ABSTRACT

Aims: To evaluate the bacterial diversity and degree of contamination obtainable on the ATM buttons as money is being collected and antibiotic susceptibility pattern of the isolates.

Study Design: Cross-sectional study including all ATM user interface in the banks within Umuahia metropolis.

Place and Duration of Study: Department of Microbiology, Michael Okpara University of Agriculture, Umudike, Abia state, between August 2015 and September 2015.

Methodology: A total number of sixty-eight (68) samples were collected from 14 different commercial banks in Umuahia metropolis. Isolation and identification of bacteria were done by standard microbiological techniques. Antibiotic susceptibility testing was carried out by disc diffusion technique.

Results: Nine (9) different organisms were isolated which include- E. coli (26.5%), S. aureus (17.6%), Bacillus spp (4.9%), Klebsiella spp (6.9%), Proteus spp (8.8%), Pseudomonas aeruginosa
(9.8%), Streptococcus spp (13.7%), Salmonella spp (4.9%) and Coagulase Negative Staphylococcus (6.9%). Most of the isolates were sensitive to Ceftriaxone, Ciprofloxacin, Amoxicillin/Clavulanate and Gentamicin and resistant to Cotrimoxazole, Ampicillin and Cephalexin.

**Conclusion:** The result of the study reveals that high levels of bacterial contamination were detected on ATM hardware user interface. This is of public health importance.

**Keywords:** Bacterial pathogens; ATM; antibiotic sensitivity pattern; South-eastern Nigeria.

1. **INTRODUCTION**

Several studies of the human environment have demonstrated colonization and contamination of objects such as door handles, faucets, phones, money, fabrics and plastics [1]. People come into daily contact with all sorts of fomites, with an increasing rate of bacterial infection [2]. The spread of infectious disease through hand contact has been an area of major concern. According to a study conducted by [3], Gram positive *Staphylococcus aureus* and Gram negative enteric bacteria such as *Escherichia Coli, klebsiella species, citrobacter species* was found to contaminate various contact surfaces including tables, chairs, windows, door handles and many other common household fixture [3]. Some epidemiological studies have suggested that contaminated surfaces may play a role in the spread of respiratory viruses and several laboratory studies have corroborated this hypothesis [4,5,6].

Bacteria that can cause severe gastroenteritis have been found on ATM machine keypads/buttons. Fomites such as ATM machines carry germs and when one touches it and then touches the mouth, nose, eye etc., there may be transfer of germs in the body. The presence of pathogenic bacteria on the user interface of ATM machines possesses a potential risk to vulnerable, immune compromised individuals. It has been shown that hard, non-porous surfaces such as ATM machines have the highest bacteria transfer rates to hands [7].

ATM machines once contaminated becomes vehicles for transmission of infection, such that the user may succeed in picking these pathogens after making use of an ATM machine, the organisms thus picked can introduce infections into such individual orally or topically or can be transferred to another person.

However, personal hygiene and good hand washing technique have been found to be an effective method of preventing the transmission of pathogens through fomites such as the user interface of ATM machines.

2. **MATERIALS AND METHODS**

2.1 **Study Area**

This study was carried out in Umuahia, Abia State, Southeastern Nigeria. It covered various commercial banks located within the Umuahia metropolis.

2.2 **Collection of Samples**

A total number of sixty-eight (68) swab samples were collected from the user interface of 14 different commercial banks situated at various parts of Umuahia metropolis with the aid of sterile cotton swab sticks moistened with sterile physiological saline before swabbing the buttons of the ATM machines. The cotton swab sticks were transferred immediately to the laboratory within one hour of collection for bacteriological analysis.

2.3 **Bacterial Inoculation**

The first phase of bacterial inoculation involved a direct streaking of the swab sticks on MacConkey agar, Mannitol salt agar and Blood agar respectively and incubated for 24 hours at 37ºC after which colonies were counted. In the second phase, individual buttons on the user interface were swabbed and soaked in 3ml of normal saline for 1hr. Serial dilution was later carried out and 0.1 ml of the10⁻³ dilution cultured by streak plate on MacConkey agar, Mannitol salt agar and Blood agar respectively and incubated for 24 hours at 37ºC. Colony forming units was calculated in CFU/cm².

2.4 **Colony Counting**

After 24 hours of incubation and the colonies were counted and assigned values (+, ++, +++).
to determine the nature and severity of growth. Where;

+ = Scanty growth (1-30 colonies)
++ = Moderate growth (31-70 colonies)
+++ = Profuse growth (71 and above)

2.5 Isolation and Identification of Bacteria Isolates

The isolation and identification of bacteria from the internal surface of handbags were done by standard methods. The isolate were identified by the modification of the methods described by [8] based on their: morphological appearance, Gram reaction and Biochemical characteristics.

2.6 Antibiotics Susceptibility Testing

The antibiotics sensitivity of the isolates was tested against the following antibiotics: streptomycin (30 mcg), tarivid (10 mcg), peflacine (10 mcg), ciproflox (10 mcg), Augmentin (30 mcg), Gentamicin (10 mcg), septrin (30 mcg), ceporex (10 mcg) and Ampicillin (30 mcg) using Kirby Bauer antibiotics disc method [9]. A colony of the test organisms was picked with sterile wire hoop and immersed in peptone water. The turbidity of the suspension was compared against a reference 0.5 Mcfarland tube. The suspension of the organism was streaked on the entire of nutrient agar and the antibiotic disc was placed on the centre of the plate using forcep. The plates were incubated at 37ºc for 24 hours. The diameter of the zone of inhibition was measured using CLSI standard guidelines [10].

3. RESULTS

Table 2 the diversity of bacteria obtained from the different ATM user interface which were screened in various banks. Banks with more customers than the others showed a wider spectrum of bacteria types.

Table 2 shows the diversity of bacteria and degree of contamination of user hardware interface in various banks. Banks with ore customers than the others showed both a wider spectrum of bacteria types and higher degree of contamination.

Table 3 the differentiation of isolates according to Gram stain reaction. Two (2) gram positive bacteria, S. aureus and Streptococcus spp showed 17.6% and 13.7% respectively while two (2) Gram negative bacteria, E. coli and Pseudomonas spp showed 26.5% and 9.8% respectively.

Table 4 the percentage of occurrence of each organism in the various banks screened. E. coli (26.5%) and S. aureus (17.6%) were the most frequently isolated organisms in the study.

Table 5 the antibiotics susceptibility of the bacterial isolates from various ATM machines in Umuahia metropolis. Most isolates were sensitive to Ofloxacin, Peflacine, Ceftriaxone but resistant to Ampicillin, Cephalexin and Septrin.

Table 6 viable bacteria count per button from the different ATM screened in different banks. E. coli was found in all the buttons enumerated.

4. DISCUSSION

ATM machines are one of the most commonly touched surfaces today. The study evaluated the bacteria contamination of shared surfaces on user hardware interface of 14 commercial banks randomly scattered within the Umuahia Metropolis in Southeastern Nigeria. A total of 102 bacterial organisms comprising nine (9) different species, were isolated. The isolation of both Gram negative and Gram positive organisms disagrees with the findings of [11] who isolated only Gram positive bacteria: Staphylococcus, Enterococcus, Micrococcus and Streptococcus from mobile phones. In comparison with the other studies [12,13] obtained Gram positive and Gram negative bacteria in their work from currency note and computer keyboards, curtains, cellphones, white coats and ties respectively.

Findings from this study revealed E. coli to be the most frequently occurring isolate with a percentage occurrence of 26.47%. This was found to be at variance to the findings of [14] who reported S. aureus (35.8%) as the frequent bacteria contaminant of electronic hardware interfaces in Ile-ife. E. coli is a normal floral of the gastrointestinal tract which can easily be picked up from toilet door handles. In a society of low hygiene, this probably explains its preponderance as a bacterial contaminant of shared user hardware interfaces. It has also been associated with numerous infectious disease conditions and nosocomial infections. It follows that since users constantly touch interfaces there is every chance of introducing E. coli onto the interface in use. Also, airborne organisms can be transported from users or passer-by.
Table 1A. Bacterial diversity and degree of contamination of user hardware interface in various banks

| Isolates          | B1   | B2   | B3   | B4   | B5   | B6   | B7   |
|-------------------|------|------|------|------|------|------|------|
| **M**             | D    | M    | D    | M    | D    | M    | D    |
| **E. coli**       | 18.3±55.9 | +++  | 19.4±50.1 | +++  | -    | -    | 31.6±53.6 | +++  | 11.6±55.9 | +++  | -    | -    | 10.5±53.7 | +++  |
| **S. aureus**     | 20.5±57.6 | +++  | 13.8±59.4 | +++  | 17.2±51 | +++  | 11.5±58 | +++  | 9.1±20    | +++  | -    | -    | -    | -    |
| **Klesiella spp** | 6.5±12.6 | +   | -    | -    | -    | -    | 7.5±38.7 | ++   | -    | -    | -    | -    | -    |
| **P. aeruginosa** | 0.7±2.5 | +   | 7.9±25 | ++   | 5±10 | +   | -    | -    | 8.6±37.8 | ++   | 9.2±20 | ++   | -    | -    |
| **Streptococcus** | 9.6±26.8 | ++   | 13.2±22.5 | ++   | 14.4±38.6 | ++   | -    | -    | -    | -    | 1.5±3.3 | +   | -    | -    |
| **Bacillus spp**  | 13.1±25.6 | ++ | -    | -    | -    | -    | -    | -    | 13.8±59.4 | +++  | -    | -    | -    | -    |
| **Proteus spp**   | 9.4±26.4 | ++   | 13.4±51 | +++  | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    |
| **CoANS**         | 7.5±6.3 | +   | 7.6±26.7 | ++   | 2.1±4.3 | +   | -    | -    | 8.2±27.5 | ++   | -    | -    | -    | -    |
| **Salmonella spp**| 6.3±11.5 | +   | -    | -    | -    | -    | -    | -    | 9.4±18.2 | +   | -    | -    | -    | -    |

**Keys:** M = Mean number of colonies per swab, + = Scanty growth (From 1-20 colonies), ++ = Moderate growth (From 21-50 colonies), D = Degree of bacterial contamination where; +++ = Profuse growth (51 colonies and above)

Table 1B. Bacterial diversity and degree of contamination of user hardware interface in various banks

| Isolates          | B8   | B9   | B10  | B11  | B12  | B13  | B14  |
|-------------------|------|------|------|------|------|------|------|
| **M**             | D    | M    | D    | M    | D    | M    | D    |
| **E. coli**       | 13.1±23 | ++   | 27.2±50.1 | +++  | 10±55 | +++  | 13.4±51 | +++  | 8.5±26.6 | ++   | 17.2±61 | +++  | 14.2±30.1 | +++  |
| **S. aureus**     | 11.4±20.7 | ++   | 18.7±51.6 | +++  | 23.6±50 | +++  | 20.5±57.6 | +++  | 13.7±56.8 | +++  | 13.8±79.4 | +++  | -    | -    |
| **Klesiella spp** | -    | -    | -    | -    | -    | -    | 1.7±2.8 | +   | -    | -    | -    | -    | 2.3±5.2 | +   |
| **P. aeruginosa** | -    | -    | 10.4±23 | ++   | 6.5±27.5 | ++   | -    | -    | -    | -    | -    | -    | -    | -    |
| **Streptococcus** | 1.7±2.7 | +   | 2.2±5.7 | +   | -    | -    | -    | -    | 10.2±30.6 | ++   | 8.4±28.2 | ++   | -    | -    |
| **Bacillus spp**  | -    | -    | 1±3  | +   | 7.5±6.3 | +   | -    | -    | -    | -    | -    | -    | -    | -    |
| **Proteus spp**   | 8.5±23.7 | ++ | -    | -    | -    | -    | 5.6±36.4 | ++   | 7.9±25 | ++   | 12.2±21.5 | ++   | -    | -    |
| **CoANS**         | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    |
| **Salmonella spp**| -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    | -    |

**Keys:** M = Mean number of colonies per swab, + = Scanty growth (From 1-20 colonies), ++ = Moderate growth (From 21-50 colonies), D = Degree of bacterial contamination where; +++ = Profuse growth (51 colonies and above)
Table 2. Types of bacteria isolates observed from different banks

| S/N | Banks | Bacterial isolated                                                                 |
|-----|-------|-----------------------------------------------------------------------------------|
| 1   | B1    | Pseudomonas aeruginosa, E. coli , proteus spp, S. aureus, Klebsiella spp, Streptococcus spp, Bacillus spp, Coagulase Negative Staphylococcus, Salmonella spp |
| 2   | B2    | Streptococcus spp, proteus spp, E. coli , S. aureus, Pseudomonas aeruginosa, Coagulase Negative Staphylococcus |
| 3   | B3    | S. aureus, Streptococcus spp, Pseudomonas aeruginosa                                |
| 4   | B4    | E. coli, Klebsiella spp, S. aureus                                                 |
| 5   | B5    | E. coli, S. aureus, Coagulase Negative Staphylococcus                               |
| 6   | B6    | Bacillus spp, Pseudomonas aeruginosa                                               |
| 7   | B7    | Pseudomonas aeruginosa, Streptococcus spp, E. coli, Coagulase Negative Staphylococcus |
| 8   | B8    | Streptococcus spp, E. coli, S. aureus, Proteus spp.                                 |
| 9   | B9    | Pseudomonas aeruginosa , E. coli, Streptococcus spp, S. aureus                      |
| 10  | B10   | S. aureus, E. coli, Pseudomonas aeruginosa , Bacillus spp.                          |
| 11  | B11   | E. coli, S. aureus, Klebsiella spp, Bacillus spp                                   |
| 12  | B12   | Proteus spp , S. aureus, E. coli                                                   |
| 13  | B13   | E. coli, S. aureus, Streptococcus spp, Proteus spp.                                 |
| 14  | B14   | Klebsiella spp, Proteus spp, E. coli, Streptococcus spp.                           |

Table 3. Differentiation of isolates from study by gram staining

| Gram stain reaction        | Bacteria isolates          | No. of bacteria | Percentage (%) |
|----------------------------|----------------------------|-----------------|----------------|
| Gram positive              | S. aureus                  | 18              | 17.6           |
|                            | Streptococcus spp          | 14              | 13.7           |
|                            | Bacillus spp               | 5               | 4.9            |
|                            | Coagulase Negative Staphylococcus | 7          | 6.9            |
| Gram negative              | Klebsiella spp             | 7               | 6.9            |
|                            | E. coli                    | 27              | 26.5           |
|                            | Proteus spp                | 9               | 8.8            |
|                            | Pseudomonas aeruginosa     | 10              | 9.8            |
|                            | Salmonella spp             | 5               | 4.9            |
|                            | Total                      | 102             | 100            |
### Table 4. Percentage of occurrence of isolates in various banks

| Isolate       | B1 (%) | B2 (%) | B3 (%) | B4 (%) | B5 (%) | B6 (%) | B7 (%) | B8 (%) | B9 (%) | B10 (%) | B11 (%) | B12 (%) | B13 (%) | B14 (%) | Total (%) |
|---------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|---------|---------|---------|---------|-----------|
| E. coli       | 8 (28.6) | 5 (26.3) | 3 (30) | 2 (40) | 1 (12.5) | 1 (20) | 0 (0) | 2 (0.12) | 0 (0) | 1 (25) | 2 (66.6) | 0 (0) | 2 (50) | 0 (0) | 27 (26.5) |
| S. aureus     | 5 (17.9) | 3 (15.8) | 1 (10) | 0 (0) | 2 (0.2) | 0 (0) | 0 (0) | 1 (50) | 2 (66.6) | 2 (50) | 0 (0) | 1 (50) | 0 (0) | 1 (50) | 18 (17.6) |
| Klebsiella spp| 2 (7.1) | 1 (5.3) | 1 (10) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 1 (50) | 0 (0) | 0 (0) | 7 (5.9) |
| P. aeruginosa | 3 (10.7) | 3 (15.8) | 1 (10) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 1 (50) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 1 (50) | 10 (9.8) |
| S. typhi       | 2 (7.1) | 2 (10.5) | 2 (20) | 1 (0.1) | 2 (0.2) | 0 (0) | 1 (0.03) | 0 (0) | 1 (50) | 1 (33.3) | 0 (0) | 0 (0) | 1 (25) | 0 (0) | 14 (13.7) |
| Bacillus spp   | 1 (3.6) | 2 (10.5) | 0 (0) | 0 (0) | 0 (0) | 1 (12.5) | 0 (0) | 0 (0) | 1 (50) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 5 (4.9) |
| Proteus spp    | 2 (7.1) | 2 (10.5) | 1 (10) | 1 (0.15) | 0 (0) | 1 (20) | 0 (0) | 0 (0) | 0 (0) | 1 (25) | 0 (0) | 0 (0) | 1 (25) | 0 (0) | 9 (8.8) |
| CoANS          | 2 (7.1) | 1 (5.3) | 1 (10) | 0 (0) | 2 (0.2) | 0 (0) | 1 (0.03) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 7 (6.8) |
| S. paratyphi   | 3 (10.7) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 2 (40) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 0 (0) | 5 (4.9) |

### Table 5. Antibiotics susceptibility of the bacterial isolates from various ATM machines in umuahia metropolis

| Isolates       | No tested | S       | OFX     | PEF     | AU      | CRO     | CEP     | SXT     | PN     | CN     |
|----------------|-----------|---------|---------|---------|---------|---------|---------|---------|--------|--------|
| E. coli        | 27        | 5 (18.5)| 25 (92.6)| 20 (74.0)| 15 (55.5)| 20 (74.0)| 6 (29.7)| 0 (0)   | 4 (14.8)| 20 (74.0)|
| S. aureus      | 18        | 10 (55.5)| 15 (83.3)| 12 (66.7)| 9 (50.0)| 10 (55.5)| 7 (38.9)| 8 (44.4)| 5 (27.8)| 12 (66.7)|
| Proteus spp    | 9         | 3 (33.3)| 5 (55.5)| 4 (44.4)| 9 (99.9)| 9 (99.9)| 2 (22.2)| 1 (11.1)| 0 (0)   | 5 (55.5)|
| Klebsiella     | 7         | 2 (28.6)| 4 (57.1)| 3 (42.8)| 5 (71.4)| 2 (28.6)| 1 (14.3)| 7 (100.0)| 1 (14.3)| 6 (85.7)|
| P. aeruginosa  | 10        | 1 (10.0)| 3 (30.0)| 9 (90.0)| 5 (50.0)| 4 (40.0)| 2 (20.0)| 0 (0)   | 0 (0)   | 7 (70.0)|
| Streptococcus  | 14        | 6 (42.9)| 6 (42.8)| 2 (14.3)| 5 (35.7)| 7 (50.0)| 12 (85.7)| 0 (0)   | 0 (0)   | 4 (28.6)|
| Bacillus spp   | 5         | 0 (0)   | 1 (20.0)| 3 (60.0)| 2 (40.0)| 3 (60.0)| 1 (20.0)| 4 (80.0)| 4 (80.0)| 2 (40.0)|
| CoANS          | 7         | 3 (42.9)| 5 (71.4)| 4 (57.1)| 7 (100) | 6 (85.7)| 5 (71.4)| 1 (14.2)| 2 (28.6)| 5 (71.4)|

**KEYS:**
- S = Streptomycin, CEP = Cephalexin, CRO = Ceftriaxone
- OFX = Ofloxacin, SXT = Septrin, PN = Ampicillin
- PEF = Peflazine
- AU = Amoxycillin/Clavulanate, CN = Gentamicin
### Table 6. Assessment of bacterial count from various bank of each ATM buttons

| Bank | Area of button (cm$^2$) | E. coli | Strept. Spp | S. aureus | Kleb. spp | Proteus spp | Sal. spp |
|------|-------------------------|---------|-------------|-----------|-----------|-------------|---------|
| B1   | 7.3                     | 2.5x10$^5$ | -           | 1.5 x 10$^5$ | -          | 1.0 x 10$^5$ | 1.0 x 10$^5$ |
| B2   | 6.2                     | 3.0x10$^5$ | 5.0 x 10$^5$ | 1.0 x 10$^5$ | 1.0 x 10$^5$ | -           | -       |
| B3   | 7                       | 3.5x10$^5$ | -           | 5.0 x 10$^2$ | -          | 5.0 x 10$^4$ | -       |
| B4   | 1.7                     | 5.0 x 10$^4$ | 5.0 x 10$^4$ | -          | -          | 5.0 x 10$^4$ | -       |
| B5   | 1.2                     | 3.5 x 10$^5$ | -           | 5.0 x 10$^4$ | -          | -           | 1.0 x 10$^5$ |
| B6   | 3.3                     | 1.0 x 10$^5$ | 3.5 x 10$^5$ | -          | -          | -           | -       |
| B7   | 6.7                     | 3.0 x 10$^5$ | -           | 5.0 x 10$^4$ | -          | -           | -       |
| B8   | 2.4                     | 2.0 x 10$^5$ | -           | 5.0 x 10$^3$ | 3.5 x 10$^4$ | -          | -       |
| B9   | 6.2                     | 2.0 x 10$^5$ | -           | 1.0 x 10$^5$ | 1.0 x 10$^5$ | -          | -       |
| B10  | 1.2                     | 3.0 x 10$^5$ | 5.0 x 10$^5$ | 5.0 x 10$^4$ | -          | -           | -       |

**Key:** SAL. = Salmonella species
Bacillus spp was isolated from the findings in this research, and its high presence 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 finding is in agreement with the research carried out by [15] who reported that Bacillus spp was found to be among the predominant organisms from user hardware interface.

The isolation of S. aureus agrees with the findings of [16]. Staphylococcus aureus is a major component of the normal floral of the skin and nostrils, which probably explains its high prevalence as a contaminant, as it can be easily discharged by several human activities including sneezing, talking, and contact with moist skin [3]. It has also been associated with numerous infectious disease conditions and noscomial infections. It follows that since users constantly touch interface and often sneeze, there is every chance of introducing S. aureus on to the interface in use. Also, airborne organisms can be transported from users to passerby.

In the present study, a sustained pattern of similarity in the bacterial diversity obtained from the user interfaces of ATM machines of different banks was observed. This could be attributed to frequent dermal contact and sharing by numerous users with different hygiene practices and health conditions.

High microbial loads were observed as in the reports of [14]. A higher number of different types of bacteria isolates and contamination were found to be more in B1 because of the high number of customers which is in agreement with the research of [17] who revealed that high proportion of organisms were found in surfaces associated with crowded public utilities and the least count in non-crowded public utilities.

Antibiotics susceptibility studies of the isolates showed a pattern of resistance to commonly used antibiotics. This agrees with the reports of [16], who worked on door handles in a tertiary institution.

5. CONCLUSION

In conclusion, interfaces such as ATM machine were found to be contaminated with potentially pathogenic bacteria, highly resistant to some commonly used antibiotics. ATMs harbor more bacterial contaminants than other electronic hardware; this can be attributed to their structural design and large surface area, coupled with the fact that ATMs are usually located in open places exposed to wind and rain.

These interfaces are therefore potential vehicles for the transmission of clinically important pathogens through human own hands.

6. RECOMMENDATION

The spread of infection can be interrupted by good hygienic practices which include adherence to hand hygiene recommendation, cleaning and disinfecting contaminated environmental surfaces. It is extremely difficult to completely eliminate all bacteria from surfaces. However, strict adherence to basic rules of hand washing and disinfection of ATM user interface will reduce possible spread of infectious agents.

CONSENT

It is not applicable.

ETHICAL APPROVAL

It is not applicable.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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