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Assessment and Antibiotic Susceptibility Profiles of Bacterial Contaminants on Mobile Phones of Students in the University of Abuja

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Abstract

Mobile phones are in near-constant contact with the hands and face, yet are rarely cleaned or disinfected, making them recognised fomites capable of harbouring and transmitting pathogenic bacteria. Despite growing evidence of mobile phone contamination in various settings, data specific to University of Abuja students combining bacterial isolation, characterisation, and antibiotic susceptibility profiling remain limited, posing a public health concern in a crowded academic environment where such data are needed to inform context-specific interventions. This study therefore assessed the bacterial contaminants present on mobile phones used by students of the University of Abuja, isolated and characterised the recovered organisms, and determined their antibiotic susceptibility patterns. Swab samples were collected from the mobile phones of twenty (20) undergraduate students and cultured on Nutrient Agar and MacConkey Agar. Isolates were identified by Gram staining and biochemical tests, and antibiotic susceptibility was determined by the disc diffusion method, interpreted using Clinical and Laboratory Standards Institute guidelines. Bacterial growth was observed on all 20 (100.0%) sampled phones on both media. Eight Gram-positive isolates were presumptively identified as *Bacillus* sp., *Enterococcus* sp., and *Staphylococcus* sp., while six Gram-negative isolates were presumptively identified as *Klebsiella* sp., *Escherichia* coli, *Enterobacter* sp. and *Shigella* sp. Complete resistance (100.0%) was recorded among Gram-positive isolates to ceftazidime, amoxicillin, and ciprofloxacin, and among Gram-negative isolates to ofloxacin, pefloxacin, and cephalexin. Gentamicin was the most effective antibiotic against both groups. These preliminary findings indicate that the sampled mobile phones harboured diverse bacterial populations, including isolates resistant to multiple antibiotic classes, suggesting that personal devices may warrant further attention as a potential contributor to antimicrobial resistance in this setting. The results support integrating mobile phone hygiene into routine public health practice and establish a baseline for future antimicrobial resistance surveillance on personal devices within comparable populations.

Introduction

Mobile phones have become essential devices in contemporary society, shaping how people communicate, access information, and carry out daily activities. Students are among the most active mobile phone users, relying on these devices for academic work, social interaction, online learning, financial transactions, and entertainment (Agboola & Sunday, 2020; Anele & Ogbuagu, 2025). This growing dependence has raised public health concerns due to the potential of mobile phones to harbour and transmit microorganisms. As objects in constant contact with the hands and face, mobile phones are widely recognised as fomites (inanimate objects) capable of supporting and transmitting pathogenic bacteria (Odiete et al., 2018; Bala et al., 2025).

Mobile phones are handled continuously across a wide range of environments (Almizwary et al., 2024), yet they are rarely cleaned or disinfected as routinely as other frequently touched personal items (Morubagal et al., 2017). The heat generated during use creates a favourable microenvironment for microbial survival and proliferation (Ugwu et al., 2021). Reported microbial loads on mobile phones have, in some studies, been found up to ten times exceeding those on recognised high-contamination surfaces such as toilet seats, inside of a user's shoe, or a toilet doorknob (Ibraheem, 2019; Almizwary et al., 2024).

Bacterial contamination of mobile phones has been documented across diverse populations and geographical settings, with reported prevalence typically exceeding 70%, depending on sampling approach, study population, and hygiene behaviour (Ahmad et al., 2021; Mushabati et al., 2021; Sadiq et al., 2021). Among student populations specifically, a study conducted in Ghana reported bacterial contamination on over 80% of sampled mobile phones (Olu-Taiwo et al., 2021), while comparable studies within Nigerian tertiary institutions have reported contamination rates above 60% (Algmati et al., 2024; Isibor et al., 2026).

The bacteria most frequently isolated from mobile phone surfaces include Gram-positive organisms such as *Staphylococcus aureus*, *Streptococcus* species, and Gram-positive bacilli, many of which form part of normal human skin flora but can cause infection under favourable conditions (Zakai et al., 2016; Erinle & Ajayi, 2022; Ezemba et al., 2022). Gram-negative organisms such as *Escherichia coli*, *Pseudomonas aeruginosa* and *Klebsiella* species are also commonly found (Bhumbla et al., 2016; Taha et al., 2026). The presence of *E. coli* in particular, is widely used as an indicator of faecal contamination and inadequate hand hygiene, and its detection on mobile phones has been linked to broader hygiene practices such as phone use during eating, after restroom visits, and after contact with contaminated surfaces (Moirangthem et al., 2026).

Growing evidence highlights that bacteria associated with mobile phones are not only diverse but increasingly antibiotic-resistant. Loyola et al. (2018) reported the isolation of antibiotic-resistant *Staphylococcus aureus* and *Pseudomonas aeruginosa* from mobile phones, with multidrug resistance observed against commonly used antibiotic classes. In densely populated academic environments, where students are in close contact and frequently share materials, personal devices may facilitate the community-level spread of antimicrobial-resistant organisms (Olsen et al., 2020; Olu-Taiwo et al., 2021).

While these findings collectively establish mobile phones as a recognised vehicle for bacterial contamination and antimicrobial resistance across various settings, data specific to University of Abuja students, combining bacterial isolation, characterisation, and antibiotic susceptibility profiling, appear limited. This gap is significant given that prevalence and resistance patterns are known to vary by institution, region, and population behaviour, making localised data necessary to inform context-specific interventions.

Despite extensive and continuous use, mobile phones are rarely cleaned or disinfected by students, who often handle them while eating, after handshakes, during laboratory sessions, and following restroom use without adequate hand hygiene (Lugova et al., 2025; Olaitan et al., 2025). Such practices increase the transfer of microorganisms from contaminated hands and surfaces onto mobile phones. The heat generated

during use and frequent storage in pockets or bags may further support microbial survival. Continuous handling of contaminated devices raises the risk of bacterial transmission among individuals, posing a public health concern in crowded academic settings where students interact closely and share materials and spaces.

This study aimed to assess the bacterial contaminants present on mobile phones used by students of the University of Abuja and to determine the antibiotic susceptibility pattern of the bacterial isolates.

Materials and methods

Study Design and Area

This study was a cross-sectional, laboratory-based investigation aimed at isolating, identifying, and determining the antibiotic susceptibility of bacteria contaminating mobile phones. The research was conducted at the University of Abuja Microbiology Laboratory, located on Mohammed Maccido Road, Airport Road, Abuja, Nigeria.

Study Population

The study population consisted of twenty (20) undergraduate students from various faculties of the University of Abuja, all of whom regularly used mobile phones. Participants were recruited through availability-based (convenience) sampling. Students who were present at the time of sampling and willing to participate were approached, until the target sample size of twenty (20) was reached. Verbal informed consent was obtained from all participants prior to sample collection, after they had been informed of the study's purpose and the voluntary and anonymous nature of their participation. No formal institutional ethical approval was sought because the study involved minimal-risk environmental sampling and did not collect personally identifiable information.

Given the preliminary scope of the study, a sample size of twenty (20) mobile phones was selected to provide baseline local data on mobile phone-associated bacterial contamination. Consequently, the findings should be interpreted as indicative of the sampled participants rather than generalised to the wider student population.

Sample Collection

Sterile cotton swabs moistened with normal saline were used to swab the surfaces of randomly selected students' mobile phones. The swabbed areas included the screen, back cover, and side buttons. Swabs were then placed into sterile containers and transported immediately to the laboratory for analysis.

Sterilisation of Materials

All glassware, pipettes, loops, and forceps used in the study were sterilised at 121°C in an autoclave for 15 minutes. Culture media and McCartney bottles were also sterilised before bacterial inoculation to prevent contamination during isolation and enumeration. All procedures were performed under sterile conditions to ensure the validity of the results.

Preparation of Culture Media

Culture media were prepared following the manufacturer's instructions. Nutrient Agar and MacConkey Agar (Titan Biotech Limited) were used, with aseptic conditions maintained throughout. Media were dissolved in distilled water, heated until fully dissolved, dispensed into appropriate containers, and autoclaved at 121°C for 15 minutes. Sterile Petri dishes were then filled with the molten media and allowed to solidify under aseptic conditions.

Sample Inoculation and Cultivation

Swab samples were directly inoculated onto prepared Nutrient Agar and MacConkey Agar plates. The plates were incubated in an inverted position at 37°C for 24 hours. After incubation, bacterial growth and colony morphology were examined. Distinct colonies were sub-cultured for purification, then identified using Gram staining and biochemical tests. Across the 20 sampled phones, a total of fourteen (14) morphologically distinct colony types were recovered and selected for identification (8 from Nutrient Agar, 6 from MacConkey Agar). Colonies that were morphologically indistinguishable from an isolate already selected from the same plate were not

separately characterised, to avoid redundant identification of what were judged to be the same organism.

Identification of Bacterial Isolates

Gram Staining

A clean glass slide was prepared, and a small drop of distilled water was placed on its surface using a sterile wire loop. A 24-hour-old bacterial colony was aseptically picked with a sterile loop and mixed thoroughly with the water to produce a thin smear. The smear was air-dried and heat-fixed by gently passing the slide over a Bunsen burner flame three times. The fixed smear was flooded with crystal violet stain for 60 seconds and rinsed gently with clean water. Gram's iodine was then applied for 30 seconds as a mordant before rinsing again with water. Decolourisation was carried out with acetone, which was immediately washed off with water to prevent over-decolourisation. The smear was counterstained with safranin for 60 seconds and rinsed gently with water. The stained slide was air-dried, and two drops of immersion oil were added before microscopic examination using the 100X objective. Bacteria that appeared purple to blue were interpreted as Gram-positive, while those that appeared pink to red were interpreted as Gram-negative.

Biochemical Characterisation

Identification was based on Gram reaction, colonial morphology, and the five-test biochemical panel described below. Given the limited biochemical panel used, all identifications in this study are presumptive at the genus/species level.

Catalase Test

Two drops of hydrogen peroxide were placed on a clean glass slide. A small portion of the bacterial colony was aseptically transferred into the reagent using a sterile wire loop. The immediate appearance of effervescence indicated a positive catalase reaction, while the absence of bubble formation was recorded as a negative result (Al-Joda & Jasim, 2021).

Oxidase Test

An oxidase reagent, tetramethyl-p-phenylenediamine, was applied to a bacterial colony impregnated onto a filter paper. A rapid colour change to dark purple or blue within 10 seconds indicated a positive reaction, while no colour change signified a negative result (Al-Joda & Jasim, 2021).

Citrate Utilisation Test

Simmons citrate agar was prepared according to the manufacturer's instructions and dispensed as slants in bijou bottles. Test organisms were inoculated onto the agar surface using a sterile wire loop and incubated at 35°C for up to 48 hours. A colour change from green to blue indicated a positive citrate utilisation reaction, while the absence of colour change indicated a negative result (Al-Joda & Jasim, 2021).

Indole Test

Test organisms were inoculated into sterile tryptone water and incubated at 37°C. Following incubation, Kovac's reagent was gently added to the medium. The formation of a red ring at the surface of the broth indicated a positive indole reaction, while no colour change was interpreted as a negative result (Al-Joda & Jasim, 2021).

Coagulase Test

A bacterial colony was emulsified in a drop of distilled water on a clean, grease-free glass slide. A loopful of plasma was added to the suspension and mixed gently. Visible clumping within 10 seconds was recorded as a positive coagulase reaction (Al-Joda & Jasim, 2021).

Antibiotic Susceptibility Testing

Pure cultures were suspended in sterile normal saline and adjusted to match the turbidity of a 0.5 McFarland standard to achieve a uniform inoculum density. The standardised suspension was evenly spread over the surface of Mueller–Hinton agar plates using sterile cotton swabs to obtain a uniform bacterial lawn. Commercially prepared antibiotic discs (Optun Laboratories Nig. LTD) were aseptically placed onto the inoculated agar surface using sterile forceps. For Gram-positive bacteria, the antibiotics tested included: Rifampicin (20 μg), Ceftazidime (30 μg), Streptomycin (30 μg), Azithromycin (15 μg), Amoxicillin (20 μg), Ciprofloxacin (10 μg), Erythromycin (30 μg),

Levofloxacin (20 µg), Gentamicin (10 µg), Cefuroxime (30 µg). For Gram-negative bacteria, the antibiotics tested included: Ofloxacin (10 µg), Augmentin (30 µg), Pefloxacin (10 µg), Ceftazidime (30 µg), Gentamicin (10 µg), Ciprofloxacin (10 µg), Cephalexin (10 µg), Ceftriaxone (30 µg), Streptomycin (30 µg), Cefuroxime (30 µg). Plates were incubated aerobically at 35°C for 24 hours. After incubation, the zones of inhibition surrounding each antibiotic disc were measured in millimetres using a transparent ruler. Susceptibility of the isolates was interpreted as susceptible, intermediate, or resistant based on the Clinical and Laboratory Standards Institute (CLSI 2025) guidelines. Zone-diameter interpretive breakpoints were applied, using the interpretive tables applicable to Enterobacterales for Gram-negative isolates and to *Staphylococcus* sp. And other Gram-positive organisms for Gram-positive isolates, as appropriate to each identified genus. The descriptive resistance-level bands used in this study (Negligible, Low, Moderate, High, Very High) are an author-defined convention adopted for ease of tabular interpretation and are not part of the CLSI M100 framework.

Statistical Analysis

This study was purely descriptive in nature. Percentages were calculated as the number of isolates showing a given result (resistant, intermediate, or susceptible) for a given antibiotic, divided by the total number of isolates tested within that Gram-reaction group, multiplied by 100.

Results and Discussions

Results

Growth of Bacterial Isolates on Nutrient Agar (NA) and MacConkey Agar (MAC) Among Mobile Phone Swab Samples (N = 20)

Among mobile phone swab samples (N = 20) growth was observed in all 20 (100.0%) sampled mobile phones on both Nutrient Agar and MacConkey Agar (Table 1).

Table 1: Bacterial Growth Patterns on Nutrient and MacConkey Agar from Mobile Phone Swabs (N = 20)

Sample Code	Growth on NA	Growth on MAC
S1	+	+
S2	+	+
S3	+	+
S4	+	+
S5	+	+
S6	+	+
S7	+	+
S8	+	+
S9	+	+
S10	+	+
S11	+	+
S12	+	+
S13	+	+
S14	+	+
S15	+	+
S16	+	+
S17	+	+
S18	+	+
S19	+	+
S20	+	+

Key: += Growth observed; – = No growth observed

Gram Reaction and Cultural Characteristics of Bacterial Isolates from Nutrient Agar (NA) Plates

Eight morphologically distinct colonies selected from Nutrient Agar plates were all Gram-positive, comprising both rod-shaped and cocci forms. Colony size ranged from small to large, shape was circular or irregular, and elevation was flat, convex, or raised. Surface appearance ranged from moist, mucoid, and slimy to dry, with pigmentation recorded as milky, cream, whitish, yellow, or colourless (Table 2).

Gram Reaction and Cultural Characteristics of Bacterial Isolates from MacConkey Agar (MAC) Plates

Six morphologically distinct colonies selected from MacConkey Agar plates were all Gram-negative rods. Colony shapes were circular or irregular, with

elevations recorded as flat, convex, or raised, and colony appearance was mostly mucoid, moist, or dry, with pigmentation recorded as pink, cream, yellow, or white (Table 3).

Biochemical Characteristics and Presumptive Identification of Bacterial Isolates

Among the Gram-positive isolates, six rod-shaped isolates (S1NAA, S1NAB, S2NAC, S3NAE, S3NAF, and S4NAH) were catalase-positive and citrate-positive and were identified as *Bacillus* sp., one cocci-shaped isolate (S2NAD) was catalase-negative and citrate-negative and was identified as *Enterococcus* sp., and one cocci-shaped isolate (S4NAG) was catalase-positive, citrate-positive, and coagulase-negative and was identified as *Staphylococcus* sp. Among the Gram-negative isolates, S1MA and S3MC were catalase-positive and citrate-positive and were identified as *Klebsiella* sp.; S2MB was catalase-positive, indole-positive, and citrate-negative and was identified as *Escherichia coli*; S5MD was identified as *Enterobacter* sp.; S6ME returned a catalase-negative result, which is atypical for the family Enterobacteriaceae and inconsistent with confident assignment to any other genus within the biochemical panel used. Rather than assigning a genus-level identity that the data did not support, this isolate was reported as an unidentified Gram-negative rod pending further confirmatory testing.; and S7MF was catalase-positive and citrate-negative and was identified as presumptive *Shigella* sp. (Table 4).

Antibiotic Susceptibility Pattern of Gram-Positive Isolates

Complete resistance (100.0%) was recorded against ceftazidime, amoxicillin, and ciprofloxacin among the Gram-positive isolates. High resistance was recorded against azithromycin and cefuroxime (75.0% each), and against erythromycin and levofloxacin (62.5% each). Resistance of 50.0% was recorded against rifampicin, and 37.5% against streptomycin. The lowest resistance was recorded against gentamicin (25.0%), which correspondingly showed the highest susceptibility rate (75.0%) (Table 5).

Antibiotic Susceptibility Pattern of Gram-Negative Isolates

Complete resistance (100.0%) was recorded against ofloxacin, pefloxacin, and cephalexin among the Gram-negative isolates. High resistance was recorded against augmentin, ceftazidime, and cefuroxime (83.3% each), and against ceftriaxone (66.7%). Resistance of 50.0% was recorded against streptomycin and ciprofloxacin. The lowest resistance was recorded against gentamicin (16.7%), which correspondingly showed the highest susceptibility rate (50.0%) (Table 6).

Table 2: Gram Staining and Cultural Characteristics of Bacterial Isolates from Nutrient Agar (NA) Plates

Isolate Code	GR	CM	Colony Size	Shape	Margin	Elevation	Surface Appearance	Opacity	Pigmentation
S1NAA	+	Rod	Medium	Circular	Entire	Raised	Mucoid, moist	Translucent	Milky
S1NAB	+	Rod	Small	Circular	Entire	Convex	Slimy	Opaque	Cream
S2NAC	+	Rod	Large	Irregular	Undulate	Flat	Moist	Opaque	Whitish
S2NAD	+	Cocci (Small)	Medium	Circular	Entire	Flat	Moist	Opaque	Cream
S3NAE	+	Rod	Medium	Circular	Entire	Convex	Dry	Opaque	Yellow
S3NAF	+	Rod	Small	Circular	Entire	Convex	Mucoid	Opaque	White
S4NAG	+	Cocci	Medium	Irregular	Lobate	Raised	Dry	Translucent	Colourless
S4NAH	+	Rod	Medium	Circular	Entire	Convex	Moist	Opaque	Milky

Keys: GR = Gram Reaction; CM = Cell Morphology

Table 3: Gram Staining and Cultural Characteristics of Bacterial Isolates from MacConkey Agar (MAC) Plates

Isolate Code	GR	CM	Colony Size	Shape	Margin	Elevation	Surface Appearance	Opacity	Pigmentation
S1MA	-	Rod	Medium	Circular	Entire	Raised	Dry	Translucent	Pink
S2MB	-	Rod	Small	Circular	Entire	Convex	Mucoid	Opaque	Cream
S3MC	-	Rod	Large	Irregular	Undulate	Flat	Mucoid	Opaque	Yellow
S5MD	-	Rod	Medium	Circular	Entire	Flat	Moist	Opaque	Cream
S6ME	-	Rod	Medium	Circular	Entire	Convex	Slimy	Opaque	Yellow
S7MF	-	Rod	Small	Circular	Entire	Convex	Mucoid	Opaque	White

Keys: GR=Gram Reaction; CM= Cell Morphology

Table 4: Biochemical Characteristics and Presumptive Identification of Bacterial Isolates

Isolate Code	GR	CM	Catalase	Oxidase	Indole	Citrate	Coagulase	Presumptive Identity
S1NAA	+	Rod	+	-	-	+	-	*Bacillus* sp.
S1NAB	+	Rod	+	-	-	+	-	*Bacillus* sp.
S2NAC	+	Rod	+	-	+	+	-	*Bacillus* sp.
S2NAD	+	Cocci (Small)	-	-	-	-	-	*Enterococcus* sp..
S3NAE	+	Rod	+	-	-	+	-	*Bacillus* sp.
S3NAF	+	Rod	+	-	-	+	-	*Bacillus* sp.
S4NAG	+	Cocci	+	-	-	+	-	*Staphylococcus* sp.
S4NAH	+	Rod	+	-	-	+	-	*Bacillus* sp.
S1MA	-	Rod	+	-	-	+	-	*Klebsiella* sp.
S2MB	-	Rod	+	-	+	-	-	*Escherichia coli*
S3MC	-	Rod	+	-	-	+	-	*Klebsiella* sp.
S5MD	-	Rod	+	-	-	+	-	*Enterobacter sp.*
S6ME	-	Rod	-	-	-	+	-	Unidentified
S7MF	-	Rod	+	-	-	-	-	*Shigella* sp.

Keys: GR=Gram Reaction; CM= Cell Morphology, + = Positive; – = Negative

Table 5: Antimicrobial Resistance (AMR) Pattern of Gram-Positive Bacterial Isolates (n = 8)

Antibiotic Class	Antibiotic Tested (Disc Potency)	Resistant n (%)	Intermediate n (%)	Susceptible n (%)	Degree of Resistance
Rifamycins	Rifampicin (20 μg)	4 (50.0)	1 (12.5)	3 (37.5)	High
Cephalosporins	Ceftazidime (30 μg)	8 (100.0)	0 (0.0)	0 (0.0)	Very High
Aminoglycosides	Streptomycin (30 μg)	3 (37.5)	4 (50.0)	1 (12.5)	Moderate
Macrolides	Azithromycin (15 μg)	6 (75.0)	2 (25.0)	0 (0.0)	Very High
Penicillins	Amoxicillin (20 μg)	8 (100.0)	0 (0.0)	0 (0.0)	Very High
Fluoroquinolones	Ciprofloxacin (10 μg)	8 (100.0)	0 (0.0)	0 (0.0)	Very High
Macrolides	Erythromycin (30 μg)	5 (62.5)	2 (25.0)	1 (12.5)	High
Fluoroquinolones	Levofloxacin (20 μg)	5 (62.5)	3 (37.5)	0 (0.0)	High
Aminoglycosides	Gentamicin (10 μg)	2 (25.0)	0 (0.0)	6 (75.0)	Moderate
Cephalosporins	Cefuroxime (30 μg)	6 (75.0)	1 (12.5)	1 (12.5)	Very High

Footnote: Degree of resistance was classified as: Negligible (0%), Low (1–20%), Moderate (21–49%), High (50–69%), and Very High (≥70%) based on the percentage of resistant isolates.

Table 6: Antimicrobial Resistance (AMR) Pattern of Gram-Negative Bacterial Isolates (n = 6)

Antibiotic Class	Antibiotic Tested (Disc Potency)	Number Resistant n (%)	Number Intermediate n (%)	Number Susceptible n (%)	Degree of Resistance
Fluoroquinolones	Ofloxacin (10 μg)	6 (100.0)	0 (0.0)	0 (0.0)	Very High
Penicillins	Augmentin (30 μg)	5 (83.3)	0 (0.0)	1 (16.7)	Very High
Fluoroquinolones	Pefloxacin (10 μg)	6 (100.0)	0 (0.0)	0 (0.0)	Very High
Cephalosporins	Ceftazidime (30 μg)	5 (83.3)	0 (0.0)	1 (16.7)	Very High
Aminoglycosides	Gentamicin (10 μg)	1 (16.7)	2 (33.3)	3 (50.0)	Low
Fluoroquinolones	Ciprofloxacin (10 μg)	3 (50.0)	0 (0.0)	3 (50.0)	High
Cephalosporins	Cephalexin (10 μg)	6 (100.0)	0 (0.0)	0 (0.0)	Very High
Cephalosporins	Ceftriaxone (30 μg)	4 (66.7)	0 (0.0)	2 (33.3)	High
Aminoglycosides	Streptomycin (30 μg)	3 (50.0)	3 (50.0)	0 (0.0)	High
Cephalosporins	Cefuroxime (30 μg)	5 (83.3)	1 (16.7)	0 (0.0)	Very High

Footnote: Degree of resistance was classified as: Negligible (0%), Low (1–20%), Moderate (21–49%), High (50–69%), and Very High (≥70%) based on the percentage of resistant isolates.

Discussion

Mobile phones are among the most frequently handled personal items in daily human activities, yet they are rarely subjected to routine cleaning or disinfection. This neglect makes them highly suitable surfaces for microbial persistence and transmission. This study revealed a 100% contamination rate, with all sampled phones showing growth on both Nutrient Agar and MacConkey Agar. This finding indicates that every sampled phone served as a potential contributor to the spread of cultivable bacteria, reflecting widespread exposure and, potentially, inadequate hygiene practices among users.

This universal bacterial growth is consistent with the findings of Galazzi et al. (2019), who reported that all the mobile phones sampled in their study of healthcare workers in a tertiary-level Italian intensive care unit were positive for bacteria. Similarly, Al-Abdalall (2010) and Selim & Abaza (2015) documented full contamination of mobile devices in a healthcare setting and other populations, attributing this to continuous handling without proper sanitation. The present study extends this evidence to a non-clinical population, suggesting that mobile phone contamination is not limited to healthcare settings but is a broader phenomenon among general device users.

Just like in a study conducted by Mushabati et al. (2021), *Staphylococcus* spp. and *Bacillus* spp. are frequently isolated from mobile phones. *Staphylococcus* spp. may be introduced from human skin during routine handling, as it is frequently carried by healthy individuals on the skin and mucous membranes, indicating that phones can serve as temporary contributors to the spread of these organisms.

In contrast, the isolation of enteric organisms such as *E. coli*, *Klebsiella* sp., *Enterobacter* sp., and presumptive *Shigella* sp. is less readily explained by normal flora transfer; previous studies have linked such organisms to external faecal-oral contamination arising from inadequate hand hygiene (Shahaby et al., 2012), although hand hygiene practices were not directly assessed among participants in the present study.

The detection of coliform organisms such as *E. coli* is notable from a public health standpoint, as it is a recognised indicator organism for faecal contamination (Some et al., 2021). Its presence on mobile phones is consistent with reports by Edrees & Al-Awar (2020), who associated its detection with poor personal hygiene or faecal contamination.

Shigella spp. are characterised by complex epidemiological and pathological features, and

gastrointestinal infections caused by these organisms continue to rise. With increasing morbidity and mortality globally, *Shigella* spp. has become a major public health concern. The isolation of *Shigella* sp. from mobile phones is therefore of particular concern, given its low infectious dose and ability to cause dysentery following minimal exposure (Bakhshi et al., 2018).

Clinically, the organisms identified in this study are associated with a range of infections: *Staphylococcus* spp. with skin, wound, and device-associated infections; *Bacillus* spp. with opportunistic infections in immunocompromised individuals; and *E. coli*, *Klebsiella* spp., and *Enterobacter* spp. with urinary tract infections, septicaemia, and hospital-acquired infections. These associations are consistent with reports that mobile phones in community and healthcare settings are frequently contaminated with potentially pathogenic bacteria, including staphylococci, coliforms, and multidrug-resistant organisms. Taken together, these findings support the view that mobile phones can act as fomites that bridge normal skin microbiota and pathogenic enteric organisms between users and their environment, thereby contributing to the potential transmission of both community- and healthcare-associated infections (Ulger et al., 2015; Debnath et al., 2018; Ikiriko et al., 2026).

The antibiotic susceptibility results indicate that a substantial proportion of isolates were resistant to the antibiotics tested. In both Gram-negative and Gram-positive groups, resistance was concentrated among penicillins, fluoroquinolones and cephalosporins, three antibiotic classes that are widely used in both clinical and self-medication settings in Nigeria, which has been suggested in Sekoni et al. (2022) and Amuzie et al. (2024) as a contributing factor to elevated antibiotic resistance, although antibiotic-use behaviour among phone owners was not directly assessed in this study. This suggests that mobile phones may also function as a potential contributor to the spread of antimicrobial-resistant bacteria, extending their public health relevance beyond simple contamination to a potential role in the community-level dissemination of resistant organisms.

The high resistance to penicillins observed in this study aligns with reports from African healthcare settings, where *E. coli* and *Klebsiella pneumoniae* exhibited resistance to penicillin-class antibiotics in ≥80% of isolates (Monk et al., 2024). Similarly, the elevated fluoroquinolone resistance documented here is consistent with findings from both clinical and environmental contexts, where fluoroquinolone-resistant *E. coli* has been isolated from diverse sources, including clinical specimens and environmental samples (Amábile-Cuevas et al., 2010). Furthermore, the substantial cephalosporin resistance observed in this study corroborates clinical reports indicating that more than half of bacterial isolates demonstrate resistance to third-generation cephalosporins such as ceftriaxone and ceftazidime (Gashe et al., 2018).

Limitations of the Study

This study has several limitations that should be considered when interpreting the findings.

The sample size was relatively small (20 mobile phones) and sampling was restricted to a single institution (University of Abuja), limiting the generalisability of the findings to the wider student population and other settings. Sampling was restricted to a single institution (University of Abuja), so the results may not reflect contamination patterns in other settings.

Bacterial identification relied solely on Gram staining and a limited panel of five conventional biochemical tests rather than molecular methods (e.g., 16S rRNA sequencing or PCR-based confirmation). This limited the precision of bacterial identification, as demonstrated by the presumptive identification of isolate S7MF as *Shigella* sp. and the inability to resolve isolate S6ME to genus level. Further biochemical, serological, or molecular testing would be required to confirm these identifications. The study did not collect data on participants' phone-cleaning habits, hand hygiene practices, or environmental exposure, which limits the ability to explain observed variation in contamination intensity.

Future Research Directions

Future studies could build on these findings by incorporating molecular identification techniques

to confirm species-level identity, expanding sample size and institutional scope to improve generalizability, and correlating contamination levels with self-reported hygiene behaviour and phone-cleaning frequency. Further investigation into the genetic basis of the antimicrobial resistance observed in this study, including screening for specific resistance genes, would also help clarify the role of mobile phones in the community spread of resistant organisms.

Conclusion

This study provides evidence that mobile phones can harbour diverse bacterial populations, encompassing both commensal skin flora and enteric organisms of public health concern. Beyond confirming widespread contamination, the findings demonstrate that resident bacteria on these devices carry a substantial burden of antibiotic resistance, positioning mobile phones as an under recognised vehicle in the broader antimicrobial resistance landscape rather than a mere hygienic nuisance.

These results contribute to the growing body of evidence linking personal electronic devices to microbial transmission and antimicrobial resistance surveillance, and reinforce the relevance of routine fomite screening as a complementary tool in community-level infection control. The findings support integrating mobile phone hygiene into routine personal and public health practices, particularly in institutional settings such as universities, where devices are frequently shared, borrowed, or used in proximity to food and communal surfaces. Furthermore, this study establishes a baseline for future surveillance of antimicrobial resistance on personal devices within this and comparable populations.

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Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of the paper.

Author Contribution

The authors confirm contribution to the paper as follows: study design: Barwa J, Oti S. C; data collection: Oti S. C; analysis and interpretation of results: Barwa J, Oti S. C; draft manuscript preparation: Barwa J, Oti S. C. All authors reviewed the results and approved the final version of the manuscript

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