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Isolation of Bacterial Contaminants from Mobile Phones Used by Students,Faculty, Members and Employees at the Faculty of science, University of Zawia

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Abstrac

This study aimed to isolate and identify bacteria contaminating the mobile phones of students, faculty members, and Employees at the University of zawia. The study was conducted on 30 mobile phones. Mobile phones were sampled using sterile swabs, and the specimens were cultured and analysed. All examined mobile phones showed bacterial contamination, and a total of 1,254 bacterial colonies were recovered. Faculty members had the highest total number of colonies (573; 45.69%) and the highest mean colony count (57.30 ± 28.80), followed by employees (472; 37.64%; 47.20 ± 15.65) and students (209; 16.67%; 20.90 ± 13.50). Pseudomonas aeruginosa was the predominant isolate, accounting for 678 colonies (54.07%), followed by Micrococcus spp. (30.54%), Micrococcus roseus (13.40%), and Bacillus spp. (1.99%). This study found that mobile phones are possible carriers for the transmission of various infections, and that a level of cleanliness must be implemented to prevent cross-contamination. Contaminated mobile phones can convey microorganisms capable of causing serious disease.

Keywords: *bacterial contaminants; mobile phones; Pseudomonas aeruginosa*

عزل الملوثات البكتيرية من الهواتف المحمولة المستخدمة من قبل الطلاب وأعضاء هيئة التدريس والموظفين كلية العلوم، جامعة الزاوية

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الملخص

هدفت هذه الدراسة إلى عزل البكتيريا الموجودة على الهواتف المحمولة الخاصة بالطلاب وأعضاء هيئة التدريس والموظفين في جامعة الزاوية .أُجريت الدراسة على 30 هاتفًا محمولًا .جمعت عينات من الهواتف المحمولة باستخدام المسحات معقمة، ثم زُرعة العينات على الأوساط الغذائية ، تم عزل البكتريا وتعريفيها .واظهرت جميع الهواتف المحمولة المفحوصة تلوثًا بكتيريًا، رصد 1,254 مستعمرة بكتيرية. سجّل أعضاء هيئة التدريس أعلى عدد كلي من المستعمرات، بواقع 573 مستعمرة(45.69%) ، كما سجّلوا أعلى متوسط لعدد المستعمرات، حيث بلغ28.80 ± 57.30 ، يليهم الموظفون بواقع 472 مستعمرة (37.64%) ومتوسط بلغ

15.65 ± 47.20، ثم الطلاب بواقع 209 مستعمرات (16.67%) ومتوسط بلغ13.50 ± 20.90. كانت بكتيريا *Pseudomonas aeruginosa* هي العزلة السائدة، إذ مثّلت 678 مستعمرة(54.07%) ، تلتها بكتيريا *Micrococcus spp.* بنسبة30.54% ، و *Micrococcus roseus* بنسبة13.40% ، و *Bacillus spp.* بنسبة1.99%. وجدت هذه الدراسة أن الهواتف المحمولة قد تكون نواقل محتملة لانتقال أنواع مختلفة من العدوى، وأنه ينبغي تطبيق مستوى مناسب من النظافة لمنع التلوث المتبادل .كما يمكن للهواتف المحمولة الملوثة أن تنقل كائنات دقيقة قادرة على التسبب في أمراض خطيرة.

Introduction

Mobile phones have become essential devices in contemporary society. They are used for communication, access to information, academic activities, online learning, financial transactions, and entertainment. Students are among the most frequent users of these devices, and their continuous dependence on mobile phones has raised concerns about possible public health risks (Agboola & Sunday,2020 ; Anele et al .,2025 ; Qadi et l., 2021 ; Abd-alla, 2015). Because mobile phones are regularly handled and often come into contact with the hands and face, they may act as fomites, or inanimate objects capable of carrying and transmitting pathogenic bacteria (Hamidu& Yunusa 2024 ; Odiete et al.,2018 ; Olsen et al.,2022). Mobile phones are used in many different environments, but they are not always cleaned or disinfected as regularly as other frequently touched personal items (Alkufeid et al.,2025 ; Almizwary et al.,2024). In addition, the heat generated during use may create a favourable microenvironment for the survival and proliferation of microorganisms (Ugwu et al., 2021). Some studies have reported that the microbial load on mobile phones may be up to ten times higher than that found on other highly contaminated surfaces, including toilet seats, the inside of a user's shoe, and toilet doorknobs (Al-Abdalall,2010; Roy,et al.,2026).These findings indicate that mobile phones can provide suitable surfaces for the persistence and transfer of bacteria.

Bacterial contamination of mobile phones has been reported in different populations and geographical settings, with prevalence commonly exceeding 70%, although the reported rate varies according to the sampling method, study population, and hygiene practices (Mushabati et al,2021;Sadeeq et al.,2021). Among students, bacterial contamination was detected on more than 80% of mobile phones examined in a study conducted in Ghana (Olu et al.,2021). Similarly, studies conducted in Nigerian tertiary institutions reported contamination rates above 60% (Barwa&Oti,2026). The organisms commonly recovered from mobile-phone surfaces include Gram-positive

bacteria such *as Staphylococcus aureus*, *Streptococcus species*, and Gram-positive bacilli. Although many of these organisms are part of the normal human skin flora, they may cause infection under favourable conditions (Zakai et al,2016; Zenbaba, 2023; Hossain, 2022; Alkufeid et al., 2025; Omran& Taha,2020). The detection of *E. coli* is of particular importance because it is commonly used as an indicator of faecal contamination and inadequate hand hygiene. Its presence on mobile phones has also been associated with practices such as using phones while eating, after visiting restrooms, or after touching contaminated surfaces (Taha et al.,2025).

In addition to the variety of organisms detected, increasing attention has been given to the antibiotic resistance of bacteria associated with mobile phones. Antibiotic-resistant *Staphylococcus aureus* and *Pseudomonas aeruginosa* have been isolated from mobile phones, with resistance reported against several commonly used antibiotic classes (Subhashini & Karunanidhi, 2025). This issue may be especially important in crowded academic environments, where students are in close contact and may frequently share materials. Under these conditions, personal devices could contribute to the community-level spread of antimicrobial-resistant organisms (Uthman& Abdulrazaq,2025; Alsaadi et al.,2026). Studies conducted in African countries, including Nigeria, Ethiopia, and Egypt, have also shown that electronic devices can serve as reservoirs for clinically significant bacteria, including *Bacillus species*, *Enterobacter aerogenes, Klebsiella pneumoniae*, and Proteus species(Pierre et al.,2020). Therefore, the present study aimed to investigate bacterial contamination on mobile phones at the Faculty of Sciences, University of Zawia, and to raise awareness of the risks associated with contaminated phones and the importance of appropriate handling practices.

Materials and Methods

Study Design and Sample Collection : A cross-sectional study was conducted at the Faculty of Sciences, University of Zawia, in May 2026 to investigate bacterial contamination of mobile phones belonging to students, faculty members, and administrative staff. A total of 30 mobile phone samples were collected and equally distributed among the three study groups, with 10 samples obtained from each group. Sterile swabs were used to collect samples from the mobile phone surfaces. The collected samples were transported immediately to the Microbiology Laboratory in the Department of Botany, Faculty of Science, University of Zawia, for bacteriological examination.

Preparation of Culture Media: Nutrient agar, blood agar, and MacConkey agar were prepared according to the manufacturer's instructions (Oxoid, Thermo Fisher Scientific). The prepared media were sterilised by autoclaving at 121°C for 15 minutes. After sterilisation, the media were allowed to cool to an appropriate temperature and were aseptically poured into sterile Petri dishes..

Isolation and Purification of Bacterial Isolates: The swabs were inoculated onto nutrient agar, blood agar, and MacConkey agar plates using the streak-plate technique. The inoculated plates were incubated aerobically at 37°C for 24–48. hours. Following incubation, the plates were examined for bacterial growth, including colony morphology, such as colony size, shape, colour, elevation.

Distinct colonies were selected and subcultured onto the appropriate culture medium to obtain pure bacterial isolates. For purification, a portion of each selected colony was transferred using a sterile inoculating loop and streaked onto a fresh agar plate. The subcultured plates were then incubated aerobically at 37°C for 24–48 hours**Identification of Bacterial Isolates:** The purified bacterial isolates were initially examined by Gram staining to determine their Gram reaction and cellular morphology. Based on the Gram-staining results and colony characteristics, appropriate biochemical tests were performed for the preliminary identification of the bacterial isolates. (AlMomani et al.,2019)

Statistical Analysis

Statistical analysis was performed using SPSS 27 to examine the bacterial contamination of mobile phones among students, faculty members, and employees at the Faculty of Science, University of Zawia. Descriptive statistics were used to summarize the findings, including frequencies, percentages, total bacterial colony counts, means, standard deviations, medians, ranges, and coefficients of variation. The relative contribution of each bacterial genus to the total number of recovered colonies was calculated and expressed as a percentage, while the frequency of positive samples was used to describe the occurrence of each bacterial genus within the examined groups. The Shapiro–Wilk test was employed to assess the normality of total bacterial colony counts within each group, while Levene's test was used to examine the homogeneity of variances. Since Levene's test indicated unequal variances and each group consisted of a relatively small sample (n = 10), the Kruskal–Wallis test was selected as the primary non-parametric procedure to compare total bacterial colony counts among the three groups. One-way analysis of variance

(ANOVA) was also performed as a supplementary analysis for comparison. Following statistically significant Kruskal–Wallis results, pairwise comparisons were conducted using the Mann–Whitney U test with Bonferroni adjustment to identify differences between specific groups. Tukey's Honestly Significant Difference (HSD) test was additionally used for post hoc comparisons following ANOVA. Furthermore, the chi–square test of independence was applied to examine the association between study group and bacterial genus distribution, with Cramér's V calculated to assess the strength of this association. Separate Kruskal–Wallis tests were also conducted to investigate differences in the colony counts of individual bacterial genera across the three groups. All statistical tests were two–tailed, and statistical significance was established at the 0.05 level . The results were interpreted using the appropriate test statistics and corresponding p–values.

Results: Bacterial Contamination of Employees'phones

ntamination of employees' phones by genus

Table (1)

Genus	Total colonies	% within group	Mean / sample	SD	Median	Range	Positive samples
Bacillus spp	0	0.00%	0.00	0.00	0.0	0 – 0	0/10
Pseudomonas aeruginosa	227	48.09%	22.70	7.01	25.0	10 – 30	10/10
Micrococcus roseus	67	14.19%	6.70	4.37	4.0	3 – 15	10/10
Micrococcus spp	178	37.71%	17.80	13.58	13.0	3 – 44	10/10
Total	**472**	**100.00%**	**47.20**	**15.65**	**47.0**	**19 – 70**	**10/10**

The results presented in Table (1) indicate that all 10 employees' mobile phones (100%) were contaminated with bacterial isolates, yielding a total of 472 bacterial colonies, with an average of 47.20 colonies per sample (SD = 15.65) and a median of 47.0 colonies, ranging from 19 to 70 colonies. Regarding the distribution of bacterial genera, *Pseudomonas aeruginosa* was the most predominant isolate, accounting for 227 colonies (48.09% of the total), with a mean of 22.70 colonies per sample (SD = 7.01) and a median of 25.0, ranging from 10 to 30 colonies. It was detected in all examined samples (10/10). Similarly, *Micrococcus spp*. represented the second most frequently isolated group, accounting for 178 colonies (37.71%), with a mean of 17.80 colonies per sample (SD = 13.58) and a median of 13.0, ranging from 3 to 44 colonies; it was also detected in all samples (10/10). In contrast, *Micrococcus roseus* accounted for 67 colonies (14.19%), with a mean of 6.70 colonies per sample (SD = 4.37) and a median of 4.0, ranging from 3 to 15 colonies, and was detected in all examined samples. No *Bacillus spp*. colonies were recovered from any of the employees' mobile phones. Overall, these findings demonstrate widespread bacterial contamination of employees' mobile phones, with *Pseudomonas aeruginosa* representing the predominant isolate, followed by *Micrococcus spp*. and *Micrococcus roseus*. The consistent detection of these bacterial groups across all samples highlights the potential role of mobile phones as reservoirs of bacterial contamination and emphasizes the importance of regular phone disinfection and appropriate hand hygiene practices among faculty members and staff.

1) Bacterial Contamination of Students' Phones

Table (2)

Contamination of students' phones by genus

Genus	Total colonies	% within group	Mean / sample	SD	Median	Range	Positive samples
Bacillus spp	9	4.31%	0.90	1.20	0.5	0 – 3	5/10
Pseudomonas aeruginosa	84	40.19%	8.40	5.08	8.0	1 – 18	10/10
Micrococcus roseus	59	28.23%	5.90	5.36	4.0	1 – 15	10/10
Micrococcus spp	57	27.27%	5.70	4.40	4.5	0 – 11	9/10
Total	**209**	**100.00%**	**20.90**	**13.50**	**17.5**	**5 – 41**	**10/10**

The results presented in Table (2) indicate that all 10 students' mobile phones (100%) were contaminated with bacterial isolates, yielding a total of 209 bacterial colonies, with an average of 20.90 colonies per sample (SD = 13.50) and a median of 17.5 colonies, ranging from 5 to 41 colonies. Regarding the distribution of bacterial genera, *Pseudomonas aeruginosa* was the most predominant isolate, accounting for 84 colonies (40.19% of the total), with a mean of 8.40 colonies per sample (SD = 5.08) and a median of 8.0, ranging from 1 to 18 colonies. It was detected in all examined samples (10/10). *Micrococcus roseus* was the second most frequently isolated bacterium, representing 59 colonies (28.23%), with a mean of 5.90 colonies per sample (SD = 5.36) and a median of 4.0, ranging from 1 to 15 colonies; it was also detected in all samples. Similarly, *Micrococcus spp.* accounted for 57 colonies (27.27%), with a mean of 5.70 colonies per sample (SD = 4.40) and a median of 4.5, ranging from 0 to 11 colonies, and was detected in 9 out of 10 samples (90%). In contrast, *Bacillus spp.* represented the least frequently isolated bacterial group, accounting for only 9 colonies (4.31%), with a mean of 0.90 colonies per sample (SD = 1.20) and a median of 0.5, ranging from 0 to 3 colonies; it was detected in 5 out

of 10 samples (50%). Overall, these findings demonstrate that bacterial contamination was widespread among students' mobile phones, with *Pseudomonas aeruginosa* being the predominant isolate, followed by *Micrococcus roseus* and Micrococcus spp. The recovery of multiple bacterial groups from the examined phones suggests that students' mobile devices may serve as potential reservoirs of bacterial contamination, highlighting the importance of regular mobile phone disinfection and appropriate personal hygiene practices within the academic environment.

2) Bacterial Contamination of Faculty members' Phones

Table (3)

Contamination of faculty members' phones by genus

Genus	Total colonies	% within group	Mean / sample	SD	Median	Range	Positive samples
Bacillus spp	16	2.79%	1.60	1.71	1.0	0 – 5	7/10
Pseudomonas aeruginosa	367	64.05%	36.70	20.96	39.5	7 – 79	10/10
Micrococcus roseus	42	7.33%	4.20	2.86	4.5	0 – 8	9/10
Micrococcus spp	148	25.83%	14.80	12.93	12.0	4 – 45	10/10
Total	**573**	**100.00%**	**57.30**	**28.80**	**57.0**	**16 – 100**	**10/10**

The results presented in Table (3) indicate that all 10 faculty members' mobile phones (100%) were contaminated with bacterial isolates, yielding a total of 573 bacterial colonies, with an average of 57.30 colonies per sample (SD = 28.80) and a median of 57.0 colonies, ranging from 16 to 100 colonies. Regarding the distribution of bacterial genera, *Pseudomonas aeruginosa* was the predominant isolate by a considerable margin, accounting for 367 colonies (64.05% of the total), with a mean of 36.70 colonies per sample (SD = 20.96) and a median of 39.5, ranging from 7 to

79 colonies. It was detected in all examined samples (10/10). *Micrococcus spp*. represented the second most frequently isolated group, accounting for 148 colonies (25.83%), with a mean of 14.80 colonies per sample (SD = 12.93) and a median of 12.0, ranging from 4 to 45 colonies; it was also detected in all samples. In comparison, *Micrococcus roseus* accounted for 42 colonies (7.33%), with a mean of 4.20 colonies per sample (SD = 2.86) and a median of 4.5, ranging from 0 to 8 colonies, and was detected in 9 out of 10 samples (90%). *Bacillus spp*. represented the least frequently isolated group, accounting for 16 colonies (2.79%), with a mean of 1.60 colonies per sample (SD = 1.71) and a median of 1.0, ranging from 0 to 5 colonies; it was detected in 7 out of 10 samples (70%). Overall, these findings demonstrate a high level of bacterial contamination among faculty members' mobile phones, with Pseudomonas aeruginosa representing the dominant bacterial isolate, followed by *Micrococcus spp*. The predominance of *P. aeruginosa*, together with the detection of multiple bacterial groups across most or all examined samples, highlights the potential role of mobile phones as reservoirs of bacterial contamination and underscores the importance of regular mobile phone disinfection and appropriate hand hygiene practices within the university environment.

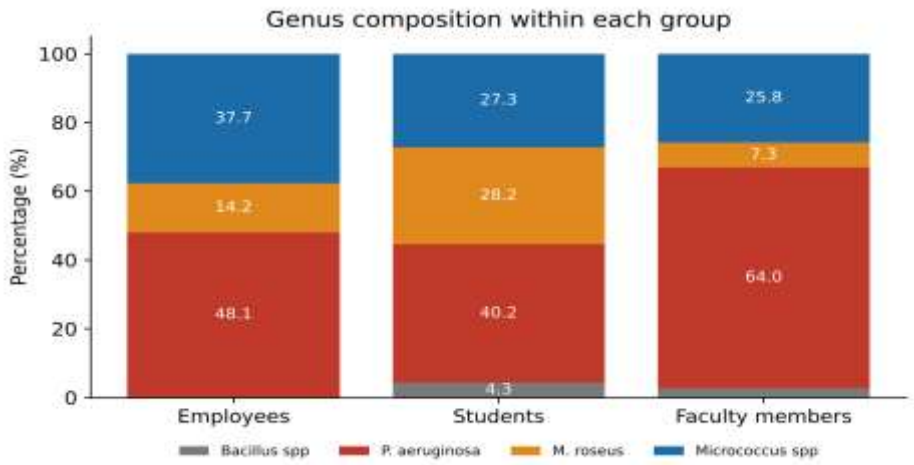


Figure 1: Genus composition within each group (%)

3) Contamination Across All Groups and the Most Contaminated Group

Table (4)

Comparison of bacterial contamination between groups

Group	**Total colonies**	**Contamination (%)**	**Mean colonies / sample**	**SD**	**CV**
Employees	472	37.64%	47.2	15.7	33.2%
Students	209	16.67%	20.9	13.5	64.6%
Faculty members	573	45.69%	57.3	28.8	50.3%
Overall	**1254**	**100.00%**	**41.8**	–	–

The results presented in Table (4) demonstrate differences in the distribution and mean levels of bacterial contamination among the three examined groups: employees, students, and faculty members. Out of the 1,254 bacterial colonies recovered from all 30 mobile phone samples, faculty members accounted for the largest proportion, with 573 colonies (45.69%), followed by employees, with 472 colonies (37.64%), while students recorded the lowest proportion, with 209 colonies (16.67%). When considering the mean number of colonies per sample, faculty members exhibited the highest level of bacterial contamination, with an average of 57.30 colonies (SD = 28.80), followed by employees, with an average of 47.20 colonies (SD = 15.70), whereas students had the lowest average, at 20.90 colonies (SD = 13.50). These

findings suggest that faculty members' mobile phones were the most heavily contaminated group in terms of both the total number of recovered colonies and the average bacterial count per sample. Regarding the coefficient of variation (CV), students demonstrated the greatest relative variability in bacterial counts (64.6%), followed by faculty members (50.3%) and employees (33.2%). This indicates that bacterial contamination levels were relatively more heterogeneous among students, whereas employees showed comparatively more consistent contamination levels across their samples. Overall, the findings identify faculty members as the group with the highest bacterial burden, while students exhibited the lowest mean bacterial count but the greatest relative variation in contamination levels .

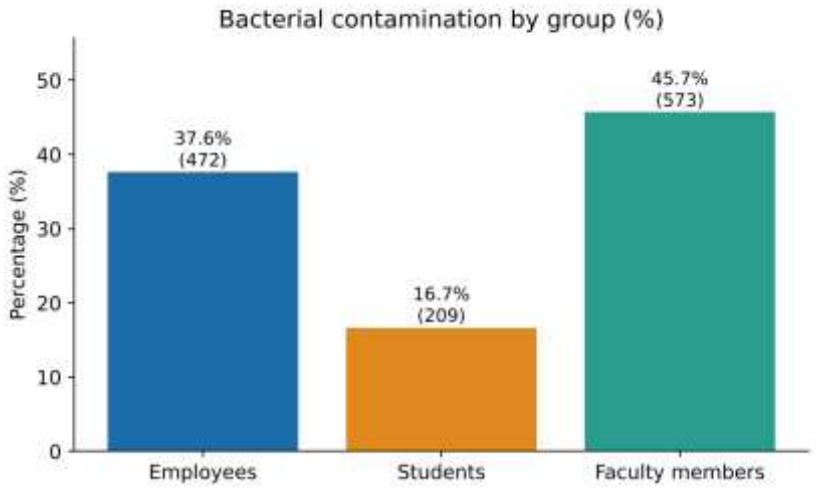


Figure 2: Bacterial contamination by group (%)

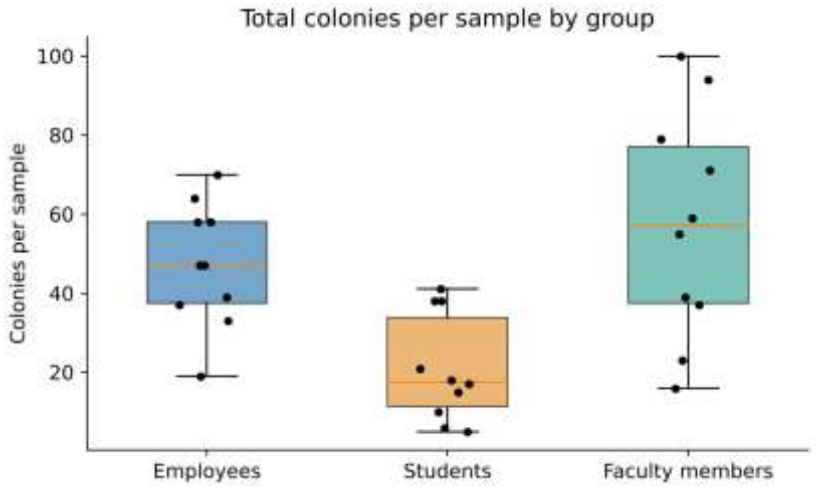


Figure 3: Total colonies per sample by group

4) Most Prevalent Bacterial Genera

Table (5)

Total colonies of each genus by group and overall share

Genus	Employees	Students	Faculty members	Total	Overall share	Rank
Bacillus spp	0	9	16	25	1.99%	4
Pseudomonas aeruginosa	227	84	367	678	54.07%	1
Micrococcus roseus	67	59	42	168	13.40%	3
Micrococcus spp	178	57	148	383	30.54%	2
Total	**472**	**209**	**573**	**1254**	**100.00%**	–

The results presented in Table (5) illustrate the overall distribution and relative prevalence of the bacterial genera isolated from the mobile phones of employees, students, and faculty members at the Faculty of Science, University of Zawia. A total of 1,254 bacterial colonies were recovered from the 30 examined mobile phone

samples. *Pseudomonas aeruginosa* was the most predominant bacterial isolate, ranking first with 678 colonies, representing 54.07% of the total bacterial isolates. It was the leading isolate across all three groups, accounting for 227 colonies among employees, 84 among students, and 367 among faculty members. *Micrococcus spp*. ranked second, with 383 colonies (30.54% of the total), distributed as 178 among employees, 57 among students, and 148 among faculty members. In contrast, *Micrococcus roseus* ranked third, accounting for 168 colonies (13.40%), with 67 colonies recovered from employees' phones, 59 from students' phones, and 42 from faculty members' phones. *Bacillus spp*. was the least frequently isolated bacterial group, ranking fourth, with only 25 colonies (1.99% of the total), including 9 among students and 16 among faculty members, while no colonies were recovered from employees' phones. Overall, the findings indicate that Pseudomonas aeruginosa constituted more than half of all recovered bacterial colonies, demonstrating its predominance among the bacterial isolates across the three study groups. Furthermore, the consistent recovery of *Pseudomonas aeruginosa and Micrococcus spp*. from the different groups suggests that these bacterial genera were the major contributors to mobile phone contamination within the study population

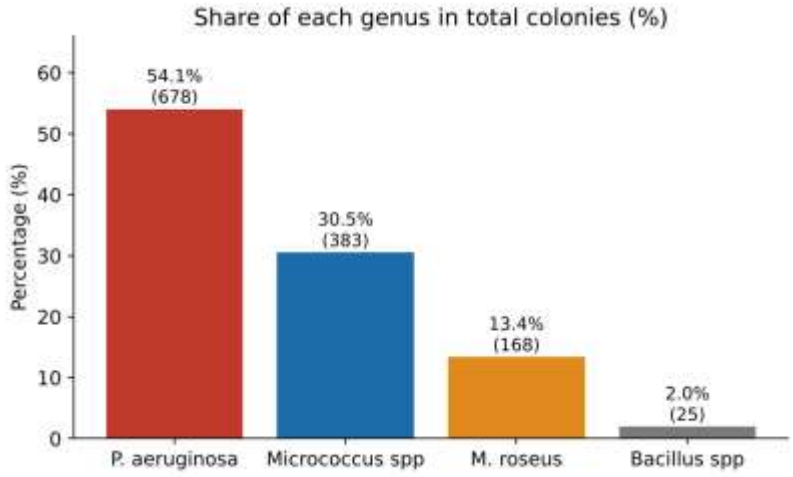


Figure 4: Share of each genus in total colonies (%)

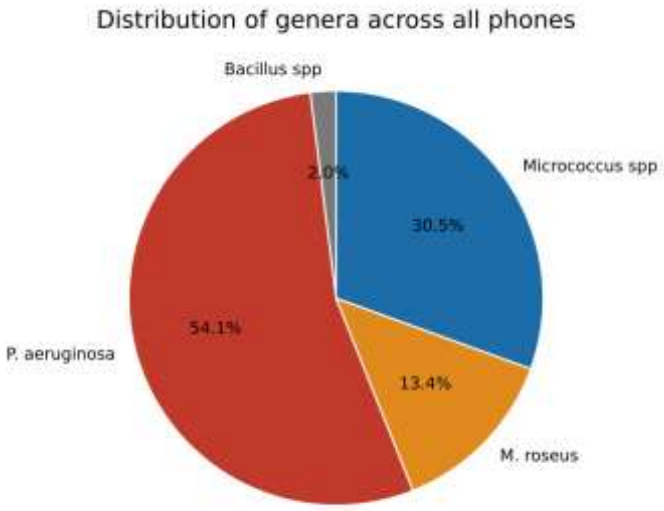


Figure 5: Distribution of genera across all phones

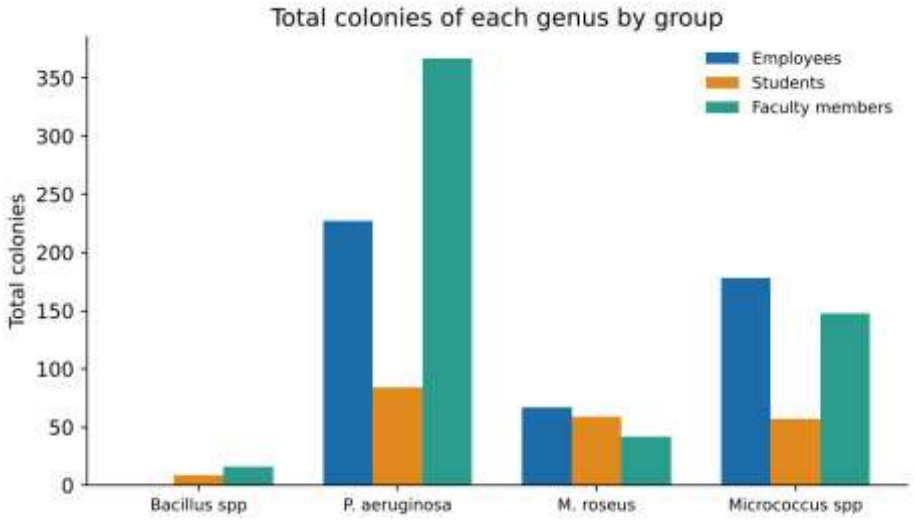


Figure 6: Total colonies of each genus by group

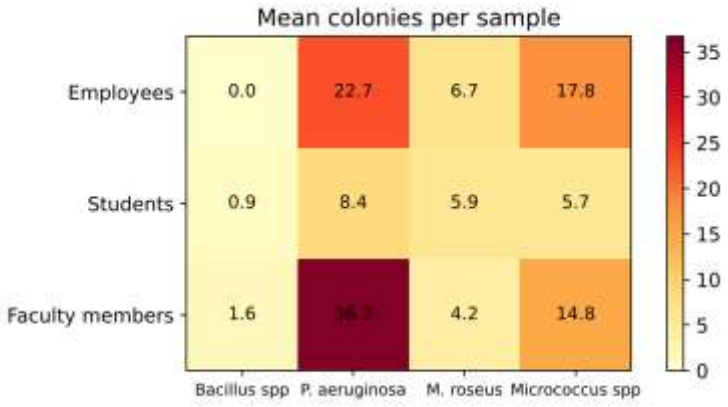


Figure 7: Mean colonies per sample (heat map) (Darker color = higher mean)

5) Inferential Statistical Tests

To test whether the differences between groups are statistically significant, the following tests were run at the 0.05 significance level.

1) Assumption checks

Table (6)

Shapiro–Wilk normality test on total colonies per sample

Group	W	P	Result
Employees	0.972	0.913	Normal
Students	0.878	0.124	Normal
Faculty members	0.960	0.781	Normal

The results presented in Table (6) show that the assumption of normality was examined using the Shapiro–Wilk test to determine the appropriate statistical approach for comparing total bacterial colony counts among employees, students, and faculty members. The findings indicated that the distribution of total colony counts did not significantly deviate from normality in any of the three groups. Specifically, the

employees' group demonstrated a Shapiro–Wilk statistic of (W = 0.972), with a non-significant result (p = 0.913\, while the students' group recorded (W = 0.878) (p = 0.124). Similarly, the faculty members' group showed (W = 0.960) (p = 0.781). Since all p-values exceeded the .05 significance level, the null hypothesis of normality was not rejected for any group. However, Levene's test revealed a statistically significant difference in variances among the three groups (F = 3.86), (p = 0.034), indicating that the assumption of homogeneity of variances was violated. Considering the relatively small sample size in each group (n = 10) and the unequal variances, the Kruskal–Wallis test was selected as the primary inferential procedure for comparing bacterial colony counts across the groups, while one-way analysis of variance (ANOVA) was retained as a supplementary comparative analysis. Overall, these preliminary assumption checks supported the use of a non-parametric approach as the main method for evaluating differences in bacterial contamination among the three study groups.

2) Comparing total contamination between groups

Table (7)

Comparison of total colonies per sample across the three groups

Test	Statistic	P	Decision
Kruskal–Wallis (H)	11.45	0.003	Significant
One-way ANOVA (F)	8.43	0.001	Significant

The results presented in Table (7) indicate that statistically significant differences existed in the total bacterial colony counts per sample among employees, students, and faculty members at the Faculty of Science, University of Zawia. The Kruskal–Wallis test revealed a statistically significant difference among the three groups, (H = 11.45), (p = 0.003), indicating that the distribution of bacterial contamination levels was not the same across the groups. This finding was further supported by the one-way analysis of variance (ANOVA), which also demonstrated statistically significant differences, (F = 8.43), (p = 0.001). Both statistical procedures therefore provided consistent evidence of differences in bacterial contamination among the study groups.

Table (8)

Pairwise comparisons (Tukey HSD and Mann–Whitney with Bonferroni correction)

Comparison	Mean difference	P (Tukey)	P (Mann–Whitney, adjusted)	Decision
Employees vs Students	26.3	0.021	0.011	Significant
Employees vs Faculty members	−10.1	0.520	1.000	Not significant
Students vs Faculty members	−36.4	0.001	0.017	Significant

The results presented in Table (8) show the pairwise comparisons of total bacterial colony counts among employees, students, and faculty members using Tukey's Honestly Significant Difference (HSD) test and the Mann–Whitney U test with Bonferroni correction. The comparison between employees and students revealed a statistically significant difference, with a mean difference of 26.30 colonies, according to both Tukey's HSD test (p = 0.021) and the adjusted Mann–Whitney test (p = 0.011). This indicates that employees' mobile phones had significantly higher bacterial colony counts than students' phones. Similarly, a statistically significant difference was observed between students and faculty members, with a mean difference of -36.40 colonies, supported by Tukey's HSD test (p = 0.001) and the adjusted Mann–Whitney test (p = 0.017). The negative mean difference indicates that faculty members' phones had higher average bacterial colony counts than students' phones. In contrast, the comparison between employees and faculty members did not reveal a statistically significant difference, despite the observed mean difference of -10.10 colonies (Tukey's HSD, (p = 0.520); adjusted Mann–Whitney, (p = 1.000). This suggests that although faculty members recorded a higher average bacterial colony count than employees, the difference was not statistically significant. Overall, the pairwise comparisons indicate that students' mobile phones had significantly lower bacterial contamination levels than both employees' and faculty members' phones, whereas

the difference between employees and faculty members was not statistically significant.

3) Relationship between group and bacterial genus

Table (9)

Kruskal–Wallis test for each genus across groups

Genus	H	P	Decision
Bacillus spp	10.05	0.007	Significant
Pseudomonas aeruginosa	15.46	< 0.001	Significant
Micrococcus roseus	1.22	0.543	Not significant
Micrococcus spp	6.69	0.035	Significant

The results presented in Table (9) indicate that the distribution of bacterial genera differed significantly across the three study groups, as demonstrated by the chi-square test of independence, which revealed a statistically significant association between group membership and bacterial genus (chi^2 = 101.10), (df = 6), (p < 0.001). The strength of this association, measured using Cramér's V, was 0.201, indicating a weak-to-moderate association between the type of mobile phone user and the composition of bacterial isolates. To examine these differences further, separate Kruskal–Wallis tests were conducted for each bacterial genus. The findings revealed statistically significant differences in the distribution of *Bacillus spp*. across the three groups ((H = 10.05), (p = 0.007)). Similarly*, Pseudomonas aeruginosa* demonstrated a statistically significant difference ((H = 15.46), (p < 0.001)), indicating that the number of recovered colonies of this genus varied significantly according to group membership. Furthermore, *Micrococcus spp*. showed a statistically significant difference across the groups ((H = 6.69), (p = 0.035)). In contrast, no statistically significant difference was observed for *Micrococcus roseus* ((H = 1.22), (p = 0.543)), suggesting that its distribution did not vary significantly among employees, students, and faculty members. Overall, these findings indicate that the bacterial composition of mobile phone contamination was associated with the category of users, with significant between-group differences identified for *Bacillus spp.*, *Pseudomonas aeruginosa*, and

Micrococcus spp., whereas Micrococcus roseus showed a relatively similar distribution across the three groups.

Summary of Results

The present study investigated the isolation and distribution of bacterial contaminants from mobile phones belonging to students, faculty members, and employees at the Faculty of Science, University of Zawia. A total of 30 mobile phone samples were examined, comprising 10 samples from each group, yielding 1,254 bacterial colonies. The findings demonstrated that all examined mobile phones (100%) were contaminated with bacterial isolates, indicating the widespread occurrence of bacterial contamination among the different categories of university members.

Regarding bacterial contamination among employees, a total of 472 bacterial colonies were recovered, with an average of 47.20 colonies per sample (SD = 15.65). *Pseudomonas aeruginosa* was the predominant isolate, accounting for 48.09% of the recovered colonies, followed by *Micrococcus spp*. (37.71%) and Micrococcus roseus (14.19%). No *Bacillus spp*. colonies were detected in this group. Among students, 209 bacterial colonies were recovered, with an average of 20.90 colonies per sample (SD = 13.50). *Pseudomonas aeruginosa* was also the most frequently recovered genus, representing 40.19% of the total colonies, followed by *Micrococcus roseus* (28.23%), *Micrococcus spp*. (27.27%), and *Bacillus spp*. (4.31%). For faculty members, the highest total number of colonies was recorded, reaching 573, with an average of 57.30 colonies per sample (SD = 28.80

. *Pseudomonas aeruginosa* was the predominant isolate, accounting for 64.05% of the colonies, followed by *Micrococcus spp*. (25.83%), *Micrococcus roseus* (7.33%), and *Bacillus spp*. (2.79%).

Comparison of bacterial contamination across the three groups revealed that faculty members accounted for the largest proportion of the total recovered colonies (45.69%), followed by employees (37.64%) and students (16.67%). Similarly, faculty members recorded the highest mean number of colonies per sample (57.30), followed by employees (47.20), whereas students had the lowest mean (20.90). Regarding the coefficient of variation, students exhibited the greatest relative variability in bacterial colony counts (64.6%), followed by faculty members (50.3%) and employees (33.2%), indicating greater heterogeneity in contamination levels among students.
;

With respect to the overall prevalence of the isolated bacterial genera, *Pseudomonas aeruginosa* was the most predominant isolate, accounting for 678 colonies $(54.07\%$ of all recovered colonies), followed by *Micrococcus spp*. with 383 colonies (30.54%), and *Micrococcus roseus*, with 168 colonies (13.40%). Bacillus spp. was the least frequently isolated group, accounting for only 25 colonies (1.99%). These findings demonstrate that *Pseudomonas aeruginosa* represented more than half of all recovered bacterial colonies was the predominant isolate across all three study groups and.

The inferential statistical analysis provided further evidence of differences in bacterial contamination among the study groups. The Shapiro–Wilk test indicated no statistically significant departure from normality in any group (employees: $(W = 0.972)$, $(p = 0.913)$; students: $(W = 0.878)$, $(p = 0.124)$; faculty members: $(W = 0.960)$, $(p = 0.781)$. However, Levene's test demonstrated unequal variances among the groups $((F = 3.86)$, $(p = 0.034))$. Consequently, the Kruskal–Wallis test was selected as the primary method for comparing total bacterial colony counts. The results revealed statistically significant differences among employees, students, and faculty members $((H = 11.45)$, $(p = 0.003))$. The one-way ANOVA also indicated statistically significant differences $((F = 8.43)$, $(p = 0.001))$, supporting the overall finding of between-group variation.

Pairwise comparisons using the Mann–Whitney U test with Bonferroni correction further clarified these differences. Statistically significant differences were observed between employees and students $(p = 0.011)$ and between students and faculty members $(p = 0.017)$. In both comparisons, students recorded lower bacterial colony counts. However, no statistically significant difference was identified between employees and faculty members $(p = 1.000)$. These findings indicate that students' mobile phones had significantly lower bacterial contamination levels than those of the other two groups, whereas employees and faculty members demonstrated statistically comparable contamination levels.

Finally, the chi-square test of independence revealed a statistically significant association between the study group and the distribution of bacterial genera $((chi^2 = 101.10)$, $(df = 6)$, $(p < 0.001))$, with Cramér's V of 0.201, indicating a weak-to-moderate association. Separate Kruskal–Wallis tests demonstrated statistically significant differences among the groups for **Bacillus spp.** $((H = 10.05)$, $(p = 0.007))$,

Pseudomonas aeruginosa ((H = 15.46), (p < 0.001)), and *Micrococcus spp*. ((H = 6.69), (p = 0.035)). In contrast, no statistically significant difference was observed for *Micrococcus roseus* ((H = 1.22), (p = 0.543)). Collectively, these findings indicate that bacterial contamination of mobile phones was widespread and that both the overall bacterial burden and the composition of bacterial isolates varied according to the category of mobile phone users

Discussion

The present study investigated bacterial contamination on mobile phones belonging to students, faculty members, and employees at the Faculty of Science, University of Zawia. All 30 examined phones yielded bacterial growth, and 1,254 bacterial colonies were recovered. This finding indicates that recoverable bacterial contamination was widespread in the study population.

The 100% contamination rate observed in this study was similar to the rate reported by Al-Abdalall, who found microbial contamination on all 202 mobile phones examined (Al-Abdalall, 2010). A comparable result was Others reported, where all 40 electronic devices examined were contaminated with bacteria (Uwizeyimana et al.,2024). In contrast, contamination was reported in 79% of mobile phones belonging to healthcare workers in Lusaka, Zambia (Mushabati et al.,2021) and in 43.5% of the phones examined at the University of Kerbala (Alsaadi et al.,2026). The Jordanian study reported bacterial growth in 29% of the total hand and mobile-phone swabs (Al AL (AlMomani et al.,2019) The high recovery rate in the current study may be related to repeated handling of mobile phones and their frequent contact with hands and other surfaces.

The most notable finding was the predominance of *Pseudomonas aeruginosa*, which accounted for 678 colonies (54.07% of all recovered colonies). This organism was the predominant isolate in each of the three study groups. It is also in agreement with those obtained by (Elbarghathi et al.,2025) the isolates obtained from mobile phones of health workers in a health facility in Libya with *P. aeruginosa*, the highest prevalence at 21.6%. on the other hand This pattern differs from most of the comparison studies. In Dammam, *P. aeruginosa* represented 8.01% of the bacterial isolates, while *Staphylococcus aureus* was predominant at 56.58% (Al-Abdalall, 2010). In the study (Gangmei,et.l,2026) of student mobile phones, *Pseudomonas spp*. accounted for 4% of isolates The corresponding proportions were 1.7% in the study (Alsaadi et al.,2026),

3.1% in the study(Mushabat,et.l2021).and 5.5% in the study of electronic devices (Uwizeyimana et al.,2024). The study (Jamalludeen,2020) reported a higher proportion of *P. aeruginosa* than these investigations, at 15.3%, but this was still substantially lower than the proportion observed in the present study .

The high proportion of *P. aeruginosa* in the current study may be related to local environmental conditions, differences in the surfaces sampled, culture media, or identification. procedures.

The second important pattern involved *Micrococcus spp*. and *Micrococcus roseus*. *Micrococcus spp*. accounted for 383 colonies (30.54%), whereas *Micrococcus roseus* accounted for 168 colonies (13.40%). The recovery of *Micrococcus spp*. and *Micrococcus roseus* may be explained by their association with frequently contacted surfaces and normal skin flora. Similar explanations were given studies for the occurrence of skin-associated bacteria on phones and electronic interfaces(Roy et al.,2026, Pierre,et.l,2024, Jamalludeen,2020).

Bacillus spp. was the least frequent bacterial group in the present study, accounting for 25 colonies (1.99%). This proportion was lower than the values reported (Hamidu& Yunusa, 2024) (11%), (Mushabati et al.,2021) (14.3%), and (Uwizeyimana,2024) (24.1%) .It was also lower than the proportion reported for *Bacillus subtilis* (2.2%) (Jamalludeen,2020). Bacillus species are widely distributed in soil and the environment, and their spores may persist under unfavourable conditions. The variation between studies may therefore be related to environmental exposure, the surfaces sampled, and the culture procedures. The bacterial profile of the present study differed from that reported in a study of healthcare workers at Alexandria University, Egypt, in which S. aureus and S. epidermidis were the predominant organisms (Selim et al., 2015). The profile also differed from that reported (Jamalludeen, 2020) study, in which *Staphylococcus aureus* was followed by P. *aeruginosa*, *Escherichia coli*, and Proteus spp. The study also reported Acinetobacter baumannii, Neisseria sicca, Enterobacter aerogenes, and *Candida spp*. These organisms were not reported among the isolates in the present study. Likewise, the (Alsaadi et al.,2026) study identified a broad range of organisms, including several Staphylococcus species, *Escherichia.coli*, Proteus mirabilis, Acinetobacter, Aeromonas, and other environmental bacteria .The Gangmei et al.,2026). study also recovered *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus spp.*, and *Staphylococcus aureus*-. These differences indicate that mobile-phone contamination is not

microbiologically uniform and may be influenced by the surrounding environment, the characteristics of the users, and the laboratory methods applied. The absence of *Escherichia coli*, *Klebsiella*, Proteus, and Enterobacter in the present results should not be interpreted as evidence that faecal or enteric contamination could not occur on phones in the study setting. These organisms were detected in several comparison studies.

The study (Al Momani et al.,2019)provides an additional comparison because it examined both students' hands and mobile phones. Bacterial recovery was higher from hands than from phones, suggesting that the hand may be an important source of organisms transferred to mobile surfaces (Al Momani et al.,2019). That study identified S. epidermidis as the most frequent organism and found a lower level of phone contamination than the present investigation. It also reported differences between academic groups, particularly among veterinary and biology students, and related these differences to contact with animals or infectious material (Al Momani et al.,2019).

Overall, the findings are consistent with previous reports showing that mobile phones and other electronic interfaces may carry skin-associated, environmental, and potentially opportunistic bacteria, although the predominant organisms differ between populations (Al-Abdalall, 2010; Elbarghathi et al.,2025). In the present study, the high proportion of *Pseudomonas aeruginosa*. aeruginosa and the significant differences between user groups support the need for practical preventive measures, such as regular cleaning of phone surfaces and appropriate hand hygiene.

Conclusions

Bacterial contamination was detected in all examined mobile phones, demonstrating that mobile devices represent potential reservoirs of bacterial contamination within the Faculty of Science, University of Zawia.

1. *Pseudomonas aeruginosa* was the predominant bacterial isolate, accounting for 54.07% of all recovered colonies, making it the most frequently recovered bacterial genus across the three study groups.
2. *Micrococcus spp*. ranked second in overall abundance, followed by Micrococcus roseus, whereas Bacillus spp. represented the least frequently recovered bacterial group.

3. Faculty members' mobile phones exhibited the highest average bacterial colony count, followed by employees' phones, while students' phones recorded the lowest average contamination level.
4. Statistically significant differences existed in total bacterial contamination among the three study groups, indicating that the bacterial burden was not uniform across different categories of mobile phone users.
5. Pairwise comparisons demonstrated that students' mobile phones had significantly lower bacterial colony counts than those of employees and faculty members. However, no statistically significant difference was observed between employees and faculty members.
6. The distribution of bacterial genera was significantly associated with the category of mobile phone users, particularly regarding *Bacillus spp*. , *Pseudomonas aeruginosa*, and *Micrococcus spp*.
7. The findings highlight the importance of mobile phone hygiene as a potential component of infection prevention and control practices within university environments.
8. Although bacterial isolates were successfully recovered and identified, the findings do not establish that all detected bacteria were pathogenic or that mobile phones directly caused infections among university members.

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