Isolation and Identification of Bacteria on Mobile Phones among Students, Staff and Food Handlers in Federal University of Technology Owerri

Emmanuel Everest Chigozie[1;] Enuma Ekpereka Mike-Anosike[1;]
[1]Department of Microbiology, School of Biological Science,
Federal University of Technology Owerri,
Imo State, Nigeria.

Gbeinbo Fiderikumo Livingstone[2]
[2]Hubei Insect Resources Utilization and Sustainable Pest Management Key Laboratory, College of Plant Science and Technology, Huazhong Agricultural University, Wuhan 430070, China

Jibrin Muhammad Yelwa[3]
[3]Department of Scientific and Industrial Research,
National Research Institute for Chemical Technology, Zaria, Kaduna State, Nigeria.

Abstract
This study investigated the microbial contamination profiles and antibiotic resistance patterns of bacteria isolated from mobile phones belonging to students, staff, and food handlers at the Federal University of Technology Owerri (FUTO). Thirty mobile phone surfaces (10 from each user group) were sampled using sterile saline-moistened swabs across a standardized 3 cm^2 area. All sampled devices (100%) showed bacterial contamination, with *Staphylococcus aureus* being the most prevalent isolate (42.9%), followed by *Bacillus cereus* (30.6%), *Streptococcus* spp. (14.2%), *Klebsiella* spp. (8.2%), and *Proteus vulgaris* (4.1%). Student devices exhibited the highest diversity of bacterial contaminants. Antimicrobial susceptibility testing revealed gentamicin (17.6%) and pefloxacin (15.1%) as the most effective antibiotics, while erythromycin (0%) and amoxicillin (4.9%) showed the lowest efficacy. These findings demonstrate that mobile phones serve as significant reservoirs for pathogenic bacteria and potential vectors for transmitting multidrug-resistant organisms within academic communities.

Keywords: Mobile phone contamination, Antimicrobial resistance, Bacterial pathogens, Hygiene practices, Public health fomites, Academic community transmission

1. Introduction
Mobile phones have become indispensable tools in modern life, with over 1.6 billion smartphones used globally as of 2013, projected to double rapidly (Strategy Analytics, 2013). While these devices offer unparalleled connectivity and convenience, their role as potential reservoirs for pathogenic microorganisms has raised

DOI: https://doi.org/10.5281/zenodo.17068555

significant public health concerns. Unlike stationary objects, mobile phones are carried everywhere, including high-risk environments like toilets, hospitals, and kitchens, where they readily accumulate and transmit microbes (Bhoonderowa et al., 2014). Their warm, humid surfaces create ideal breeding conditions for bacteria, turning them into fomites capable of spreading infections (Srikanth et al., 2009). Studies have shown that mobile phones harbor more bacteria than toilet seats or door handles, with contamination rates exceeding 90% in some populations (Ulger et al., 2009; Nwankwo et al., 2014). Pathogens such as Staphylococcus aureus, Pseudomonas aeruginosa, and multidrug-resistant (MDR) strains like methicillin-resistant S. aureus (MRSA) are frequently isolated, posing risks for nosocomial and community-acquired infections (Karabay et al., 2007; Tagoe et al., 2011).

The human skin is constantly in contact with microorganisms and becomes readily colonized by certain microbial species. The adult human is covered with approximately 2m2 of skin, with a surface area supporting about 1012 bacterial cells/person (Mackowiak, 1982). Microorganisms can be transferred from the hands, face, and ears to mobile phone surfaces during use, especially when proper hygiene measures are not followed (Elkholy and Ewees, 2010). Healthcare workers (HCWs) are especially vulnerable, as mobile phones often contact patients and clinical environments, facilitating pathogen transmission (Mehta et al., 2013). Alarmingly, 20% of S. aureus isolates from HCWs' phones are MRSA, while Gram-negative bacteria like Escherichia coli and Klebsiella spp. Indicate fecal contamination (Shahaby et al., 2012). Despite these risks, fewer than 5% of users regularly clean their devices, and hand-washing compliance remains low (Alex-Hart and Opara, 2001; Heyba et al., 2015).

Research gaps persist in non-clinical settings, particularly in densely populated environments like universities. For instance, students' mobile phones exhibit higher bacterial diversity and contamination rates (65–98%), in contrast to other groups, possibly due to frequent device sharing and prolonged use (Singh et al., 2010; Jagadeesan et al., 2013). However, limited studies focus on academic communities in Nigeria, where mobile phone usage intersects with communal living and food handling—a potential hotspot for pathogen transmission. This study addresses this gap by examining bacterial contamination on mobile phones used by students, staff, and food handlers at the Federal University of Technology Owerri (FUTO).

Using standard microbiological methods, the study successfully isolated and characterized bacterial species from 30 mobile phones, with equal representation (n=10) from each participant group. All sampled phones were contaminated, with Staphylococcus aureus (42.9%) being the most prevalent, followed by Bacillus cereus (30.6%), Streptococcus spp. (14.2%), Klebsiella spp. (8.2%), and Proteus vulgaris (4.1%). Students' phones had the highest microbial diversity. Antimicrobial susceptibility testing revealed concerning resistance patterns: gentamicin (17.6% susceptibility) and pefloxacin (15.1%) were the most effective, while erythromycin (0%) and amoxicillin (4.9%) were the least effective. These findings underscore mobile phones as potential vectors for MDR pathogens, necessitating improved hygiene protocols in academic and public settings.

By characterizing prevalent pathogenic species and their antimicrobial resistance patterns, this study provides critical insights into the urgent need for awareness campaigns and institutional policies on mobile phone sanitation. Simple interventions, such as alcohol-based cleaning (Arora et al., 2009), could

DOI: https://doi.org/10.5281/zenodo.17068555

significantly reduce microbial loads, mitigating infection risks in similar environments globally.

2. Materials and Methods

2.1 Study Design and Sample Collection

A cross-sectional microbiological analysis was conducted on 30 mobile phones obtained from three distinct groups at the Federal University of Technology Owerri (FUTO), Nigeria:

- Students (SD, n = 10): Undergraduate students residing both on and off campus.
- Staff (ST, n = 10): Academic and non-academic university employees.
- Food handlers (FH, n = 10): Individuals involved in food preparation and vending within the campus.

Sample collection protocol:

A standardized 3 cm^2 surface area of each mobile phone was swabbed using sterile cotton swabs (HiMedia, India) moistened with 0.9% NaCl (saline solution). Swabs were immediately transferred into 1 mL sterile saline tubes and transported to the laboratory under aseptic conditions within 1 hour of collection to preserve microbial viability.

2.2 Culture Media Preparation

Selective and non-selective media were prepared following standard protocols:

MacConkey Agar (Oxoid, UK): Prepared by suspending 50 g of powder in 1 L distilled water, followed by autoclaving (121°C, 15 min).

Blood Agar (Thermo Fisher Scientific, USA): Prepared using trypticase soy base, autoclaved, and supplemented with 5% defibrinated sheep blood post-sterilization.

Mueller Hinton Agar (Merck, Germany): 18 g of powder was dissolved in 500 mL distilled water, autoclaved (121°C, 15 min), and poured into plates to a uniform depth of 4 mm for antibiotic susceptibility testing.

2.3 Microbial Isolation and Incubation

Swabsampleswereinoculatedonto MacConkey Agar (for Gram-negative selection) and Blood Agar (for general bacterial growth) using the quadrant streaking method to obtain isolated colonies.Plates were incubated aerobically at 37°C for 24–48 hours to facilitate microbial growth.

2.4 Bacterial Characterization

2.4.1 Morphological Analysis

Colony morphology (size, shape, color, hemolysis on Blood Agar) was recorded. Gram staining was performed using crystal violet, iodine, and safranin (Sigma-Aldrich, USA) to differentiate Gram-positive and Gram-negative bacteria.

2.4.2 Biochemical Identification

- **Catalase Test:** Bacterial isolates were exposed to 3% H_2O_2; effervescence indicated catalase-positive organisms (e.g., *Staphylococcus* spp.).
- **Coagulase Test:** Isolates were mixed with rabbit plasma; clotting within 10 sec confirmed *Staphylococcus aureus*.
- **TripleSugarIronAgar (TSIA):** Inoculated slants exhibiting yellow butt (acid production) and black precipitate (H_2S) suggested *Proteus* spp.
- **Indole Test:** Addition of Kovac's reagent to tryptophan broth; a red ring indicated indole-positive bacteria (e.g., *Escherichia coli*).
- **Oxidase Test:** Colonies were tested with oxidase reagent; development of a blue-purple color within 10 sec indicated oxidase-positiveorganisms (e.g., *Pseudomonas* spp.).

2.5 Antibiotic Susceptibility Testing (AST)

Mueller Hinton Agar (Merck, Germany) was used for AST following Clinical and Laboratory Standards Institute (CLSI,

DOI: https://doi.org/10.5281/zenodo.17068555

2022) guidelines. Bacterial suspensions (0.5 McFarland standard, $OD_{600} \approx 0.5$) were spread onto plates, and antibiotic disks (Abtek Biologicals, USA) were aseptically placed: Amoxicillin (10 µg), Gentamicin (10 µg), Pefloxacin (5 µg), Erythromycin (15 µg). Plates were incubated at 37°C for 24 hrs, and inhibition zone diameters were measured to determine susceptibility.

2.6 Quality Control

Sterility checks: Uninoculated media were incubated to confirm absence of contamination. Reference strains: *Escherichia coli* ATCC 25922 (Gram-negative control) and *Staphylococcus aureus* ATCC 25923 (Gram-positive control).

3. Results and Discussion

All 30 mobile phone samples collected from students, staff, and food handlers at the Federal University of Technology, Owerri (FUTO), yielded bacterial growth after 24 hours of incubation at 37°C. The bacterial isolates were identified using standard microbiological techniques, including colonial morphology, Gram staining, motility testing, and biochemical assays based on BERGEY'S Manual (1994). The colonial morphology revealed small, round, pink, creamy, mucous, and shiny colonies on MacConkey and Blood agar. Gram staining results showed a mix of Gram-positive cocci (GPC), Gram-positive bacilli (GPB), and Gram-negative bacilli (GNB). Motility tests indicated that all isolates were non-motile, except for the isolate from Student Sample 6 (SD6), which exhibited motility. The biochemical tests, including Indole, Oxidase, Urease, Methyl Red, Voges-Proskauer, Catalase, and Coagulase, further confirmed the identity of the isolates.

TABLE 1: MICROBIOLOGICAL AND BIOCHEMICAL CHARACTERISTICS OF THE ISOLATES

ISOLATE CODE	GRAM STAIN	MOTILITY	INDOLE	OXIDASE	UREASE	M-R	V-P	CATALASE	COAGULASE	T H2S	S Slope	I Butt	A Gas	MOST PROBABLE ORGANISM
STUDENTS (SD)	GPC	-						+	+					*Staphylococcus aureus*
	GPB	-	-	-	-	-	-	+		-	R	R	-	*Bacillus cereus*
	GPC	-						-	-					*Streptococcus* sp.
	GNB	+	-	-	+	-	+	-		+	R	Y	+	*Proteus vulgaris*
	GNB	-	-	-	+	-	+	-		-	Y	Y	+	*Klebsiella* sp.
STAFF (ST)	GPC	-						+	+					*Staphylococcus aureus*
	GPB	-	-	-	-	-	-	+		-	R	R	-	*Bacillus cereus*
	GPC	-						-	-					*Streptococcus* sp.
	GNB	-	-	-	+	-	+	-		-	Y	Y	+	*Klebsiella* sp.
FOOD HANDLERS (FH)	GPC	-						+	+					*Staphylococcus aureus*
	GPB	-	-	-	-	-	-	+		-	R	R	-	*Bacillus cereus*
	GPC	-						-	-					*Streptococcus* sp.
	GNB	-	-	-	+	-	+	-		-	Y	Y	+	*Klebsiella* sp.

KEY WORDS: = -NEGATIVE = +POSITIVE M-R= METHYL RED TEST, V-P= VOGES PROSKAUER TEST, T.S.I.A= TRIPLE SUGAR IRON AGAR, Y= YELLOW, R= RED

Microbiological analysis revealed the following prevalence among isolated organisms: *Staphylococcus aureus* (42.9%), *Bacillus cereus* (30.6%), *Streptococcus* spp. (14.2%), *Klebsiella* spp. (8.2%), and *Proteus vulgaris* (4.1%). While most isolates Were distributed across all user groups, *P. vulgaris* exhibited exclusive detection in student samples. *S. aureus* emerged as the predominant contaminant, consistent with previous reports on mobile device microbiota. The high prevalence of *B. cereus* reflects its environmental persistence and ubiquitous nature. The detection of *Streptococcus* and *Klebsiella* species across all user categories indicates potential contamination from cutaneous, respiratory, and/or enteric sources. These findings demonstrate that mobile phones act as effective fomites for microbial transmission, with isolated distribution patterns reflecting differential hygiene practices among user populations.

Table 2: BACTERIAL ISOLATES FROM MOBILE PHONES USED BY USER GROUP.

MOBILE PHONE USERS	ORGANISMS ISOLATED
STUDENTS (SD)	*Staphylococcus aureus*
	Bacillus cereus
	Streptococcus sp.
	Proteus vulgaris
	Klebsiella sp.
STAFF (ST)	*Staphylococcus aureus*
	Bacillus cereus
	Streptococcus sp.
	Klebsiella sp.
FOOD HANDLERS (FH)	*Staphylococcus aureus*
	Bacillus cereus
	Streptococcus sp.
	Klebsiella sp.

DOI: https://doi.org/10.5281/zenodo.17068555

Antibiotic susceptibility testing revealed varied sensitivity patterns across the isolates. *Staphylococcus aureus* was sensitive to Gentamicin, Ampiclox, Zinacef, and Ciprofloxacin, but resistant to Amoxicillin, Rocephin, Streptomycin, Septrin, Erythromycin, and Pefloxacin. *Proteus vulgaris* exhibited broad sensitivity, being susceptible to most antibiotics tested except for resistance to Ampiclox and intermediate sensitivity to Septrin. *Streptococcus* species showed high resistance, particularly to Gentamicin, Ampiclox, Zinacef, Amoxicillin, and most other antibiotics tested, highlighting their potential for multidrug resistance. *Klebsiella* species were sensitive to Gentamicin, Rocephin, Ciprofloxacin, Septrin, and Pefloxacin but showed resistance to Ampiclox and Amoxicillin. *Bacillus cereus* was largely sensitive, though it displayed resistance to Amoxicillin and Erythromycin.

TABLE 3: PERCENTAGE OCCURRENCE OF THE ISOLATES

ORGANISMS ISOLATED	PERCENTAGE OCCURRENCE (%)
Staphylococcus aureus	42.9
Bacillus cereus	30.6
Streptococcus sp.	14.2
Klebsiella sp	8.2
Proteus vulgaris	4.1

The percentage sensitivity patterns to individual antibiotics were as follows: Gentamicin (17.55%), Ampiclox (6.12%),

TABLE 4: ANTIBIOTIC SENSITIVITY TEST RESULT ON THE ISOLATES

ORGANISMS ISOLATED	SENSITIVITY TEST									
	CN	APX	Z	AM	CRO	CPX	ST	SXT	ERY	PEF
Staphylococcus aureus	S	S	S	R	R	S		R	R	R
Proteus vulgaris	S	R	S	S	S	S	S	I		S
Streptococcus sp.	R	R	R	R	S	R	R	R	R	R
Klebsiella sp.	S	R	R	R	S	S	I	S		S
Bacillus cereus	S	S	S	R	S	S	S	S	R	S

KEY WORDS:
CN=GENTAMICIN CPX=CIPROXOLACIN
APX=AMPICLOX ST=STREPTOMYCIN
Z=ZINNA\CEFUROXIME SXT=SEPTRIN
AM=AMOXICILLIN ERY=ERYTHROMYCIN
RO=ROCEPHIN\CEFTRIAXONE PEF=PEFLOXACIN

Zinacef (14.29%), Amoxicillin (4.89%), Rocephin (6.94%), Ciprofloxacin (14.29%), Streptomycin (7.76%), Septrin (13.06%), Erythromycin (0%), and Pefloxacin (15.10%). Notably, Erythromycin recorded no sensitivity, indicating its ineffectiveness against the isolates in this study. Ciprofloxacin and Gentamicin showed the highest efficacy among the antibiotics tested.

Table 5: PERCENTAGE OCCURRENCE OF THE ANTIBIOTIC SENSITIVITY PATTERN FOR ISOLATES OBTAINED

ANTIBIOTICS	SENSITIVITY PATTERN	PERCENTAGE OCCURRENCE (%)
CN	43	17.55
APX	15	6.12
Z	35	14.29
AM	12	4.89
RO	17	6.94
CPX	35	14.29
ST	19	7.76
SXT	32	13.06
E	0	0
PEF	37	15.10

KEY:
CN = GENTAMICIN CPX = CIPROXOLACIN
APX = AMPICLOX ST = STREPTOMYCIN
Z = ZINNA\CEFUROXIME SXT = SEPTRIN
AM = AMOXICILLIN ERY = ERYTHROMYCIN
RO = ROCEPHIN PEF = PEFLOXACIN

When analyzed by user groups, the isolates from food handlers showed the highest overall sensitivity (87 sensitive responses), followed by staff (85), and students (73). The resistance profile was highest among isolates from food handlers (64 resistant responses), suggesting the potential for antibiotic misuse or environmental selection pressure in this group.

DOI: https://doi.org/10.5281/zenodo.17068555

Table 6: SUMMARY OF SENSITIVITY TEST RESULTS BY USER CATEGORY

RESULT	STUDENT	STAFF	FOODHANDLER
S	73	85	87
I	11	18	10
R	55	54	64

KEY WORDS: S= SENSITIVE (Drug killed the Bacteria)
I= INTERMEDIATE (More concentration will kill the Bacteria)
R= RESISTANT (Did not kill the Bacteria)

These findings emphasize the need for enhanced hygiene practices and routine disinfection of mobile phones, especially in high-contact environments such as food handling areas. The antibiotic resistance observed, particularly among *Streptococcus* species and food handler isolates, also underscores the public health implications of indiscriminate antibiotic use and the necessity of monitoring resistance trends. Comparisons with previous studies on microbial contamination of mobile phones corroborate these findings, affirming mobile phones as significant reservoirs for potentially pathogenic and drug-resistant bacteria.

4.0 Conclusion

This study has demonstrated that mobile phones, as personal electronic devices in constant contact with the human body and environment, are significantly colonized by various microorganisms, including potential pathogens. The consistent detection of bacterial contaminants across all sampled phones emphasizes the role of these devices as vectors in the transmission of infectious agents. Among the bacterial isolates identified, *Staphylococcus aureus*, *Bacillus cereus*, and *Streptococcus* species were the most prevalent, aligning with previous research and highlighting the likelihood of skin and hand contact as the primary routes of contamination. The results further showed that students' phones harbored the highest number of bacterial contaminants, likely due to frequent and varied use in high-risk areas such as toilets, kitchens, and laboratories.

Antibiotic susceptibility testing revealed that many isolates displayed resistance to commonly used antibiotics such as Erythromycin and Amoxicillin, while Gentamycin and Pefloxacin demonstrated higher effectiveness, suggesting their potential as drugs of choice for treating infections related to mobile phone contamination. The presence of multidrug-resistant organisms on mobile phones raises public health concerns, particularly in environments with immunocompromised individuals. As such, this study underscores the importance of regular hand hygiene, routine disinfection of mobile phones with 70% isopropyl alcohol, and public awareness of the risks posed by contaminated devices. Simple interventions, including the use of hands-free accessories and surface-friendly phone materials, could further mitigate microbial transmission. Continued research is encouraged to deepen understanding of the diversity of microorganisms present on mobile phones and the mechanisms underlying their resistance and survival.

DOI: https://doi.org/10.5281/zenodo.17068555

References

Akinyemi, O., Atapu, D., Adetona, O., & Coker, A. (2009). The potential role of mobile phones in the spread of bacterial infections. Journal of Infection in Developing Countries, 3(8), 628–632.

Arora, U., Devi, P., Chadha, A., & Malhotra, S. (2009). Cell phones: A modern stay house for bacterial pathogens. Journal of Medical Education and Research Science, 11(3), 127–129.

Brady, R. R. W., Damani, N. N., McAllister, C., Stirling, I., & Wasson, A. (2006). Is your phone bugged? The incidence of bacteria known to cause nosocomial infection on healthcare workers' mobile phones. Journal of Hospital Infection, 62(2), 123–125. https://doi.org/10.1016/j.jhin.2005.07.010

Brady, R. R. W., Fraser, S. F., Dunlop, M. G., Paterson-Brown, S., & Gibb, A. P. (2007). Bacterial contamination of mobile communication devices in the operative environment. Journal of Hospital Infection, 66(4), 397–398. https://doi.org/10.1016/j.jhin.2007.04.015

D'Alò, G. L., Cicciarella Modica, D., Maurici, M., Mozzetti, C., Messina, A., & Distefano, A. (2020). Microbial contamination of the surface of mobile phones and implications for the containment of the COVID-19 pandemic. Travel Medicine and Infectious Disease, 37, 101870. https://doi.org/10.1016/j.tmaid.2020.101870

Dhayhi, N., Kameli, N., Salawi, M., Shajri, A., Basode, V. K., Algaissi, A., & Alhazmi, A. H. (2023). Bacterial contamination of mobile phones used by healthcare workers in critical care units: A cross-sectional study from Saudi Arabia. Microorganisms, 11(8), 1986. https://doi.org/10.3390/microorganisms11081986

Ilusanya, O., Adesanya, O., Adesemowo, A., & Amushan, N. (2012). Personal hygiene and microbial contamination of mobile phones of food vendors in Ago-Iwoye Town, Ogun State, Nigeria. Pakistan Journal of Nutrition, 11(3), 276–278.

Karabay, O., Koçoglu, E., & Tahtaci, M. (2007). The role of mobile phones in the spread of bacteria associated with nosocomial infections. Journal of Infection in Developing Countries, 1(1), 72–73.

Kilic, I., Ozaslan, M., Karagoz, I., Zer, Y., & Davutoglu, V. (2009). The microbial colonisation of mobile phones used by healthcare staff. Pakistan Journal of Biological Sciences, 12(11), 882–884.

Modica, D. C., Maurici, M., D'Alò, G. L., Mozzetti, C., Messina, A., & Distefano, A. (2020). Taking screenshots of the invisible: A study on bacterial contamination of mobile phones from university students of healthcare professions in Rome, Italy. Microorganisms, 8(7), 1075. https://doi.org/10.3390/microorganisms8071075

Olsen, M., Lohning, A., Campos, M., Jones, P., Bannach-Brown, A., & Gordin, F. (2021). Mobile phones of paediatric hospital staff are never cleaned and commonly used in toilets: Implications for healthcare-associated infections. Scientific Reports, 11, 12999. https://doi.org/10.1038/s41598-021-92555-5

Simmonds, R., Lee, D., & Hayhurst, E. (2020). Mobile phones as fomites for potential pathogens in hospitals: Microbiome analysis reveals hidden contaminants. Journal of Hospital Infection, 104(2), 207–213. https://doi.org/10.1016/j.jhin.2020.07.024

Tagoe, D. N. A., Gyande, V. K., & Ansah, E. O. (2011). Bacterial contamination of mobile phones: When your mobile phone could transmit more than just a call. WebmedCentral Microbiology, 2(10), WMC002294.

DOI: https://doi.org/10.5281/zenodo.17068555