and inadequately cleansed hands. The presence of bacteria associated with human skin flora suggested introduction of microbes as a result of poor hygiene practices among toilet users. All the gram-negative bacteria isolated were resistant to Augmentin, Ceftriazone and Tetracycline which should be a source of concern. All of the gram-negative bacteria recovered were Augmentin, Ceftriazone, and Tetracycline resistant, which is cause for concern. Therefore, this calls for an immediate intervention by the University administration in

implementing efficient and systematic approaches to improving hygienic and sanitation initiatives. Hence, in order to prevent the spread of disease, modern hand washing facilities should be installed and used prior to entry and exit to ensure hygienic hand disinfection.

Acknowledgment

Appreciation goes to Dr Kehinde O. Awojobi of the department of Microbiology, Obafemi Awolowo University, Ile-Ife for making his laboratory available for this study and to all technical staff of Microbiology laboratory for their support.

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