Natural Resources for Human Health
eISSN: 2583-1194

Original Research

Received 22 May 2026
Revised 13 July 2026
Accepted 26 July 2026

Natural Resources for Human Health 2026, Vol. 6 (13s): 418–433

KEYWORDS:
bacterial contamination; mobile phones; healthcare workers; healthcare-associated infection; antimicrobial resistance; fomite

Bacterial Contamination of Mobile Phones used by Healthcare Workers: A Cross-Sectional Microbiological Study

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ABSTRACT: Mobile phones are widely used tools in healthcare but can also function as fomites in clinical environments. This cross-sectional study evaluated bacterial contamination, antimicrobial resistance, and behavioral factors linked to contamination on mobile phones used by healthcare workers (HCWs) at a tertiary-care hospital. Two hundred phones from the Intensive Care Unit (ICU), medical and surgical units, and Outpatient Department (OPD) were sampled. Swab isolates were cultured, biochemically identified, evaluated for antimicrobial susceptibility using disk diffusion, and selectively examined by polymerase chain reaction (PCR) targeting mecA, blaCTX-M, blaTEM, blaSHV, blaOXA-23-like, and blaNDM. Of 200 phones, 174 (87.0%) yielded bacterial growth; 18 (10.3%) positive phones were polymicrobial, yielding 192 isolates. Coagulase-negative staphylococci (44.8%) predominated, followed by Staphylococcus aureus (20.3%), Escherichia coli (9.4%), Klebsiella pneumoniae (7.3%), Pseudomonas aeruginosa (6.3%), and Acinetobacter baumannii (4.2%). Thirteen of 39 S. aureus isolates were phenotypically methicillin resistant, and mecA was detected in 12/13 (92.3%). Among Enterobacterales, 13/32 (40.6%) were ESBL-positive by the double-disk synergy test; four additional DDST-positive non-fermenting isolates were treated as exploratory. blaCTX-M was the most frequently detected targeted ESBL gene among the 17 DDST-positive

Natural Resources for Human Health
eISSN: 2583-1194

gram-negative isolates (82.4%), and blaOXA-23-like was detected in all three meropenem-non-susceptible A. baumannii isolates. In the adjusted behavioral model, never cleaning the phone (AOR 4.6, 95% CI 1.5-13.9) and phone use during patient care (AOR 3.0, 95% CI 1.2-7.4) remained statistically significant; phone-case use showed a borderline association (AOR 2.5, 95% CI 1.0-6.4). HCW mobile phones were commonly contaminated and harbored clinically important resistant organisms. The findings support evidence-based phone-hygiene guidance and prospective evaluation of standardized decontamination practices.

1. INTRODUCTION

Healthcare-associated infections (HAIs) remain a major patient-safety challenge worldwide, contributing to considerable mortality, longer hospital stays, and higher healthcare costs (Dhayhi et al., 2023). While conventional infection-control measures emphasize hand hygiene, environmental surfaces, and aseptic techniques, mobile phones have emerged as a largely neglected fomite in clinical settings (De Groote et al., 2022).

The adoption of smart devices in health care has expanded rapidly and has become almost ubiquitous among health care professionals (HCPs). Many HCPs access and manage health records on the go, consult drug resources, and communicate and coordinate care (Mushabati et al., 2021). Like most technologies, mobile smart devices offer benefits but also create opportunities for cross-contamination because they are repeatedly touched and may contact multiple hands and environmental surfaces. Because HCW hands are an important route of pathogen transfer in hospitals, frequent hand-phone contact may contribute to contamination cycles.

Bacterial load is a concern for HCW mobile devices in various global locations, such as Asia, the Pacific, Europe, and the Middle East, in addition to Africa. A systematic analysis of 39 studies revealed Staphylococcus aureus was present in 66.7% of studies, and CoNS was present in 48.7% of studies. A more recent analysis of 26 studies focused on the African region estimated a pooled prevalence of contamination at 84.5% (Zenbaba et al., 2023). Of greater clinical concern is the presence of multidrug-resistant organisms including methicillin-resistant S. aureus (MRSA), extended-spectrum beta-lactamase (ESBL)-producing Enterobacterales, and carbapenem-resistant organisms on these devices (Cavari et al., 2016; Qadi et al., 2021; Tännhäuser et al., 2022).

The "cyclic contamination" model by Ulger et al. (2015) expands on how pathogens transfer from patients and hospital surroundings to health care workers' (HCWs') hands, phones, and then back to patients' hands via HCWs' hands. This cycle of bidirectional contamination is facilitated by the surface of phones, which becomes warm when in contact with skin, hence becoming favorable to the survival of microbes, coupled with a high frequency of contact and almost no routine disinfection (Chang et al., 2017).

Despite the increasing evidence, many countries have not developed institutional policies, and most surveys of phone contamination rely on phenotypic culture and susceptibility testing without molecular confirmation of selected resistance genes (Zenbaba et al., 2023). The present study was therefore designed to answer three questions: (1) what are the prevalence, species distribution, and departmental patterns of bacterial contamination of HCW mobile phones at a tertiary-care hospital; (2) which phenotypic and genotypic antimicrobial resistance determinants are detected among the contaminating organisms; and (3) which modifiable behavioral factors are associated with contamination? By pairing conventional microbiology with PCR-based resistance-gene detection and behavioral association modeling, the study aims to provide an evidence base for targeted infection-prevention interventions.

2. MATERIALS AND METHODS

2.1. Study design and setting

A descriptive cross-sectional study was carried out over a six-month period (January-June 2025) at a 600-bed tertiary-care teaching hospital in Baghdad, Iraq. The study was conducted in accordance with the Declaration of Helsinki and reported in line with the STROBE (Strengthening the Reporting of Observational Studies in Epidemiology) guidelines. Ethical approval

was granted by [AUTHOR TO INSERT APPROVING ETHICS COMMITTEE AND APPROVAL NUMBER]. Written informed consent was provided by all participants.

2.2. Study population and sampling

Healthcare workers were eligible if they were employed in direct patient care roles (physicians, nurses, laboratory technicians) or supporting roles (administrative staff, pharmacy staff), owned a personal mobile phone, and consented to participate. HCWs on leave, students on rotation, or those who declined were excluded. Administrative and pharmacy staff were pooled into a single supporting-role category because both groups share comparatively limited direct patient contact and their combined number (n = 30) was too small to support separate analysis; this grouping is acknowledged in the limitations.

The minimum required sample size was 82 phones, estimated using the single-population proportion formula $n = Z2p(1 - p)/d2$, assuming a contamination prevalence of 94.4% reported by Ulger et al. (2015), a 95% confidence level (Z = 1.96), with an absolute precision of 0.05; 200 phones were enrolled to permit subgroup analyses by department and profession. Of 232 eligible healthcare workers approached, 200 (86.2%) consented and were enrolled using department-based quota sampling. Quotas were set according to departmental size, and HCWs were recruited consecutively during shift rounds until each quota was reached in the Outpatient Department (OPD), medical wards, surgical wards, and Intensive Care Unit (ICU). The quotas were 60 HCWs from the ICU, 50 from surgical wards, 50 from medical wards, and 40 from the OPD.

Sociodemographic data and mobile phone use behaviors were collected through a pretested, self-administered questionnaire evaluating frequency of phone use during patient care, phone cleaning habits, use of protective covers, hand hygiene after phone use, and phone use in the bathroom. The questionnaire was developed following a review of the available literature, pretested on a convenience pilot of 15 HCWs from departments outside the sampling frame, and refined for clarity of wording; pilot responses were excluded from the final analysis. Laboratory personnel processing the samples were blinded to participants' questionnaire responses and departmental assignment to minimize measurement bias.

2.3. Sample collection

Swab samples were collected under aseptic conditions. Each phone was swabbed over the entire front screen, back surface, and side edges with sterile cotton-tipped applicators moistened beforehand with 0.9% normal saline, following previously validated methods (Punj et al., 2022; Tännhäuser et al., 2022). Because the rear surface of smartphones has been reported to be contaminated even more frequently than the touchscreen (Kuriyama et al., 2021), the entire device screen, back surface, and side edges was sampled. Swabs were promptly transported to the clinical microbiology laboratory in Stuart's transport medium and processed within two hours. **An illustrative image of mobile-phone handling is provided in Appendix Figure A1.**

2.4. Bacteriological analysis

Swabs were plated onto blood agar (5% sheep blood), MacConkey agar, mannitol salt agar (MSA), and chocolate agar plates. Plates were aerobically incubated at 37 °C for 24-48 hours. Colony morphology, Gram staining, catalase and coagulase tests were performed for initial characterization. Final species identification relied on standard biochemical tests and, when available, the VITEK 2 automated system (bioMérieux, Marcy-l'Étoile, France). Staphylococcus aureus was verified by the tube coagulase test and DNase activity. Environmental commensals of low clinical significance were recorded as "other organisms" and identified to genus level only (see Table 3 note).

2.5. Antimicrobial susceptibility testing

Antibiotic susceptibility testing was carried out using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar following the Clinical and Laboratory Standards Institute document M100, 33rd edition (CLSI, 2023). Antibiotics tested included: oxacillin (1 ug), ampicillin (10 ug), ciprofloxacin (5 ug), gentamicin (10 ug), tetracycline (30 ug), erythromycin (15 ug), trimethoprim-sulfamethoxazole (1.25/23.75 ug), vancomycin (30 ug), imipenem (10 ug), ceftazidime (30 ug), and meropenem (10 ug). Vancomycin susceptibility was assessed by disk diffusion only, in line with the study protocol; MIC-based screening for VISA/VRSA was not performed. Colistin (polymyxin B) susceptibility was not tested for A. baumannii isolates because disk diffusion is unreliable for polymyxins and broth microdilution was not available at the study site; this omission is acknowledged as a limitation.

Phenotypic methicillin resistance in S. aureus was determined by oxacillin disk diffusion with cefoxitin (30 ug) disk screening. ESBL production was evaluated with the double-disk synergy test (DDST) using cefotaxime (30 ug) and ceftazidime (30 ug) disks alone and combined with clavulanic acid (10 ug), with a ≥5 mm increase in inhibition zone used as the phenotypic criterion (CLSI, 2023; Araya et al., 2021). The DDST is established for ESBL detection in Enterobacterales but has inconsistent performance in non-fermenting bacilli; therefore, DDST-positive findings in P. aeruginosa and A. baumannii (two isolates each) were treated as exploratory and interpreted separately from the Enterobacterales findings in Section 3.6.

2.6. Statistical analysis

Data were entered twice and verified against original laboratory records before analysis using IBM SPSS Statistics version 29.0 (IBM Corp., Armonk, NY, USA). Categorical variables were summarized using frequencies and percentages and compared using the Pearson chi-square test or Fisher's exact test when expected cell counts were below five. Questionnaire and laboratory records were complete for all 200 participants, so no missing-data methods were required; isolate-level analyses (Tables 3-8) were based on the 192 confirmed isolates. For the behavioral association model, candidate behavioral variables with a bivariate p value below 0.20 were included in a multivariable binary logistic regression model with the enter method, with culture status (positive versus negative) as the dependent variable. Results are presented as crude odds ratios (ORs) and adjusted odds ratios (AORs) along with 95% confidence intervals (CIs). Reference categories were prespecified for each categorical predictor (cleaning frequency: at least weekly cleaning; all binary predictors: absence of the behavior). Model calibration was evaluated using the Hosmer-Lemeshow test and multicollinearity with variance inflation factors. Because bacterial contamination was common (87.0%), ORs were interpreted as odds-based measures of association and not as risk ratios. A two-sided p value below 0.05 was regarded as statistically significant.

2.7. Molecular detection of antimicrobial resistance genes by PCR

To further characterize the phenotypic resistance findings, a subset of clinically significant isolates underwent polymerase chain reaction (PCR)-based molecular screening for selected resistance determinants. All S. aureus isolates phenotypically classified as methicillin resistant by oxacillin/cefoxitin testing (n = 13) were screened for mecA. All 17 gram-negative isolates that were DDST-positive were screened by PCR for blaCTX-M, blaTEM, and blaSHV; findings from P. aeruginosa and A. baumannii were considered exploratory because DDST is not validated for ESBL confirmation in these non-fermenters. A. baumannii isolates demonstrating non-susceptibility to meropenem (n = 3) were additionally screened for blaOXA-23-like and blaNDM.

Bacterial genomic DNA was extracted from pure 18-24-hour cultures with a commercial genomic DNA extraction kit following the manufacturer's instructions, preceded by a boiling-lysis step (95 °C for 10 minutes before centrifugation) for crude template preparation. DNA concentration and purity were verified by spectrophotometry (NanoDrop) prior to amplification, and extracted DNA was kept at −20 °C until use.

PCR assays were conducted in a final reaction volume of 25 uL containing template DNA (2 uL), gene-specific primer pairs adapted from the cited source protocols, a ready-to-use PCR master mix comprising Taq DNA polymerase, dNTPs and MgCl2, and nuclease-free water. Amplification conditions followed the corresponding published protocols, with gene-specific annealing temperatures summarized in Supplementary Table S1. Reference strains S. aureus ATCC 43300 (mecA-positive), K. pneumoniae ATCC 700603 (blaSHV-positive), and E. coli ATCC 25922 (pan-susceptible) served as documented assay controls. Amplification products were separated by agarose gel electrophoresis, viewed under UV transillumination, and sized against a 100 bp DNA ladder; a band of the expected amplicon size (Supplementary Table S1) was considered positive for the orresponding target. Primer sequences and assay conditions were adapted from previously published protocols (Oluduro et al., 2023; Pishtiwan and Khadija, 2019; Jalil Alawi et al., 2025).

Supplementary Table S1. Target resistance genes, amplicon sizes, annealing temperatures, and source protocols used for molecular screening

Target gene	Resistance mechanism detected	Amplicon size (bp)	Annealing temp. (°C)	Reference
mecA	Methicillin/oxacillin resistance (altered PBP2a) - MRSA confirmation	533	55	Oluduro et al., 2023

Target gene	Resistance mechanism detected	Amplicon size (bp)	Annealing temp. (°C)	Reference
*bla*CTX-M	ESBL production (CTX-M group)	593	58	Pishtiwan and Khadija, 2019
*bla*TEM	ESBL production (TEM-type)	516	54	Pishtiwan and Khadija, 2019
*bla*SHV	ESBL production (SHV-type)	392	54	Pishtiwan and Khadija, 2019
*bla*OXA-23-like	Carbapenemase - Ambler class D oxacillinase	501	56	Jalil Alawi et al., 2025
*bla*NDM	Carbapenemase - Ambler class B metallo-b-lactamase	621	56	Jalil Alawi et al., 2025

Note: PBP2a = penicillin-binding protein 2a; ESBL = extended-spectrum beta-lactamase; MRSA = methicillin-resistant Staphylococcus aureus. References indicate the source protocols from which primer sequences and assay conditions were adapted; the table outlines target genes, expected amplicon sizes, annealing temperatures, and source references.

3. RESULTS AND DISCUSSION

3.1. Overall contamination rate

The median age among the 200 healthcare workers was 31 years (IQR 27-39), and 108 (54%) were female. Of the 200 mobile phones assessed, 174 (87.0%) showed bacterial growth. This prevalence was comparable with reports from Saudi Arabia (81.1%; Dhayhi et al., 2023), Zambia (79%; Mushabati et al., 2021), and Germany (99.3%; Tännhäuser et al., 2022), and was similar to the pooled prevalence of 84.5% (95% CI 81.7-87.4) reported across African studies (Zenbaba et al., 2023). Differences between studies may reflect variation in sampling techniques, culture methods, clinical environments, and device-hygiene behaviors (Zenbaba et al., 2023; De Groote et al., 2022). Eighteen (10.3%) of the 174 culture-positive phones were polymicrobial, and 192 bacterial isolates were recovered overall. Contamination rates showed no significant difference across HCW occupational categories (Fisher's exact test, p = 0.71). Nurses had the highest overall contamination rate (90.0%; Table 1).

Table 1. Mobile-phone bacterial contamination by healthcare worker category

HCW category	No. sampled	Contaminated (n)	Contamination rate (%)	Isolates recovered (n)	MRSA* (n)
Physicians	55	47	85.5	52	4
Nurses	80	72	90.0	79	7
Lab technicians	35	30	85.7	33	2
Administrative/pharmacy	30	25	83.3	28	0
Total	**200**	**174**	**87.0**	**192**	**13**

Note: Differences between HCW categories did not show statistical significance (Fisher's exact test, p = 0.71). MRSA* counts in this table refer to phenotypically methicillin-resistant *S. aureus identified by oxacillin/cefoxitin testing; 12 of 13 were subsequently mecA-positive by PCR.*

3.2. Contamination by hospital department

Contamination was numerically highest in the ICU (93.3%), followed by surgical wards (90.0%), medical wards (86.0%), and the OPD (75.0%; Figure 1). The overall four-department comparison was borderline and did not reach the prespecified 0.05 threshold (Pearson chi-square = 7.66, df = 3, p = 0.054). An exploratory pairwise comparison showed higher contamination in the ICU than in the OPD (p = 0.010). ICU phones also had the highest absolute counts of gram-negative bacteria and phenotypic MRSA (Table 2). Higher contamination in high-acuity environments is biologically plausible because these settings involve critically ill or postoperative patients, frequent handling of equipment, and greater antimicrobial selection pressure (Chang et al., 2017; Dhayhi et al., 2023). However, the present cross-sectional data do not demonstrate a hand-phone-patient transmission loop. Rather, the observed departmental pattern is compatible with the proposed contamination pathway described in previous literature (Ulger et al., 2015; De Groote et al., 2022).

Table 2. Bacterial contamination stratified by hospital department

Department	Sampled (n)	Positive (n)	Rate (%)	*S. aureus* (n)	GNB (n)	MRSA* (n)
ICU	60	56	93.3	14	18	6
Surgical wards	50	45	90.0	11	14	4
Medical wards	50	43	86.0	9	12	3
Outpatient (OPD)	40	30	75.0	5	8	0
Total	**200**	**174**	**87.0**	**39**	**52**	**13**

Note: Overall comparison across the four departments: Pearson chi-square = 7.66, df = 3, p = 0.054. The ICU-versus-OPD comparison (p = 0.010) is presented as an exploratory pairwise comparison. GNB = gram-negative bacteria; MRSA counts refer to phenotypically methicillin-resistant* S. aureus; OPD = outpatient department.

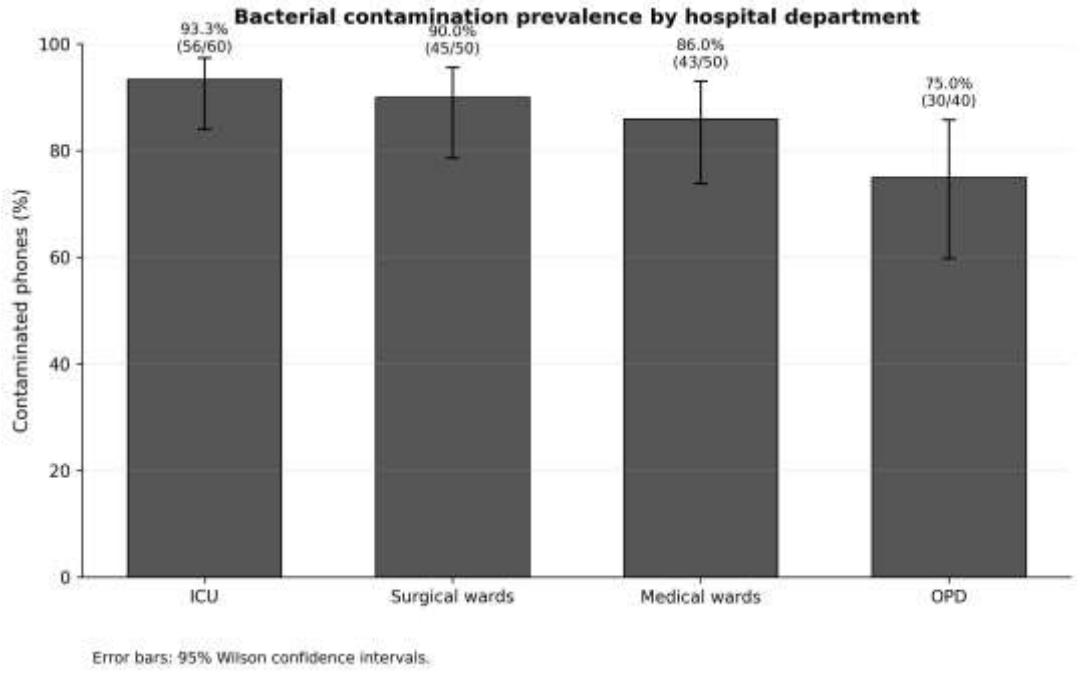

Figure 1. Bacterial contamination prevalence by hospital department. Bars show the proportion of sampled phones with bacterial growth; error bars show 95% Wilson confidence intervals. The overall four-department comparison was Pearson chi-square = 7.66, df = 3, p = 0.054; the ICU-versus-OPD comparison (p = 0.010) was exploratory.

3.3. Bacterial isolate profile

CoNS (44.8%) were the most abundant isolates and are common commensal skin flora. Of clinical importance, S. aureus accounted for 20.3% of all isolates (methicillin-susceptible and phenotypically methicillin-resistant isolates combined). Gram-negative bacteria constituted 27.1% of all isolates, including E. coli (9.4%), K. pneumoniae (7.3%), P. aeruginosa (6.3%), and A. baumannii (4.2%). Among Enterobacterales, 13/32 (40.6%) were DDST-positive for ESBL production. Four additional DDST-positive isolates were non-fermenters (two P. aeruginosa and two A. baumannii) and were treated as exploratory because the DDST is not validated for ESBL confirmation in these organisms. The distribution of recovered isolates is summarized in Figure 2.

CoNS are common skin commensals and can persist for extended periods on dry surfaces, which may help explain their predominance among recovered isolates. Although often regarded as low-virulence organisms, CoNS can serve as opportunistic pathogens, especially in immunocompromised patients, neonates, and individuals with indwelling medical devices. S. aureus represented 20.3% of all isolates; 13/39 (33.3%) were phenotypically methicillin resistant, of which 12 were subsequently mecA-positive. This phenotypic methicillin-resistance proportion was comparable with the 25% reported among S. aureus isolates in Zambia (Mushabati et al., 2021) and higher than the <2% reported in Germany (Tännhäuser et al., 2022). Gram-negative organisms are also important in infection control because they include important causes of healthcare-associated infection and often exhibit antimicrobial resistance (Bayraktar et al., 2021; Nwankwo et al., 2014). Yao et al. (2022) identified *A. baumannii* on 3.6% of HCW phones in China, close to the 4.2% observed here. Araya et al. (2021) identified ESBL-producing gram-negative bacteria on 79.4% of phones in Ethiopia; in the present study, 13/32 (40.6%) Enterobacterales were DDST-positive, while DDST findings in four non-fermenting isolates were exploratory. Differences between studies may reflect local resistance epidemiology, sampling methods, and laboratory definitions.

Table 3. Frequency profile of bacterial isolates from contaminated mobile phones

Bacterial isolate	n	%	Gram stain	Classification
Coagulase-negative staphylococci (CoNS)	86	44.8	Positive	Commensal/opportunistic
Staphylococcus aureus (MSSA)	26	13.5	Positive	Pathogen
Phenotypic MRSA	13	6.8	Positive	MDR pathogen
Enterococcus spp.	10	5.2	Positive	Pathogen
Escherichia coli	18	9.4	Negative	Pathogen
Klebsiella pneumoniae	14	7.3	Negative	Pathogen
Pseudomonas aeruginosa	12	6.3	Negative	Pathogen
Acinetobacter baumannii	8	4.2	Negative	MDR pathogen
Other organisms	5	2.6	Mixed	Variable
Total	**192**	**100**	—	—

Note: Percentages are rounded to one decimal place and may not total exactly 100%. The row labeled phenotypic MRSA comprises 13 oxacillin/cefoxitin-resistant S. aureus isolates; 12 were mecA-positive by PCR and one remained genotypically unconfirmed. Other organisms comprised *Micrococcus* spp. (n = 2), *Bacillus* spp. (n = 2), and coryneform diphtheroid (n = 1), identified to genus level only given their low clinical significance as environmental commensals. CoNS = coagulase-negative staphylococci; MSSA = methicillin-susceptible *S. aureus;* MDR = multidrug-resistant.

Natural Resources for Human Health
eISSN: 2583-1194

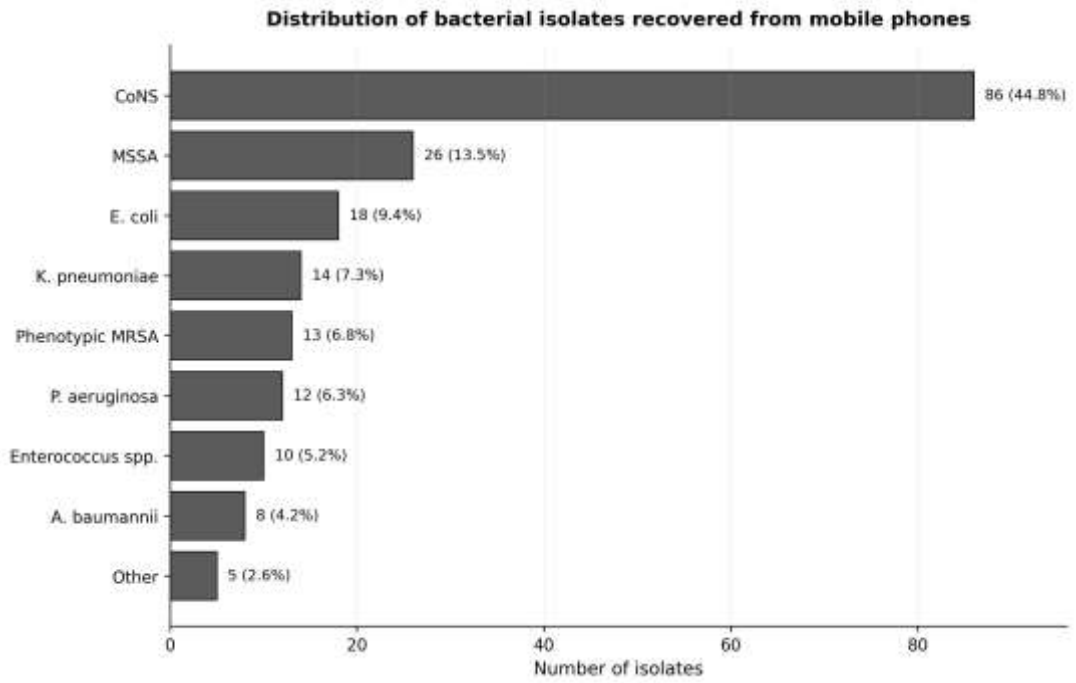

Figure 2. Profile of bacterial isolates recovered from contaminated mobile phones (n = 192 isolates). Bars show isolate counts, with labels reporting the count and percentage of all isolates. Phenotypic MRSA refers to oxacillin/cefoxitin-resistant S. aureus; 12 of 13 isolates were mecA-positive by PCR.

3.4. Antibiotic susceptibility patterns

Antibiotic susceptibility testing showed substantial resistance among several organism groups (Table 4). Among staphylococci, 13/39 S. aureus isolates (33.3%) were phenotypically methicillin resistant, and 50/86 CoNS isolates (58.1%) were oxacillin resistant. No vancomycin resistance was identified by the study's disk-diffusion method; however, MIC-based testing was not performed, so reduced vancomycin susceptibility cannot be reliably excluded. Among Enterobacterales, susceptibility to ceftazidime was 56% in E. coli and 50% in K. pneumoniae, consistent with the 13 DDST-positive Enterobacterales isolates. Four additional DDST-positive non-fermenters were analyzed exploratorily. Carbapenem non-susceptibility was observed in 3/8 A. baumannii isolates (37.5%). Ciprofloxacin susceptibility was below 65% for all gram-negative species, whereas gentamicin susceptibility was 71-72% among Enterobacterales and 50% for A. baumannii.

The reduced susceptibility observed to both fluoroquinolones and aminoglycosides among Enterobacterales, together with carbapenem non-susceptibility in A. baumannii and P. aeruginosa, broadly parallels resistance patterns reported in regional clinical isolates (Bayraktar et al., 2021; Jalil Alawi et al., 2025). This similarity indicates that phones could accumulate resistant organisms present in patient-care environments, but the study did not include paired patient or environmental isolates and therefore cannot establish a shared strain source. Colistin susceptibility was not tested for the carbapenem-non-susceptible A. baumannii isolates; future studies of phone-derived isolates should include reference broth microdilution if polymyxin susceptibility is to be characterized.

Table 4. Antibiotic susceptibility of major bacterial isolates (% susceptible by the study disk-diffusion method)

Antibiotic	***S. aureus***	**CoNS**	***E. coli***	***K. pneumoniae***	***P. aeruginosa***	***A. baumannii***
Oxacillin/methicillin	67	42	—	—	—	—
Ampicillin	44	38	28	—	—	—

Antibiotic	*S. aureus*	CoNS	*E. coli*	*K. pneumoniae*	*P. aeruginosa*	*A. baumannii*
Ciprofloxacin	72	78	61	57	58	38
Gentamicin	79	84	72	71	58	50
Tetracycline	56	60	50	50	—	—
Erythromycin	51	47	—	—	—	—
Trimethoprim-sulfamethoxazole	69	72	44	43	—	—
Vancomycin	100	100	—	—	—	—
Imipenem	—	—	94	86	75	63
Meropenem	—	—	94	93	83	63
Ceftazidime	—	—	56	50	58	38

Note: — = not routinely tested. Ampicillin is intrinsically ineffective against *K. pneumoniae* and was not reported. Vancomycin values reflect the study's disk-diffusion results only; MIC-based testing was not performed, and reduced vancomycin susceptibility cannot therefore be reliably excluded. *S. aureus* = *Staphylococcus aureus;* CoNS = coagulase-negative staphylococci.

3.5. Behavioral factors associated with contamination

In the multivariable behavioral model, never cleaning the phone was linked to greater odds of contamination (AOR 4.6, 95% CI 1.5-13.9, p = 0.005), as was phone use during patient care (AOR 3.0, 95% CI 1.2-7.4, p = 0.017) (Table 5). Phone-case or cover use showed a borderline adjusted association (AOR 2.5, 95% CI 1.0-6.4, p = 0.049), with the rounded lower confidence bound at the null value. Absence of hand hygiene after phone use was not statistically significant after adjustment (AOR 2.3, 95% CI 0.9-5.7, p = 0.075), and bathroom use was also not significant after adjustment (AOR 1.8, 95% CI 0.5-6.0, p = 0.34). In univariable analysis, never cleaning the phone (OR 4.9, 95% CI 1.7-14.1) and using the phone during patient care (OR 3.3, 95% CI 1.4-7.7) showed the strongest associations. The final behavioral model showed adequate calibration (Hosmer-Lemeshow chi-squared = 6.83, df = 8, p = 0.556), and all variance inflation factors were ≤1.42. Because only 26 phones were culture-negative and the outcome prevalence was high, the adjusted ORs should be interpreted cautiously as measures of association rather than risk. Adjusted effect estimates and 95% confidence intervals are shown in Figure 3.

These behavioral associations are broadly consistent with the wider literature (Ulger et al., 2015; Zenbaba et al., 2023) and identify potentially actionable hygiene practices. The associations with infrequent cleaning and phone use during patient care support attention to device hygiene within infection-control programs. Phone-case use also showed a borderline adjusted association with contamination and should be interpreted cautiously because residual confounding by department-specific practices or other hygiene behaviors cannot be excluded. Previous studies have suggested that cases may create crevices that are difficult to clean (Yao et al., 2022; Qureshi et al., 2020; Ozkaya et al., 2020). Institutions may therefore consider guidance on cleaning both phones and cases. Disinfection approaches such as 70% isopropyl alcohol wipes and ultraviolet-C (UV-C)

devices have reduced microbial load in previous studies (De et al., 2024), but the present cross-sectional study did not compare disinfection interventions or establish an optimal cleaning frequency.

Table 5. Logistic regression of behavioral factors linked to mobile-phone bacterial contamination

Behavioral factor	Contaminated n (%)	Not contaminated n (%)	OR (95% CI)	Crude p	Crude sig.	AOR (95% CI)
Phone cleaning: never	78 (92.9)	6 (7.1)	4.9 (1.7–14.1)	0.003	**	4.6 (1.5–13.9)
Phone cleaning: monthly or less	64 (88.9)	8 (11.1)	3.0 (1.1–8.1)	0.030	*	2.7 (0.9–7.6)
Phone cleaning: weekly (reference)	32 (72.7)	12 (27.3)	1.0	—	—	1.0
Uses phone during patient care	138 (90.8)	14 (9.2)	3.3 (1.4–7.7)	0.006	**	3.0 (1.2–7.4)
No hand hygiene after phone use	108 (91.5)	10 (8.5)	2.6 (1.1–6.1)	0.026	*	2.3 (0.9–5.7)
Phone case/cover present	114 (91.9)	10 (8.1)	3.0 (1.3–7.1)	0.010	*	2.5 (1.0–6.4)
Uses phone in toilet/bathroom	54 (93.1)	4 (6.9)	2.5 (0.8–7.5)	0.110	NS	1.8 (0.5–6.0)

*Note: OR = crude odds ratio from univariable logistic regression; AOR = adjusted odds ratio from the multivariable behavioral model (enter method); CI = confidence interval; NS = not significant. The p-value and significance columns report crude, univariable results; * crude p < 0.05 and ** crude p < 0.01. Adjusted p values are stated in the accompanying text where available. Reference category for cleaning frequency: at least weekly cleaning. The model showed adequate calibration (Hosmer-Lemeshow chi-squared = 6.83, df = 8, p = 0.556); all variance inflation factors were ≤1.42. Because contamination prevalence was high (87.0%), ORs should not be interpreted as risk ratios.*

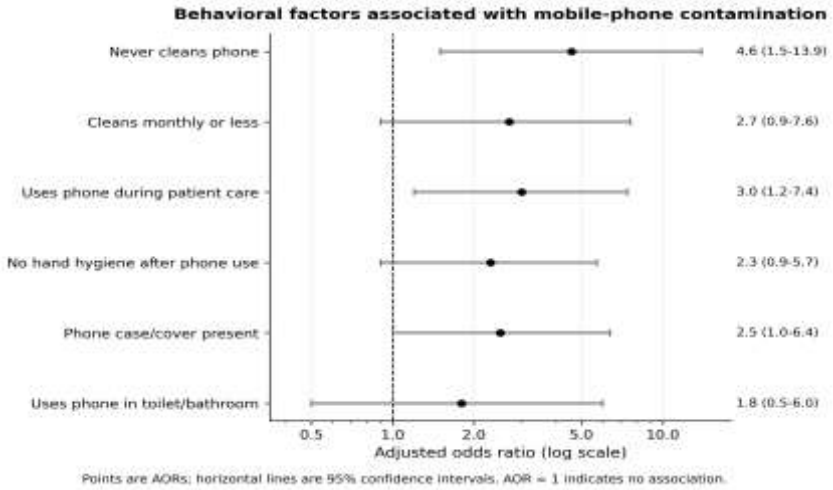

Figure 3. Adjusted odds ratios (AORs) with 95% confidence intervals from the multivariable behavioral logistic-regression model for mobile-phone bacterial contamination. The vertical line at AOR = 1 indicates the null value. Cleaning-frequency estimates use at-least-weekly cleaning as the reference; binary predictors use absence of the behavior as the reference. Because contamination was common (87%), the odds ratios should be interpreted as association measures rather than prevalence ratios or causal effects.

3.6. Molecular screening of resistance genes by PCR

PCR-based molecular screening was performed on selected phenotypically resistant isolates as described in Section 2.7. Overall, the targeted assays showed substantial but not complete concordance with the phenotypic findings and supported the presence of selected acquired resistance determinants. Because only a limited gene panel was tested, absence of a targeted gene does not exclude other resistance mechanisms. The targeted PCR findings are summarized in Figure 4.

mecA gene detection among phenotypically methicillin-resistant S. aureus isolates. Of the 13 S. aureus isolates classified as methicillin resistant by oxacillin/cefoxitin testing, mecA was detected in 12 (92.3%) (Table 6). The remaining isolate was mecA-negative despite the phenotypic result and was therefore retained as a phenotypically methicillin-resistant, genotypically unconfirmed isolate. Alternative mechanisms of oxacillin resistance were not investigated, so a specific mechanism such as BORSA should not be assigned from these data alone.

Table 6. PCR detection of *mecA* among phenotypically methicillin-resistant S. aureus isolates (n = 13)

PCR result	n	%
mecA detected (genotypically confirmed MRSA)	12	92.3
mecA not detected (phenotypically resistant; genotypically unconfirmed)	1	7.7
Total	**13**	**100.0**

Note: All 13 phenotypically methicillin-resistant S. aureus isolates were tested. Twelve were mecA-positive; one was mecA-negative and remained genotypically unconfirmed because alternative resistance mechanisms were not tested.

Detection of ESBL-encoding genes among DDST-positive gram-negative isolates. PCR screening was performed on the 17 DDST-positive gram-negative isolates rather than on all 52 gram-negative isolates. The primary Enterobacterales analysis comprised 13/32 isolates (7 E. coli and 6 K. pneumoniae) that were DDST-positive; all 13 carried at least one of the targeted genes. Four additional DDST-positive isolates were non-fermenters (2 P. aeruginosa and 2 A. baumannii), for which the DDST result was considered exploratory. Across all 17 DDST-positive isolates, at least one targeted gene (blaCTX-M, *blaTEM,* or *blaSHV)* was detected in 16/17 (94.1%) (Table 7). *blaCTX-M* was detected in 82.4%, *blaTEM* in 64.7%, and *blaSHV* in 41.2%; several isolates carried more than one targeted gene. One *DDST-positive A. baumannii* isolate was negative for all three targets. This discordance may reflect an untested resistance mechanism and also underscores the limited validity of DDST-based ESBL classification in non-fermenting species.

Table 7. PCR detection of targeted ESBL-associated genes among DDST-positive gram-negative isolates, by species (n = 17)

Species	n tested	*bla*CTX-M n (%)	*bla*TEM n (%)	*bla*SHV n (%)	≥1 gene n (%)
E. coli	7	6 (85.7)	5 (71.4)	2 (28.6)	7 (100.0)
K. pneumoniae	6	5 (83.3)	4 (66.7)	4 (66.7)	6 (100.0)
P. aeruginosa	2	2 (100.0)	1 (50.0)	0 (0.0)	2 (100.0)
A. baumannii	2	1 (50.0)	1 (50.0)	1 (50.0)	1 (50.0)
Total	**17**	**14 (82.4)**	**11 (64.7)**	**7 (41.2)**	**16 (94.1)**

Note: All 17 DDST-positive isolates underwent testing. Enterobacterales (E. coli and K. pneumoniae) constitute the primary ESBL analysis; findings for P. aeruginosa and A. baumannii are exploratory because DDST is not validated for ESBL confirmation in these non-fermenters. Percentages for individual genes do not sum to the ≥1 gene column because several isolates carried more than one targeted gene.

Carbapenemase gene detection in meropenem-non-susceptible A. baumannii isolates. Among the 8 A. baumannii isolates recovered (Table 3), 3 (37.5%) were non-susceptible to meropenem by disk diffusion (Section 3.4) and were screened for blaOXA-23-like and blaNDM (Table 8). blaOXA-23-like was identified in all three isolates (100%), while blaNDM was co-detected in one (33.3%). These findings support the occurrence of acquired carbapenemase determinants among the meropenem-non-susceptible isolates. The blaNDM-positive isolate also carried blaOXA-23-like, consistent with reports of co-occurrence of class B and class D carbapenemase genes among carbapenem-resistant A. baumannii in the region (Jalil Alawi et al., 2025).

Table 8. PCR detection of carbapenemase genes among meropenem-non-susceptible *A. baumannii* isolates (n = 3)

Gene(s) detected	**n**	**%**
*bla*OXA-23-like only	2	66.7
*bla*OXA-23-like + *bla*NDM (co-carriage)	1	33.3
*bla*NDM only	0	0.0
Total isolates with ≥1 carbapenemase gene	**3**	**100.0**

Note: All meropenem-non-susceptible *A. baumannii* isolates recovered were tested.

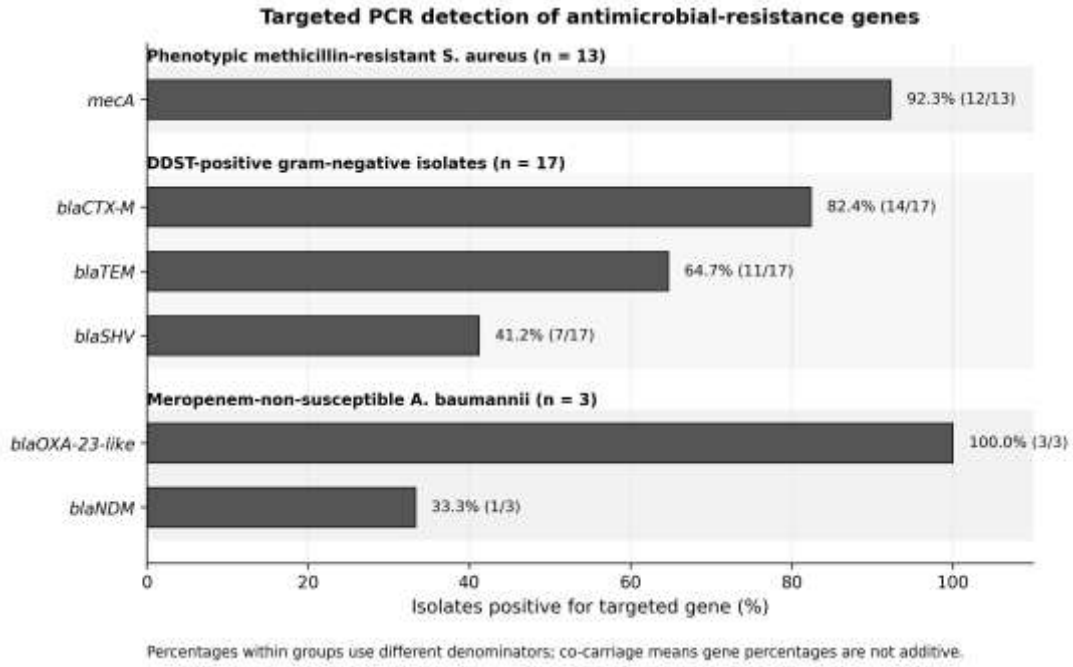

Figure 4. Targeted PCR detection of antimicrobial-resistance genes among phenotypically resistant isolates. mecA was detected in 12/13 phenotypically methicillin-resistant S. aureus isolates. Among 17 DDST-positive gram-negative isolates, blaCTX-M, blaTEM, and blaSHV were detected in 14/17, 11/17, and 7/17 isolates, respectively; these percentages are not mutually exclusive because co-carriage occurred. Among three meropenem-non-susceptible A. baumannii isolates, blaOXA-23-like was detected in 3/3 and blaNDM in 1/3. Denominators therefore differ across the three assay groups.

Detection of mecA in 12/13 (92.3%) phenotypically methicillin-resistant S. aureus isolates supports the value of molecular confirmation; Oluduro et al. (2023) detected mecA in only 25% of phenotypically resistant S. aureus recovered from mobile phones in Nigeria, illustrating that phenotypic-genotypic concordance can vary by setting and method. The frequent detection of blaCTX-M among the DDST-positive isolates is consistent with reports from Iraqi clinical E. coli and K. pneumoniae, where

blaTEM and blaCTX-M were frequently reported (Pishtiwan and Khadija, 2019). This overlap is compatible with shared regional resistance determinants, although the present study did not include paired clinical isolates and cannot demonstrate a common strain or transmission source. blaOXA-23-like was detected in all three meropenem-non-susceptible A. baumannii isolates, and blaNDM was co-detected in one. Jalil Alawi et al. (2025) also reported blaOXA-23 and blaNDM among carbapenem-resistant A. baumannii in Iraq, supporting regional circulation of these determinants. The present PCR assays establish gene detection only; plasmid localization, horizontal transfer, and patient-to-phone transmission were not investigated.

3.7. Strengths and limitations

This study has multiple methodological strengths. First, phenotypic identification and antimicrobial susceptibility testing were combined with PCR screening for six clinically important resistance genes (mecA, *blaCTX-M, blaTEM, blaSHV, blaOXA-23-like,* and *blaNDM),* providing additional molecular context beyond culture-based findings alone. Second, four culture media (blood agar, MacConkey agar, mannitol salt agar, and chocolate agar) were used to enhance recovery of both gram-positive and gram-negative organisms. Third, multivariable logistic regression with prespecified reference categories and model diagnostics estimated adjusted associations among behavioral exposures. Fourth, department-based quota sampling across four clinically distinct settings (ICU, surgical, medical, and outpatient) allowed descriptive comparison of contamination patterns across clinical environments.

Several limitations should be acknowledged. First, swab-based sampling may underestimate contamination compared with contact-plate methods because recovery varies with organism density and surface type. Second, the cross-sectional design prevents causal inference and cannot determine patient-to-phone or phone-to-patient transmission. Molecular epidemiological typing (e.g., whole-genome sequencing or multilocus sequence typing) and paired patient, hand, or environmental isolates were not available. Third, the behavioral regression model was limited to reported behavioral exposures and did not account for all potential departmental, occupational, or demographic confounding; with only 26 culture-negative phones and an 87.0% outcome prevalence, adjusted ORs may also be unstable and should not be interpreted as risk ratios. Fourth, the overall departmental comparison was borderline ($p = 0.054$), so the ICU-versus-OPD pairwise result should be viewed as exploratory. Fifth, DDST-based ESBL findings in P. aeruginosa and A. baumannii were exploratory because this method is not validated for ESBL confirmation in non-fermenters. Sixth, vancomycin was assessed by disk diffusion without MIC testing, and colistin susceptibility was not tested for carbapenem-non-susceptible *A. baumannii. Seventh, PCR targeted a limited resistance-gene panel and did not establish plasmid localization or transferability. Eighth,* participants within departmental quotas were recruited consecutively rather than randomly, and 32/232 eligible HCWs (13.8%) declined participation, so selection and non-response bias cannot be excluded. Administrative and pharmacy staff were pooled into one supporting-role category, this was a single-center study, and behavioral data were self-reported, allowing social-desirability bias. Future studies should use longitudinal or intervention designs, reference susceptibility methods, broader molecular characterization, and paired clinical/environmental sampling.

4. CONCLUSIONS

Mobile phones used by healthcare workers were commonly contaminated and harbored clinically important organisms, including phenotypically methicillin-resistant S. aureus and DDST-positive gram-negative bacteria. PCR detected mecA in 12/13 phenotypically methicillin-resistant S. aureus isolates, identified blaCTX-M in most DDST-positive isolates, and detected blaOXA-23-like in all three meropenem-non-susceptible A. baumannii isolates, with blaNDM co-detected in one. These results demonstrate carriage of important resistance determinants on HCW phones but do not establish their transferability or prove transmission to patients. Contamination was numerically highest in the ICU and surgical wards, although the overall departmental comparison was borderline. Within the behavioral model, never cleaning the phone and using the phone during patient care were associated with higher odds of contamination, while the phone-case association was borderline and absence of hand hygiene was not significant after adjustment.

These findings support consideration of institutional mobile-phone hygiene guidance, HCW education, and incorporation of device hygiene into infection-control programs. Validated approaches such as 70% isopropyl alcohol wipes or UV-C devices may be considered where compatible with device-manufacturer guidance, but the optimal frequency and clinical impact of disinfection were not tested in this study. Prospective intervention studies are needed to determine whether standardized phone decontamination reduces microbial burden and healthcare-associated transmission.

Declarations

Acknowledgements: The authors thank all healthcare workers who took part in the study.

Author contributions: Methodology: all authors; Investigation: Khudhur Raheem Obayes; Formal analysis: Hassan Fahim Kamel; Writing - original draft: Ali Hamzah Makttoof Al-Taee and Dhay Ali Abed; Writing - review and editing: all authors. All authors reviewed and approved the published version of the manuscript.

Funding: This research did not receive external funding.

Conflicts of interest: The authors report no conflicts of interest.

Use of artificial intelligence: Generative AI-assisted editorial support was used during manuscript revision to improve language, internal consistency, and reporting clarity. The authors reviewed all revisions and take full responsibility for the final scientific content.

Data availability statement: The de-identified aggregate data supporting the findings of this study are contained in the article tables; individual-level records are available from the corresponding author upon reasonable request, subject to institutional data-protection approval.

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Appendix A

Appendix Figure A1. Illustrative image of a healthcare worker handling a mobile phone in a clinical setting. The image is provided for contextual illustration only and does not represent a quantitative study outcome.