



ANTIBIOGRAM AND CONVENTIONAL HAEMOLYTIC VIRULENCE POTENTIAL OF BACTERIA ISOLATED FROM AUTOMATED TELLER MACHINES IN OTA, OGUN STATE, NIGERIA

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Abstract

Bacteria are widespread in the environment and can survive on, or even thrive on, surfaces, including Automated Teller Machine (ATM) terminals. This study aimed to determine the occurrence of bacteria isolated from automated teller machines of commercial banks in Ota, Ogun State, Nigeria, with special reference to their antibiograms and conventional haemolytic virulence potential. A total of thirteen (13) swab samples were collected from different Automated Teller Machines (ATMs) in four commercial banks in Ota, Ado-Odo Ota Local Government, Ogun State, Nigeria. All swab samples were processed in duplicate. Gram staining, biochemical tests, haemolysis tests, and antibiotic susceptibility testing (AST) were performed on the bacterial isolates. Of the 26 cultured samples, three (3) different bacteria were isolated. *Escherichia coli* and *Staphylococcus aureus* were the most prevalent, each occurring in 38.5%, while *Pseudomonas spp.* was the least prevalent (23%). Of the bacteria tested, all (100%) were resistant to ceftazidime (CAZ) and ceftriaxone (CTR); 84.6% and 65.5% of isolates were resistant to ampicillin-clavulanic acid and ofloxacin, respectively. Furthermore, 84.6% (22/26) of all isolates were resistant to ≥ 3 classes. Alpha haemolysis was observed in 11.5% (3/26), beta haemolysis in 34.6% (9/26), and gamma haemolysis in 53.9% (14/26). Complete (beta - β) haemolysis was most prevalent in *Staphylococcus aureus* (77.8%). However, there was no significant association between haemolysis pattern and antibiotic resistance status (P -value=.1445). The current findings demonstrate that ATM keypads may be contaminated with *Escherichia coli*, *Pseudomonas spp.*, and beta (β) haemolytic *Staphylococcus aureus*. Additionally, these keypads may serve as platforms for cross-contamination with antibiotic-resistant strains. As a result, proper cleaning methods should be developed for all automated teller machines. Further work should incorporate molecular detection of haemolysis-associated genes to confirm the haemolytic potential of the bacterial isolates.

Keywords: Bacteria, ATMs, Haemolysis, Keypads, Virulence

Introduction

Bacteria are found throughout the environment and can live on or even thrive on surfaces, including Automated Teller Machine (ATM) terminals. Despite the fact that most bacteria are harmless, some of them can nevertheless be pathogenic, especially for people with weakened immune systems (Duhaniuc *et al.*, 2024).

The Automated Teller Machines (ATMs), as they are known, are a technological advancement from the 20th century that allow customers of financial institutions to conduct financial transactions without the assistance of a bank teller or cashier

(Nachimuthur *et al.*, 2015). Since its development and widespread use in the late 1960s, ATMs have become the most frequently used type of computer-driven public technology, with millions of devices in use (Cardaooli *et al.*, 2021).

The conventional way to use an ATM is to insert a card into the card slot and then, after reading the instructions on the screen, use the numeric keypad to enter the codes and ask the machine for the kind of service that is needed. Over time, ATMs have developed into a necessary component of social survival (Mehmet *et al.*, 2013). Daily, they are utilised for a variety of financial activities, including cash transactions,

stock market transactions, and even bill payments. As a result, hundreds of individuals utilise them every day, especially since many governments are implementing cashless policies in different nations (Nigmatulin and Chaganova, 2022).

ATM keypads and touch displays are frequently used by people with varying levels of hygiene and health, making them possible habitats for bacteria that could spread various diseases (Arulazhagan, 2015). One of the bacteria that can be most frequently detected on ATMs is *Escherichia coli* (Adonu *et al.*, 2025). It is the most prevalent pathogen causing urinary tract infections (UTIs) and is also a major cause of bloodstream infections, wound infections, otitis media, etc. (Khan, 2002). Other bacteria that can be found on the surfaces of ATMs include *Klebsiella* spp., *Pseudomonas aeruginosa*, *Enterobacter* spp., *Serratia marcescens*, *Escherichia coli*, *Streptococcus* spp and *Staphylococcus aureus* (Adonu *et al.*, 2025)

Many ATM users are not aware that touch screens and keypads could contain bacteria that can spread many contagious diseases (Arulazhagan, 2015). As a result, people are careless or completely unaware of the need to practice good hygiene after using this equipment. The spread of these pathogenic bacteria is aided by this unhygienic behaviour, generating strains of bacteria causing diseases, multidrug-resistant (MDR) and extended-spectrum beta-lactamase (ESBL) bacteria (Sulaiman and Adam, 2025).

Currently, there are no rules governing the sanitary use of an ATM at a bank or restrictions on who is permitted to use the facility. Like other surfaces, most of these ATMs are exposed to microbial colonisation. The frequent use of the ATMs by hundreds of people with very varying socioeconomic status and sanitary standards increases the microbial load and the spread of disease. As a regularly used surface that frequently comes into contact with human users, the ATM keypad can be compared to benches, turnstiles and railings in urban transit systems (Nachimuthur *et al.*, 2015).

Additionally, the keypads of ATMs, where harmful bacteria could live, offer an often-overlooked reservoir for gastrointestinal disorders. On dry surfaces like the keypads of ATMs, a significant number of microorganisms can survive (Porter *et al.*, 2024). These devices are now used as a means of spreading contagious diseases; if the keyboard is contaminated, the user may end up getting the microorganisms after using the ATM (Arulazhagan, 2015). As a result, it has been suggested that human hands are vital in the spread and cross-contamination of organisms among environmental surfaces (Cantrell *et al.*, 2023).

This research is driven by the need to raise awareness of ATMs as a potential source of community-acquired diseases. This is necessary to prevent the spread of bacteria isolated from these surfaces and to mitigate the associated risk. The findings from this study will be used to develop evidence-based hygiene procedures for the use of ATMs. Currently, few studies have identified bacteria and assessed the conventional haemolytic virulence potential of bacteria

isolated from automated teller machine surfaces in Ota, Ogun State, Nigeria.

Materials and methods

Study Area

This study was carried out in Ado-Odo Ota, Local Government Area, Ogun State, Nigeria. Ado-Odo/Ota borders on metropolitan Lagos. The Local Government Area is the second largest in Ogun State.

Sample collection and processing

A total of thirteen (13) different Swab samples were collected from different Automated Teller Machines (ATMs) in four commercial banks (Anonymised Bank S, Z, W and A) in Ota, Ado-Odo Ota Local Government, Ogun State. ATMs at these banks were the most visited during the study period. Using sterile swab sticks, all the swab samples collected from the banks were processed in duplicate. Distinct sterile swab sticks moistened with sterile distilled water were rubbed on the ATM keypads and/or touch screen of the ATM, labelled appropriately and then transported within one hour to the Microbiology Laboratory in an ice pack without delay to prevent drying of samples for microbiological analysis.

Bank sample coding

For easy identification and differentiation of bank samples obtained from different ATM outlets, codes were adopted for the samples as shown in Table 1. Individual isolate identifiers follow a two-letter convention (e.g. AS) in which the first letter identifies the specific isolate and the second letter represents the initial of the anonymised source bank.

Sample Analysis

All the samples were processed in the laboratory according to the standard microbiological methods under very strict, complete aseptic conditions. The swabs were inoculated on appropriate media.

Culturing of Bacteria

Swab samples were directly streaked on Nutrient agar, Eosin Methylene Blue, MacConkey and mannitol salt agar plates and incubated at 37 °C for 24 hours. Upon establishment of growth, each culture plate was examined for distinct colonies; mixed growth was further subcultured on nutrient agar plates to obtain pure colonies. The colonies were identified phenotypically by colony characteristics, Gram staining and biochemical tests as per standard protocol (Cheesbrough, 2006).

Gram Staining and Biochemical Tests

Gram staining and biochemical tests were performed on all observed colonies. The biochemical tests include catalase test, coagulase test, motility test, oxidase test, citrate utilisation test, methyl red test, Voges-Proskauer test, and indole test, as described by Dawodu and Akanbi (2021).

Haemolysis test

This Haemolysis test was performed as described by Lai *et al.* (2025). Briefly, Pure colonies of isolates obtained from ATMs were streaked onto blood agar (HiMedia(India)) plates and incubated at 37°C for 24 h. Following incubation, the

observed haemolysis and morphologies of the isolates were recorded. Beta (β) haemolysis is a complete lysis of red cells in the medium around and under the colonies. The area appears lightened (yellow) and transparent. Alpha (α) haemolysis is also known as incomplete haemolysis or green haemolysis because of the colour change in the agar; the area under the colony is light and greenish. Gamma (γ) haemolysis is known as non-haemolytic. If an organism does not induce haemolysis, the agar under and around the colony is unchanged, and the organism is said to display gamma-haemolysis (γ -haemolysis) (Lai *et al.*, 2025).

Antibiotic Susceptibility Testing

Antibiotic susceptibility testing was carried out as described by Sulaimon & Adam (2025) and interpreted according to CLSI (2021) and EUCAST (2025) guidelines. The antibiotic discs were placed aseptically on Mueller-Hinton agar plates and incubated at 37 °C for 24 hours. Antibiotics used for Gram-negative bacteria were Ofloxacin (OFL) 5 µg, Amoxicillin-clavulanic acid (AUG) 30 µg, Nitrofurantoin (NIT) 100 µg, Ciprofloxacin (CIP) 5 µg, Ceftazidime (CAZ) 10 µg, Ceftriaxone (CTR) 30 µg, Gentamicin (GEN) 10 µg and Cefuroxime (CXM) 30 µg. The antibiotics used for Gram-positive bacteria include Ofloxacin (OFL) 5 µg, Amoxicillin-clavulanic acid (AUG) 30 µg, Erythromycin (ERY) 15 µg, Ceftazidime (CAZ) 10 µg, Cefuroxime (CXM) 30 µg, Gentamicin (GEN) 10 µg, Ceftriaxone (CTR) 30 µg and Cloxacillin (CXC) 5 µg.

Statistical Analysis

VassarStats R x C Fisher Exact Test Calculator (<http://vassarstats.net/fisher2x3.html>) was used to determine whether the haemolysis pattern was associated with antibiotic resistance status (MDR or non-MDR).

Table 1: Sample codes used for different anonymised banks

S/N	Sample Code
1	AS
2	BS
3	CS
4	NS
5	DZ
6	EZ
7	FZ
8	GZ
9	HW
10	IW
11	JA
12	KA
13	LA

The first letter of each sample code denotes the specific isolate, and the second letter corresponds to the initial of the anonymised source bank. Each sample was performed in duplicate

Results

Frequency of Occurrence of Bacteria Isolates Associated With Automated Teller Machines

From the 26 cultured samples, three (3) different bacteria were isolated and biochemically identified across all 26 cultured plates (Table 2). *Escherichia coli* and *Staphylococcus aureus* were the most prevalent bacteria isolated, each occurring in 38.5%, while the least prevalent was *Pseudomonas* spp. (23%) (Table 3). Commercial Bank S and Commercial Bank Z had the highest number of occurrences of bacterial contamination (Figure 1).

Antibiogram Pattern of the Bacteria Isolated from the Automated Teller Machines

Both the Gram-positive and Gram-negative bacteria were tested against five different classes of antibiotics. Of the bacteria tested, all (100%) were resistant to ceftazidime (CAZ) and ceftriaxone (CTR); 84.6% and 65.5% of isolates were resistant to ampicillin-clavulanic acid and ofloxacin (AUG), respectively. Additionally, all (100%) of the Gram-positive *S. aureus* isolates tested were resistant to cloxacillin (CXC). 84.6% (22/26) of all the isolates were resistant to ≥ 3 classes of antibiotics, and 15.4% (4/26) showed no multidrug resistance. The classes of MDR were 3-5 classes (Table 4).

Haemolysis Test

Alpha (α), beta (β), and gamma (γ) types of haemolysis were observed; alpha haemolysis was found in 11.5% (3/26), Beta haemolysis in 34.6% (9/26), and gamma haemolysis in 53.9% (14/26). Complete (Beta - β) haemolysis was more predominant in *Staphylococcus aureus* (77.8%). While 22.2% complete (Beta - β) haemolysis was recorded in *Pseudomonas* spp. (Table 4).

Association between Haemolysis Pattern and the antibiotic Resistance Status (MDR or Non-MDR)

Due to the small size, association in 3 x 2 Contingency tables were evaluated using the Fisher-Freeman-Halton Exact test and there was no significant association (P -value=.1445) at $p < 0.05$ (Table 5)

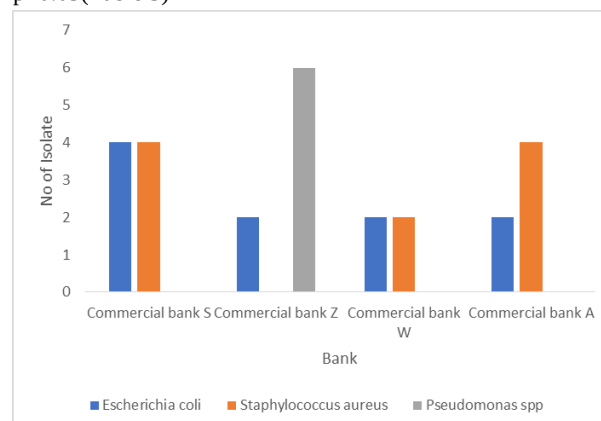


Figure 1: Distribution of the bacterial isolates obtained from ATMs in different banks

Table 2: Gram Staining and Biochemical tests of the Bacteria Isolated from the surfaces of the ATMs of four Commercial Banks

Isolate S/N ID	Gram test	Agar	Catalase	Citrate	Indole	Coagulase	Oxidase	Presumptive Isolates
1 AS(1)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
2 AS(2)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
3 BS(1)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
4 BS(2)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
5 GZ(1)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
6 GZ(2)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
7 HW(1)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
8 HW(2)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
9 KA(1)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
10 KA(2)	-ve rod	EMB	+ve	-ve	+ve	-ve	-ve	<i>E. coli</i>
11 CS(1)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
12 CS(2)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
13 IW(1)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
14 IW(2)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
15 JA(1)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
16 JA(2)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
17 LA(1)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
18 LA(2)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
19 NS(1)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
20 NS(2)	+ve cocci	MSA	+ve	-ve	-ve	+ve	-ve	<i>S. aureus</i>
21 DZ(1)	-ve rod	MAC	+ve	+ve	-ve	-ve	+ve	<i>Pseudomonas spp</i>
22 DZ(2)	-ve rod	MAC	+ve	+ve	-ve	-ve	+ve	<i>Pseudomonas spp</i>
23 EZ(1)	-ve rod	MAC	+ve	+ve	-ve	-ve	+ve	<i>Pseudomonas spp</i>
24 EZ(2)	-ve rod	MAC	+ve	+ve	-ve	-ve	+ve	<i>Pseudomonas spp</i>
25 FZ(1)	-ve rod	MAC	+ve	+ve	-ve	-ve	+ve	<i>Pseudomonas spp</i>
26 FZ(2)	-ve rod	MAC	+ve	+ve	-ve	-ve	+ve	<i>Pseudomonas spp</i>

Table 3: Percentage occurrence of bacterial isolates obtained from ATMs in four different banks

Bacterial Isolate	Commercial bank S	Commercial bank Z	Commercial bank W	Commercial bank A	Frequency	Percentage (%)
<i>Escherichia coli</i>	4	2	2	2	10	38.5
<i>Staphylococcus aureus</i>	4	0	2	4	10	38.5
<i>Pseudomonas spp</i>	0	6	0	0	6	23
Total	8	8	4	6	26	100

Table 4: Haemolysis pattern and multi-drug resistant status of the different bacteria isolated from different bank ATM keypads in Ota, Ogun-State

S/N	Isolate ID	Bacteria	Haemolysis α, β, γ	Resistance profile	MDR status
1	AS(1)	<i>E.coli</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
2	AS(2)	<i>E.coli</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
3	BS(1)	<i>E.coli</i>	γ	CAZ, CTR, CXM	Non- MDR (1 class)
4	BS(2)	<i>E.coli</i>	γ	CAZ, CTR, CXM	Non- MDR (1 class)
5	GZ(1)	<i>E.coli</i>	γ	AUG, NIT, CIP, CAZ, CTR, GEN, CXM	MDR (5 classes)
6	GZ(2)	<i>E.coli</i>	γ	AUG, NIT, CAZ, CTR, GEN, CXM	MDR (4 classes)
7	HW(1)	<i>E.coli</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
8	HW(2)	<i>E.coli</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
9	KA(1)	<i>E.coli</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
10	KA(2)	<i>E.coli</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
11	CS(1)	<i>S.aureus</i>	β	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (5 classes)
12	CS(2)	<i>S.aureus</i>	β	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (5 classes)
13	IW(1)	<i>S.aureus</i>	β	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (5 classes)
14	IW(2)	<i>S.aureus</i>	α	AUG, CAZ, GEN, ERY, CTR, CXC	MDR (4 classes)
15	JA(1)	<i>S.aureus</i>	β	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (5 classes)
16	JA(2)	<i>S.aureus</i>	α	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (3 classes)
17	LA(1)	<i>S.aureus</i>	α	AUG, CAZ, CXM, GEN, ERY, CTR, CXC	MDR (5 classes)
18	LA(2)	<i>S.aureus</i>	β	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (5 classes)
19	NS(1)	<i>S.aureus</i>	β	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (5 classes)
20	NS(2)	<i>S.aureus</i>	β	OFL, AUG, CAZ, CXM, GEN, ERY, CTR, CXC (All)	MDR (5 classes)
21	DZ(1)	<i>Pseudomonas spp</i>	β	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
22	DZ(2)	<i>Pseudomonas spp</i>	β	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
23	EZ(1)	<i>Pseudomonas spp</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
24	EZ(2)	<i>Pseudomonas spp</i>	γ	OFL, AUG, NIT, CIP, CAZ, CTR, GEN, CXM (All)	MDR (5 classes)
25	FZ(1)	<i>Pseudomonas spp</i>	γ	CAZ, CTR, CXM	Non- MDR (1 class)
26	FZ(2)	<i>Pseudomonas spp</i>	γ	CAZ, CTR, CXM	Non- MDR (1 class)

Antibiotics used for Gram- negative bacteria were Ofloxacin (OFL) 5 μ g, Amoxicillin-clavulanic acid (AUG) 30 μ g, Nitrofurantoin (NIT) 100 μ g, Ciprofloxacin (CIP) 5 μ g, Ceftazidime (CAZ) 10 μ g, Ceftriaxone (CTR) 30 μ g, Gentamicin (GEN) 10 μ g and Cefuroxime (CXM) 30 μ g. The

antibiotics used for Gram-positive bacteria include Ofloxacin (OFL) 5 μ g, Amoxicillin-clavulanic acid (AUG) 30 μ g, Erythromycin (ERY) 15 μ g, Ceftazidime (CAZ) 10 μ g, Cefuroxime (CXM) 30 μ g, Gentamicin (GEN) 10 μ g, Ceftriaxone (CTR) 30 μ g and Cloxacillin (CXC) 5 μ g.

Table 5: Association between Haemolysis Pattern and the antibiotic Resistance Status (MDR or Non-MDR)

Antibiotic Resistance status (MDR/non-MDR)	Haemolysis Alpha (α)	Haemolysis Beta (β)	Haemolysis Gamma (γ)	Total (%)	P-value
MDR	3	9	10	22 (84.6)	0.1445
Non-MDR	0	0	4	4 (15.4)	
Total	3	9	14	26 (100)	

Discussion

Microorganisms are everywhere and exhibit a remarkable capacity for environmental adaptation as well as rapid multiplication (Wani *et al.*, 2022). According to a systematic review by Wißmann

et al. (2021), a variety of bacterial, fungal, and viral pathogens might live on inanimate objects for several months

and could spread to "hand-object- sensitive patients" through direct or indirect contact.

From this study, Gram-positive and Gram-negative bacteria were present in significant numbers on Automated Teller Machines (ATMs), with more Gram-negative bacteria. This research identified *Escherichia coli*, *Staphylococcus aureus* and *Pseudomonas* species on ATM surfaces in Ota, Ogun State, Nigeria. These findings align with previous reports (Nworie *et al.*, 2012; Anele *et al.*, 2021; Ofonime *et al.*,

2021). The isolated *Escherichia coli* and *Pseudomonas* species belong to the Enterobacteriaceae family, which normally cause hand-to-mouth infections in humans if hands are not thoroughly cleaned after using ATMs. Additionally, medical professionals who use ATMs in hospital environments and their surroundings without properly sanitizing their hands tend to spread nosocomial infections, exposing ATM users to severe hospital-acquired infections, such as *Escherichia coli* and *Pseudomonas* spp. In a study by Bashir *et al.* (2019), Gram-negative bacteria (GNB) were reported to cause over 80% of nosocomial infections (NIs).

The isolation of *Staphylococcus aureus* at 38.5% is in conformity with the findings of Agu *et al.* (2018), where 32% was reported in Calabar Metropolis. However, a very high prevalence of *Staphylococcus* spp. was reported by Mbajiuka (2015). *Staphylococcus aureus* commonly inhabits the human skin and nasal passages (Laux *et al.*, 2019), which may account for its high prevalence as a contaminant, as it can be readily discharged by a variety of human actions, such as sneezing, talking, and coming into contact with moist skin.

The results of antimicrobial susceptibility testing for all isolates showed that both Gram-positive and Gram-negative isolates were 100% resistant to ceftazidime and cefuroxime. The resistance patterns observed in *E. coli*, *Staphylococcus aureus* and *Pseudomonas* spp. suggest that ceftazidime and ceftriaxone may not be suitable as first-line agents in the empirical treatment of these infections. Similarly, Oli *et al.* (2017) reported significantly higher resistance to several commercial antibiotics among these bacteria. In addition, all 10 isolates phenotypically identified as *Staphylococcus aureus* showed 100% resistance to amoxicillin-clavulanic acid, ceftazidime, ceftriaxone and cloxacillin, and 90% to cefuroxime. Similar results were reported for *S. aureus* isolated from ATMs at a private university in Nigeria, where it was 100% resistant to amoxicillin-clavulanic acid, ceftazidime, ceftriaxone, cloxacillin and cefuroxime (Akinola *et al.*, 2022).

These results demonstrated that 84.6% of the isolated bacteria exhibited multiple drug resistance to antibiotics. This aligns with the previous study by Aquino *et al.* (2021), which also reported multidrug-resistant bacteria from an automated teller machine elsewhere. Highly pathogenic multidrug-resistant microorganisms (MDR) are becoming more prevalent every day and are a major threat to human health (Bharadwaj *et al.*, 2022). The World Health Organisation has designated these bacteria as bacterial priority pathogens for research and development of novel antibiotics (Hetsa *et al.*, 2025).

Gamma (γ) haemolysis was the predominant haemolytic pattern observed, followed by beta (β) and alpha (α) haemolysis among the bacterial isolates examined. Haemolysins are proteins produced by certain microbes that lyse, or destroy, the red blood cell membrane in the growth substrate, causing a process called haemolysis (Savardi *et al.*, 2018). The presence of beta-haemolytic *S. aureus* indicates the circulation of virulent *S. aureus* on the keypads of automated teller machines. However, there was no significant

association between haemolytic pattern and antibiotic resistance status.

Conclusion

The current findings demonstrate that ATM keypads may be contaminated with *Escherichia coli*, *Pseudomonas* spp., and beta (β)-haemolytic *Staphylococcus aureus*. Additionally, these keypads may serve as platforms for cross-contamination with antibiotic-resistant strains. As a result, proper cleaning methods aimed at reducing the presence of microorganisms on the surfaces of automated teller machines should be developed, using suitable sanitizers, and handwashing with soap and water after using ATMs. Further work should incorporate molecular detection of haemolysis-associated genes to confirm the haemolytic potential of the bacterial isolates, complementing conventional phenotypic assessment using blood agar.

Competing Interest

The authors have declared that there are no conflicting interests.

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