Journal of Medical Bacteriology

Microbial Contamination and Public Health Risk Associated with the Use of Biometric Fingerprinting Clocking Device in Ekiti State, Nigeria

Akinseye Janet Funmilayo, Ajayi Deborah Damilola, Oluboyo Bernard Oluwapelumi, Akele Richard Yomi, Ayuba Sunday Buru[*]

Department of Medical Laboratory Science, College of Medicine and Health Sciences, Afe Babalola University, Ado-Ekiti, Nigeria.

ARTICLE INFO

Article type:
Research Article

Article history:
Received: 27 Nov 2021
Revised: 04 Dec 2021
Accepted: 10 Dec 2021
Published: 25 Dec 2021

Keywords: *Biometric Fingerprinting Clocking Devices, Microbial Contaminants, Public Health, Risk.*

ABSTRACT

Background: The biometric fingerprinting clocking devices are now commonly being used in Nigeria to record human biodata. This system involves physical contact between the skin and surface of the device, which is likely to be contaminated by microorganisms of multiple users. This study aimed to investigate the role of biometric fingerprinting clocking devices as a potential source for microbial contaminants spreading.

Methods: This study was conducted from February to May 2018 and involved samples collected from the surfaces of the biometric fingerprinting device using sterile swabs. Samples were inoculated on MacConkey, Blood, Nutrient, and Sabouraud dextrose agar media and incubated aerobically at 37^{o}C for 24 hours. Colonies from the agar media were characterized biochemically to identify microbial species and their antibiotic susceptibility test was determined by the Kirby Bauer disc diffusion method.

Results: Totally, 221 samples (92%) containing microbial organisms grew. Bacteria isolated included: *Staphylococcus aureus* (29.6%), *Escherichia coli* (19.4%), *Bacillus* species (17.43%), *Klebsiella* species (10.2%), *Streptococcus* species (8.55%), *Pseudomonas* spp (7.24%), *Proteus* spp (2%) and *Enterococcus* spp (0.66%). The majority of the bacteria were resistant to at least two antibiotics used. the fungi isolated were *Trichophyton mentagrophytes* (25%), *Trichophyton rubrum* (20%), *Epidermophyton* species (19%), *Mucor* species (17%), *Aspergillus* species (11%), and *Microsporum* species (5%) to decrease occurrence.

Conclusion: Hand disinfection with a proper cleaning regimen is recommended to reduce contamination on the biometric fingerprinting clocking devices.

- ***Please cite this paper as*** Funmilayo AJ, Damilola AD, Oluwapelumi OB, Yomi AR, Buru AS. Microbial Contamination and Public Health Risk Associated with The Use of Biometric Fingerprinting Clocking Device in Ekiti State, Nigeria. *J Med Bacteriol.* 2021; **10** (3, 4): **pp**.39-50.

*Corresponding Authors: Ayuba Sunday Buru, Department of Medical Laboratory Science, College of Medicine and Health Sciences, Afe Babalola University, Ado-Ekiti, Nigeria.
Email: asburu2002@yahoo.com.

Introduction

The major source of community-acquired infections are fomites (1,2). Biometrics technology has recently begun to enter into public consciousness. It is gradually commonly used technology in both the public and private sectors in Nigeria (including the educational sector) for national record-keeping, access Control, security, time, and attendance management. The biometric fingerprinting device recognition is with the physical contact between the skin and the device surface (3). Through the direct physical application of the finger on the glass plate, the biometric fingerprinting devices can serve as an environmental vehicle for transmission of pathogens as well as commensals from one user to subsequent users. The biometric device has a large number of users who introduce their microbial flora and other organisms they may have been contaminated with, there is the chance of transmission of these microorganisms from one person to another by depositing them on the biometric fingerprinting device while clocking in and out (4). Microorganisms may be present on visibly clean hands and can remain viable in the hands for up to 30 minutes or more depending on the temperature, humidity and the presence of the organic matter (5, 6). The hand is a common vehicle responsible for cross-contamination. because of contact with different surfaces, hands are likely to be contaminated with disease-causing microorganisms. Human hands usually harbor (7) pathogens that may be present on the hands as transient type include: *Escherichia coli*, *Salmonella* species, *Shigella* spp, *Clostridium perfringens*, *Giardia lamblia*, *Norwalk* virus, and *Hepatitis A* virus; (8) studies showed that *Staphylococcus epidermis* is found on almost every healthy hand. Other microorganisms are members of *Corynebacterium*, *Micrococcus* species, and some members of the *Enterobacteriaceae* family (9) all organisms that have contaminated the hands by contact on the surfaces, can be transferred to other users of the same device if proper hygiene and washing of hands are not followed. In this study, the fingerprint devices in a tertiary educational institution were studied to assess the risk of transmission of pathogenic bacteria by isolating the bacterial and fungal flora which may be present on the surface of the biometric fingerprinting device.

Materials and Methods

Study Design

All biometric fingerprinting clocking devices used for the research work were tagged alphabetically (A, B, C, D, E, F, G, H, I, J) for simple identification. The samples were taken in the morning (9-11 am) after the employees have clocked in the evening (4-6 pm) after the employees have clocked out.

Ethical approval

Ethical approval was sought for and received from the Ethical Committee, College of Medicine and Health Sciences, Afe Babalola University, Ado-Ekiti, Ekiti State. Informed consent of the students was obtained.

Study area

The study was carried out in Afe Babalola University, Ado-Ekiti (ABUAD), Ekiti State. The experimental work was done in the Medical Microbiology laboratory of the Department of Medical laboratory science, Afe Babalola University, Ado-Ekiti, (ABUAD), Ekiti State.

Study duration

The study was conducted during the period of February-May, 2018.

Sample size

A total of 240 swabs were collected in batches from eight clocking machines and included in this study about the estimated prevalence (10).

Collection of samples

The samples were collected from the biometric fingerprinting device using sterile cotton swabs moistened with sterile distilled water before swabbing. The samples were collected in the morning (9-11 am) after the employees have clocked in and the evening (4-6 pm) after the employees have clocked out to maximize the chances of isolation. The moistened swabs were wiped firmly over the entire fingerprinting surface of the biometric fingerprinting device. The tubes were re-capped, labeled, and transported to the Medical Microbiology laboratory of the Department of Medical laboratory science, ABUAD immediately for further processing and analysis. All the samples were collected using the same procedure.

Method for Sample Analysis

Laboratory analysis was conducted within one hour after sample collection. Each swab sample was cut aseptically into 2ml of nutrient broth enriched with blood to allow the present organisms to multiply. These nutrient broths were incubated at 37◦C for 24 hours (11). For cultural techniques, Nutrient agar, MacConkey agar, and Blood agar were used (11, 12). All plates were incubated at 37^{o}C for 24 hours. Characterization and identification of bacterial isolate were carried using the routine procedural systems and standard biochemical tests to identify the organism (13, 14).

Results

A total of 240 samples were collected from the biometric fingerprinting devices. The 221 bacterial contaminants were isolated amounting to 92% of samples collected being contaminated. The results obtained from the biometric fingerprinting devices showed nine different bacteria isolates: *Staphylococcus aureus*, *Streptococcus* spp, *Enterococcus* spp, *Bacillus* spp, *Escherichia coli*, *Klebsiella* spp, *Proteus* spp, and *Pseudomonas* spp. with different frequencies at different periods. Among the identified isolates, both the Gram-positive and Gram-negative organisms were found. The Gram-positive identified organisms were *Staphylococcus* spp, *Streptococcus* spp, *Enterococcus, and Bacillus* spp. while Gram-negative organisms isolated include *Escherichia coli, Klebsiella* spp, *Proteus* spp, and *Pseudomonas* spp. as presented in table 1. From 304 bacterial isolates, One hundred and eighty-six (61.18%) of the isolates were Gram-positive bacteria while 115(37.82%) were Gram-negative. Figure 1 showed the percentage diversity of the obtained isolates. A total of 8 organisms were identified. The confirmed isolates include *Staphylococcus aureus*, *Bacillus* species, *E. coli*, *Enterococcus* species, *Pseudomonas* species, *Proteus* species, *Streptococcus* species, *Klebsiella* species. *Staphylococcus aureus* was the most common organism isolated (30%) followed by *E. coli* (19%) *and Bacillus* spp (17%). *Proteus* spp (2%) and *Enterococcus* species (1%) showed the least percentage occurrence, respectively. Figure 2 showed the distribution of the isolates in the morning and the evening. It was observed that most organisms were isolated more in the morning

than the evening. However, *Bacillus* spp, Coagulase-negative *Staphylococcus* and *Klebsiella* spp were isolated more in the evening. Figure 3 showed the distribution of isolates in all weeks. All the isolated organisms were found in Week 2. *Staphylococcus aureus, Bacillus* species, and *Klebsiella* spp were most isolated in week 1. *Enterococcus* species was only isolated in weeks 2 and 3 at an equal frequency. *Streptococcus* species was most isolated in week 3. *Pseudomonas* species were isolated in week 4. Coagulase-negative *staphylococcus* was isolated in weeks 2 and 4 equally and *Escherichia coli* and *Proteus* species were most isolated in week 5.

Table 1. The distribution of the isolates according to Gram's Reaction (n=304)**.**

Gram's Reaction	Number of isolates found	Percentage (%)
Gram-positive	186	61.18
Gram-negative	115	37.82

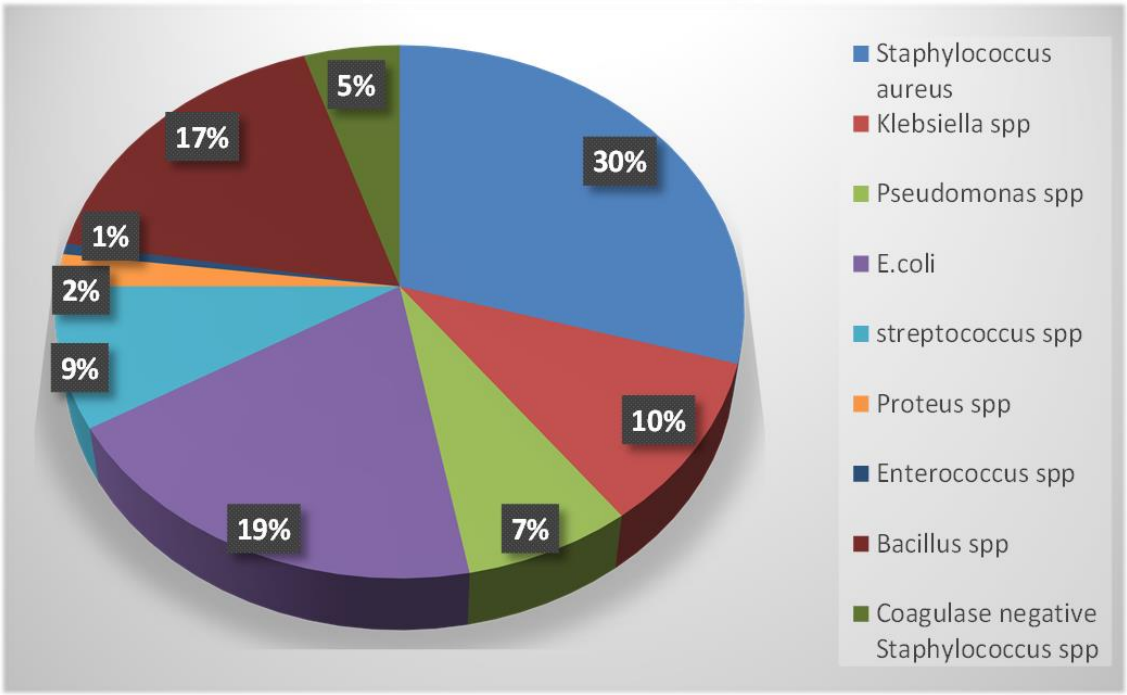

Figure 1. Bacterial isolates were obtained from the samples and their percentage of prevalence**.**

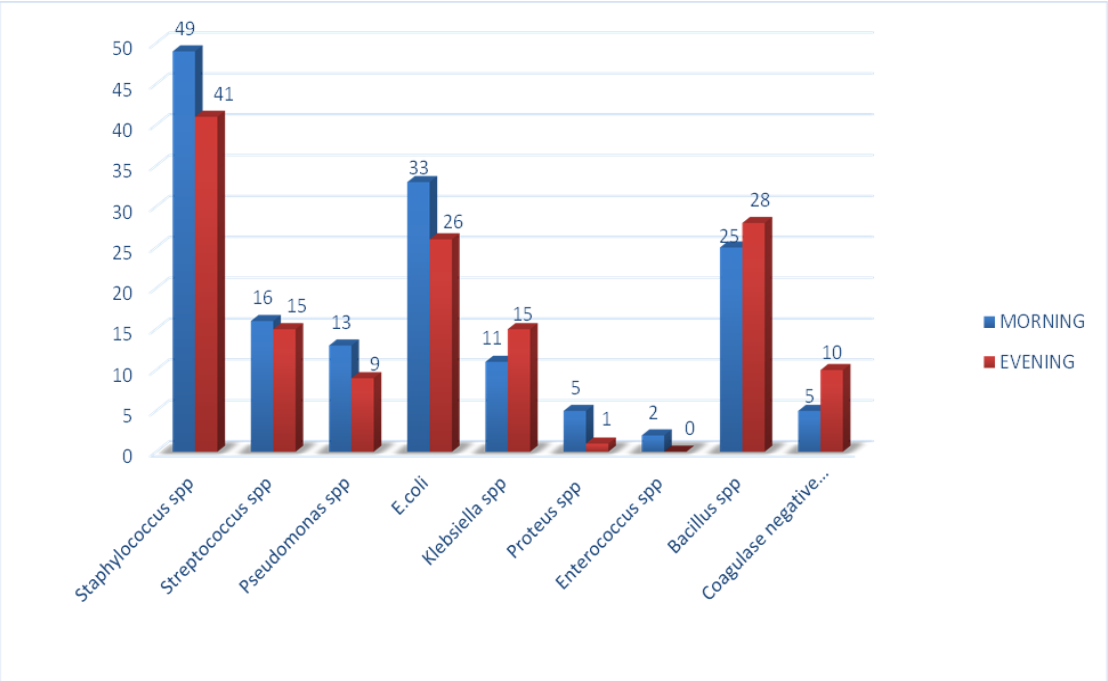

Figure 2. Distribution of the isolates in the morning and in the evening**.**

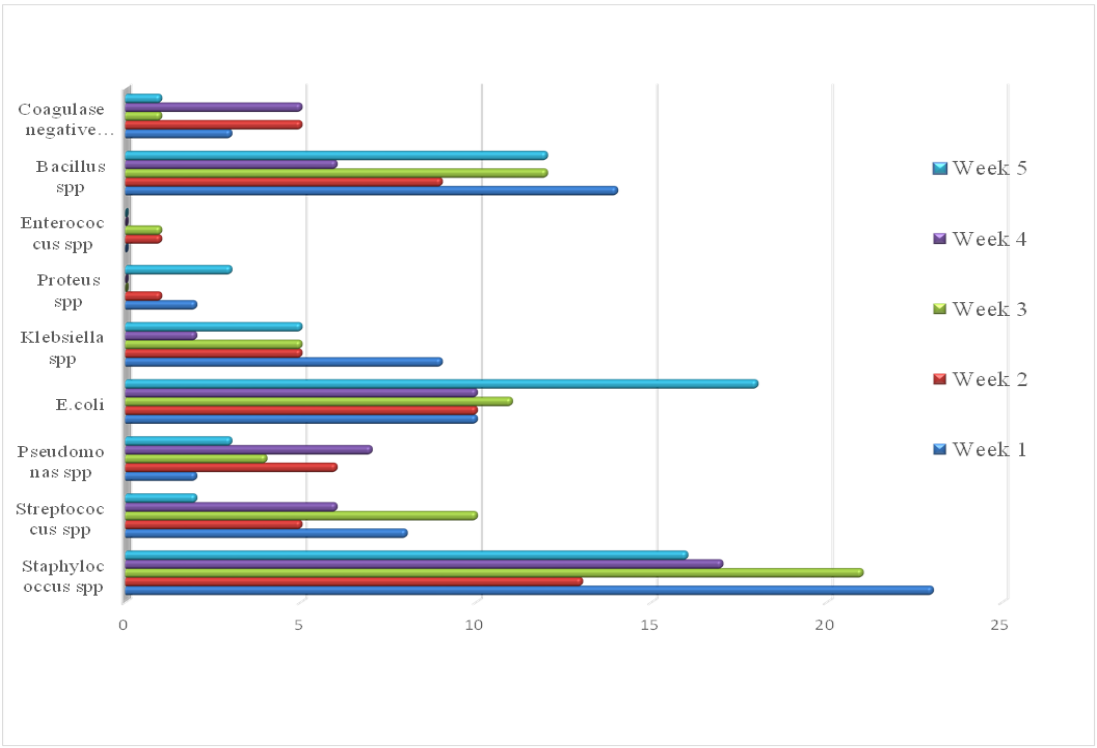

Figure 3. Distribution of isolates in all weeks**.**

Table 2. Antibiogram of the Gram-positive bacterial isolates to commonly used antibiotics**.**

Antibiotics	*S. aureus*		CNS			*Streptococcus* spp			*Enterococcus* spp			*Bacillus* spp		
	S	I	R	S	I	R	S	I	R	S	I	R	S	I
AUG(30µg)	6	17	67	1	0	4	4	0	22	0	0	2	50	0
OFL(5µg)	63	8	19	1	4	0	24	2	0	1	1	0	0	7
CXC (5µg)	86	0	4	13	0	2	22	4	0	2	0	0	47	0
ERY(5µg)	19	0	71	0	0	5	4	1	21	0	0	2	10	5
CTR(30µg)	50	0	40	12	0	3	16	0	10	2	0	0	41	7
GEN(10µg)	83	2	5	4	1	0	8	18	0	0	2	0	50	0
CRX(30µg)	50	10	30	10	2	3	20	0	6	1	1	0	48	5
CAZ(30µg	47	9	34	9	0	6	4	0	22	0	0	2	53	0

Key: AUG = Augmentin, OFL=Ofloxacin, CXC=Cloxacillin, ERY= Erythromycin, CTR= Ceftriaxone, GEN= Gentamycin, CRX=Cefuroxime ,CAZ=Ceftazime, S= susceptible, I= Intermediate susceptible, R= Resistant, CNS= C*oagulase negative Staphylococcus aureus*

Table 3. Antibiogram of the Gram-negative bacterial isolates to commonly used antibiotics**.**

Antibiotics	*Pseudomonas* spp			*Escherichia coli*			*Proteus* spp			*Klebsiella* spp		
	S	I	R	S	I	R	S	I	R	S	I	R
AUG(30µg)	0	2	20	9	43	7	6	0	0	28	0	3
OFL(5µg)	9	0	13	2	8	49	0	1	5	27	4	0
CTR(30µg)	12	0	10	44	0	15	4	0	2	18	0	13
GEN(10µg)	0	0	22	57	2	0	6	0	0	25	4	3
CRX(30µg)	10	0	12	47	5	7	6	0	0	27	4	0
CAZ(30µg	2	5	15	3	6	50	5	1	0	0	5	26
NIT(300µg)	19	0	3	42	8	9	5	0	1	22	7	2
CXM(5µg)	12	0	10	26	0	25	6	0	0	22	5	4
CPR(5µg)	15	0	7	40	6	13	4	0	4	30	1	0

Key: AUG = Augmentin, OFL= Ofloxacin, CTR= Ceftriaxone, GEN= Gentamicin , CRX= Cefuroxime , CAZ= Ceftazidime , NIT= Nitrofurantoin, CXM=Cefixime , CPR= Ciprofloxacin. S= susceptible ,I= Intermediate susceptible , R= Resistant.

Table 4. Percentage resistance of the isolates to common antibiotics**.**

Antibiotics	*S. aureus*	CNS	*Streptococcus*	*Enterococcus*	*Bacillus* spp	*Escherichia coli*	*Proteus* spp	*Klebsiella* spp	*Pseudomonas* spp
AUG(30µg)	74.50%	26.70%	84.60%	100%	5.70%	11.90%	0%	9.70%	90.90%
OFL(5µg)	21.10%	0%	0%	0%	86.80%	83.10%	83.30%	0	13%
CXC (5µg)	4.50%	13.30%	0%	0%	11.30%	-	-	-	-
ERY(5µg)	78.90%	33.30%	80.80%	100%	71.70%	-	-	-	-
CTR(30µg)	44.5%	20%	38.50%	0%	9.40%	25.40%	33.30%	41.90%	45.50%
GEN(10µg)	5.60%	0%	0%	0%	5.70%	0%	0%	9.70%	100%
CRX(30µg)	33.30%	20%	23.10%	0%	0%	11.90%	0%	0%	54.50%
CAZ(30µg	37.80%	40%	84.60%	100%	5%	84.70%	0%	83.90%	68.20%
NIT(300µg)	-	-	-	3%	-	15.30%	16.70%	6.50%	13.60%
CXM(5µg)	-	-	-	10%	-	42.40%	0%	12.90%	45.50%
CPR(5µg)	-	-	-	7%	-	22.00%	66.70%	0%	31.80%

Key: AUG = Augmentin, OFL=Ofloxacin, CXC=Cloxacillin, ERY= Erythromycin, CTR= Ceftriaxone, GEN= Gentamicin, CRX= Cefuroxime, CAZ=Ceftazidime, NIT= Nitrofurantoin, CXM=Cefixime, CPR= Ciprofloxacin, S= susceptible, I= Intermediate susceptible, R= Resistant, CNS= Coagulase negative *Staphylococcus aureus*.

Table 5. Frequency and percentage frequency of the fungi isolated from the devices**.**

Fungi isolated	Frequency	Percentage
Aspergillus spp	7	10.94%
Trichophyton rubrum	13	20.31%
Trichophyton mentagrophtes	16	25%
Epidermophyton species	12	18.75%
Microsporum species	5	7.81%
Mucor species	11	17.19%

Discussion

Contact with environmental surfaces can expose users to pathogens. Biometric fingerprinting clocking devices are important reservoirs of microorganisms. There is a public health risk implication in transmitting microorganisms to other surfaces and individuals since every user must have to make direct contact with the same surface. This study aimed at isolating, identifying and determining the antibiotic resistance pattern of the bacteria isolated from the biometric fingerprinting devices which revealed a high level of bacterial contaminants. Out of 240 samples processed, 221 samples (92%) showed bacterial contamination. Records are scanty on microbial contamination of biometric fingerprinting. However, (16) observed 86.7% positive bacterial cultures from toilet doorknobs of public conveniences and (17) observed 84.7% bacterial contamination in public toilets. A lesser prevalence was reported by (18) who found 65.7% bacterial growth from some fomites in a teaching hospital in Nigeria and (19) who found only 50% bacterial growth from toilet doorknobs in secondary schools in Nigeria. This variation in the number of positive samples from one place to the other maybe because of differences in the number of users. The isolated bacteria were both Gram-positive bacteria and Gram-negative bacteria. However, Gram-positive bacteria were found to occur more than Gram-negative bacteria. This revealed a similar result to the study of Nirupa (2016) where gram-positive bacteria were more prevalent (20). In this study, the most prevalent bacterial contaminant found was *Staphylococcus* species (30%), this high prevalence maybe because it is a major component of the normal flora of the skin and nostrils and can be easily discharged by several human activities. The biometric fingerprinting clocking device requires contact with the fingers on which *Staphylococcus* is a normal flora. This observation is consistent with the findings of other studies (16). *Bacillus* species (17%) recorded a high prevalence in this study. This high prevalence could be because *Bacillus* species are ubiquitous, they also produce spores that are resistant to environmental changes, withstand dry heat and certain chemical disinfectants for prolonged periods. This is also in agreement with the research carried out by (21) and (22) who reported that *Bacillus* spp were the predominant organisms that were isolated from door handles. *Escherichia coli* (19%) was the most prevalent Gram-negative bacilli isolated in this study. This indicates the possibility of the presence of fecal contamination on the biometric

fingerprinting devices. This might be because most people go to the toilet and end up contaminating their hands with fecal and urinal material and fail to wash their hands properly. The fecal matter remains a major source of human pathogens, which in the adverse situation may bring about outbreaks of infection. The prevalence in this work is lower than the report of (23) who recorded 36.7% *Escherichia coli* isolates from students' toilets in Tanzania. However, such a prevalence is higher than the work (17) that reported only 13.9% of the *E. coli* isolates. Prevalence of more Gram-positive organisms compared to Gram-negative organisms correspond with previous studies [23]. It is probably because Gram-positive organisms are the members of the body flora of both asymptomatic carriers and sick persons. These organisms can be transmitted by the hand, expelled from the respiratory tract, or spread by animate or inanimate objects (23). Organisms isolated in this study (*Staphylococcus aureus*, Coagulase Negative *Staphylococcus (CNS), Bacillus* species, *Klebsiella* species, *Pseudomonas* species, *Proteus* species, *Streptococcus* species, *Escherichia coli, and Enterococcus* species) are capable of causing diseases through hand-to-mouth transmission if the hands are not sanitized after each use. Possible diseases that can be caused by the isolated bacteria include foodborne diseases (*Staphylococcus aureus, Escherichia coli, Bacillus* species), Urinary tract infections (*Escherichia coli*), Skin infections (*Staphylococcus* species), and Diarrhoea (*Escherichia coli*) (25) Given the level of contamination of the biometric fingerprinting device, it can be inferred that the device can serve as a potential means of spreading organisms capable of causing epidemics if such organisms happen to be transferred to the biometric fingerprinting device. Determination of antibiotic susceptibility pattern revealed that all bacterial isolates tested were resistant to at least two antibiotics. If there is infection with these organisms, treatment might be a challenge because of the resistant nature of the organisms. This research will not be complete without awareness and cautionary notes. As it seems, we are being served the card of re-emergent epidemics- cholera (26), meningitis, Severe Acute Respiratory Syndrome (SARS) (27, 28) monkeypox virus (29), and Lassa fever (30). It would just be logical that caution is taken when accessing or coming in contact with public utilities like Automated Teller Machines (ATM), biometric fingerprinting clocking devices, swimming pools, doorknobs and handles as well as balcony railings. Minimal contact or total avoidance where necessary is a great step. Total personal hygiene and public awareness help further in nipping any impending epidemic or infection in the bud.

Conclusion

In conclusion, this study confirmed that the biometric fingerprinting clocking devices were variously contaminated with known bacterial and fungal pathogens that demonstrated a varying degree of antibiotic resistance.

Conflict of interest

Not declared

Funding information

This study received no form of funding from any organization. It was funded by the authors.

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