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# Comparison of Bacterial Contamination between I Phone and Galaxy Devices

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**Abstract:** ***Ninety eight mobile samples, (54) galaxy phone and (44) I phone, were swabbed for bacterial culture determination by culturing on MacConky agar , Blood agar , Mannitol salt agar , Muller Hinton agar .Staphylococcuswas the highest frequent isolated bacteria from Galaxy phone (33%) and I phone (37%). This study revealed that galaxy phone appears less contaminated with bacteria, the ratio of non-contaminated devices is (44%) when compared with I phone (9%). Sensitivity test showed that Ogmintin have the lowest effect on Staphylococcusisolated from both type of devices while cefitriaxone have the highest effect. DNA of isolate from galaxy 31 that exhibit highest resistance against antibiotics was extracted and 16S rRNA gene was polymerized by PCR and sequenced by microgencompany , the result identified as Staphylococcus aureus.***

**Keywords:** galaxy, I phone, *Staphylococcus aureus*

## 1. Introduction

Cell phones are commonly used almost everywhere as one of the essential devices used for communication in daily life. [1]Mobile devices act as a vehicle for transmitting pathogenic bacteria and other microorganisms as a result of heavy use of it [2,3].In recent years much importance of contaminated mobile phones has been noticed. 5-21% of mobile phones of healthcare workers were seem contaminated, and therefore it considered as important source of nosocomial infections [4]. Another studies confirmed the previous results and indicate that phones of medical students can act as transmission vehicles for both pathogenic and nonpathogenic organisms [5] Healthcare workers cell phones were contaminated with microorganism in high percentage that may reach > 90% of them and pathogenic bacteria that cause nosocomial infections compromise > 14% of them [6]. Mobile phones showed in several results as harbor a number of pathogenic bacteria including **methicillin resistant *Staphylococcus aureus*** (MRSA) and for that it considered as a potential threat in spreading nosocomial infections [7]Teachers and lectures mobile phones also may be serving as a potential vehicle for spreading pathogenic microorganisms. [1]. Mouthpiece, earpiece and the handles part of mobile phone seems to be as highest microbial concentrations than other parts. In the past public payphones considered as a considerable source for person to person infection but now it decreased dramatically after the mobile be as a popular device that most of peoples have their own one. Generally, cell phones with buttons and keyboards and other personal mobile phones have been found to be more conducive to bacterial contamination [8]. Normal flora of the skin and body compromise the majority of bacterial species that have been found on phone surfaces, due to the constant contact with the hands and face. The most common species being *Staphylococcus epidermidis* and *Corynebacteria* .That considered as normal flora of the skin includes with very high account up to $10^{12}$ bacterial cells[9] In our study we compared the bacterialcontamination on Galaxy phone and I phone

## 2. Materials and Methods

**Sample collection**

Near of 100 swab samples were collected from I phone and galaxy female mobile, Theswabs were analyzed using streak plate technique, cell phones belonging to 98 female students (54 galaxy and 44 Iphone) at Baghdad University were screened. The mobile phone was first held with caring of all sterile conditions and swabbed with the sterile swab moisturized with saline ,itrotated over the surface of both sides of the mobile phone.

**Swab culture**

The sampled mobile phone swab was streaked onto blood agar and preserved in nutrient broth. The inoculated plates and tubes were incubated aerobically in at 37 °C for 48 hours. MacConky agar wasstreaked by swabs. The plates were then observed for the presence of isolated colonies. The isolated microorganisms were transfer from the petriplate to a tube containing the nutrient agar (slant) for preservation .then, cultures of isolates colony of bacterial were characterized based on morphological and biochemical tests of Bergy's manual of systematic bacteriology was used as reference for identification.

**Antibiotic sensitivity test**

Some of bacteria obtained during the research were examined for antibiotic sensitivity by preparing the appropriate suspension of bacterial culture depending on McFarland standard tube and swabbed on Muller Hinton agar then four types of antibiotics were used Vancomycin , Augmentin , Ceftriaxone and Cloxacillin and incubated in right manner at 37°C for 24 hr. The inhibition zonewere measured for all tested isolates with antibiotics.

**DNA Extraction**

*S. aureua*bacterial samples used for DNA extraction, bacterial using G- spin DNA extraction kit, intron biotechnology and according to the kit protocol. Primers were, Forward5'- AGAGTTTGATCCTGGCTCAG- 3', Reverse 5'- GGTTACCTTGTTACGACTT- 3'. Annealing temperature was 52.

**Prepare of the Agarose gel**
Agarose gel was prepared according to Sambrook et al,.1989, the agarose gel has been made in 1.7% condensation.

**Sequencing for *S. aureua* PCR product**
The samples were sent to Microgen /koria, for gene sequencing. Using genetic analyzer (Applied Biosystem) and homology search was performed and also using (BLAST) program online blastn and blastx algorithms at NCBI.

## 3. Result and Discussion

When compare results of culturing of two types of devices we can notice the followings:33% of galaxy phone were contaminated with ***Staphylococcus*** comparing with I phone that 37% of them were contaminated with the same genus. The most commonly species found was ***Staphylococcus epidermidis*** on phone surfaces .It form a large part of the normal skin flora,and it can be a pathogen in hospital patients that have compromised immune systems [10].Phones considered as a poor environment for ***S. epidermidis*** growth and colonize but it can serve as vectors that can transmit the bacteria via contactwith plastic surfaces, such as that used in the body like, catheters and prosthetic implants inside the body. [11]. Seasonal variations have small effect on contamination rate of ***S.epidermidis*** on phones [12](Table 1).

**Table 1:** bacterial isolated from galaxy phone and I phone

| | Galaxy | | i phone | |
|---|---|---|---|---|
| *Staphylococcus* | 18 | 33% | 16 | 37% |
| *Streptococcus* | - | 0% | 4 | 9% |
| *Staph + Strep* | 3 | 6% | 1 | 2% |
| *Bacillus* | 9 | 17% | 19 | 43% |
| No growth | 24 | 44% | 4 | 9% |
| Total no. | 54 | 100% | 44 | 100% |

Nosocomial infections was common caused by ***Staphylococcus aureus*** [2]. Itnormally found on the skin, as well the human respiratory tract [13]. Mobile phones may be a health hazard with thousands of microbes living on each square inch of the devise. ***Staphylococci***and***S. epidermidis*** are normal flora of the human skin, respiratory and gastrointestinal tracts (14). Nasal carriage of ***S. aureus***may be in 20-50% of human beings. ***Staphylococci***also may be found on clothes, beds (15). ***Staphylococcus aureus***, a common bacterium that found on the skin and in noses of up to 25% of healthy people and also animals which can cause diseases from pimples and boils to pneumonia and may be meningitis that is aclose relative of methicillin resistant ***Staphylococcus aureus*** (MRSA) (16).*Streptococcus* contamination appears in 9% of I phone devices and didn't appear in galaxy phone but it appear in with *Staphylococcus* in 6%. Low number of *Streptococcus* comparing to *Staphylococcus* may be to their site, in tonsil and who suffered from respiratory disease, for that we notice that Streptococcus appear with students who have some disease, another thing is the ability of*Staphylococcus* to tolerate adverse condition more than *Streptococcus.*

Contamination with *Bacillus* seems very high in I phone (43%) comparing to galaxy phone (17%). We can't decide her that the phone is the main causative agents for this type of bacteria according to its wide distribution in the environment especially dusty place, it may be as a resulted from personal behavior and habit. Furthermore, its wide spread and it have the ability to tolerate different environmental factors by having spores that make the mobile phone as a mean for their transition and according to that its effect on medically important transmitted bacteria are neglected in most researches.

Finally, 44% of galaxy phone gave negative result (no bacteria founded) that is representing 5 times more than I phone devices that gave only 9% without any growth. This difference may be as a result to the personal behavior and to the physical properties of the device program (temperature). Galaxy phone note device warms during the use and its temperature elevates many time more than that happened with I phone devices. So high temperature of galaxy phone during the use can be represent as good character (biologically) that can act as inhibitor factor for bacterial contaminant. So we can see that I phone devices are more contaminated with all types of bacteria comparing with galaxy device.

Constant handling of mobile device will generate good heat for bacterial growth especially skin flora by two ways: first one by body temperature that will transfer to the phone device, second one come from the prolong usage of mobile that generate heat from their processor, and according to that some types of bacteria will thrive especially when this factor accompanied with low hygiene behavior. Rising in infection rates as a result of mobile phone was increasedin the last years and it may be as a reflect the wide range distribution of these devices among all people despite their origin , work, sex and even age. Gram negative bacteria appeared in very small number, two genus appeared , *E.coli*and *Klebsiella* , I phone have larger proportion of *E.coli* contamination (9%) comparing with galaxy(3.7%), the same thing noted with *Klebsiella*9% 0f I phone contaminated with it comparing to 5.5% of galaxy that have contaminated with same bacteria. This small number may be as a result of the group of people that selected for sample collection, we selected female students of science collage in Baghdad university, female college students care themselves and their personal cleaning more than others, if we select another group we think the proportion of these genus would be raised more than what obtained in this study(table 2)

**Table 2:** G-ve Bacteria isolated from galaxy phone and I phone

| | Galaxy | | I phone | |
|---|---|---|---|---|
| E. coli | 2 | 3.7% | 4 | 9% |
| Klebsiella | 3 | 5.5% | 4 | 9% |

**Antibiotic Sensitivity Result**
From table 3 we can conclude that ogmintin have the lowest effect on different ***Staphylococcus*** isolated from Galaxy phone with 12 mm inhibition zone mean while cefitriaxone have the highest effect with 18.5 mm inhibition zone mean. The same conclusion was reached with table 4 that ogmintin have the lowest effect on different ***Staphylococcus*** isolated

from I phone with 10.7 mm inhibition zone mean while cefitriaxone have the highest effect with 23 mm inhibition zone mean. In general *Staphylococcus aureus* isolated from Galaxy 31 seems as highest resistance so its identification was confirmed by sequencing of 16S rRNA gene.

**Table 3:** Inhibition Zone Diameter of antibiotics on Staphylococcus isolated from Galaxy Phone

| | Galaxy -3- | Galaxy -15- | Galaxy -23- | Galaxy -31- | Mean |
|---|---|---|---|---|---|
| Vanco | 16 mm | 14 mm | 16 mm | 12 mm | 14.5 |
| Cefitri | 25 mm | 23 mm | 13 mm | 13 mm | 18.5 |
| Ogmin | 11 mm | 12 mm | 14 mm | 11 mm | 12 |
| Cloxlli | 17 mm | 18 mm | 12 mm | 12 mm | 14.75 |

**Table 4:** Inhibition Zone Diameter of antibiotics on Staphylococcus isolated from I phone

| | I phone-14- | I phone -15- | I phone -30- | Mean |
|---|---|---|---|---|
| Vancomycin | 15 mm | 9 mm | 19 mm | 14.3 |
| Cefitriaxone | 23 mm | 13 mm | 33 mm | 23 |
| Ogmintin | 13 mm | 10 mm | 9 mm | 10.7 |
| Cloxacillin | 18 mm | 12 mm | 23 mm | 17.7 |

**Identification of isolate by 16S rRNA**

The Identification of ***S. aureus*** as it is the highest resistant bacteria isolated in our study from galaxy device no. 31 confirmed by PCR to the 16S ribosomal RNA gene(fig 1). The sequencing results of the gene confirmed our findings. As shows in table 1our strain was compared with 11 submitted strains to create the relationship.When the strain sequence compared with submitted strain of staphylococci it seems highly resembling that the query sequence and subject sequence mismatched in 3 base pairing only, in the 65,403 and 953 sites labeled in red color in figure 2. The relationship between them presented as a phylogenetic tree as shown in figure 3.

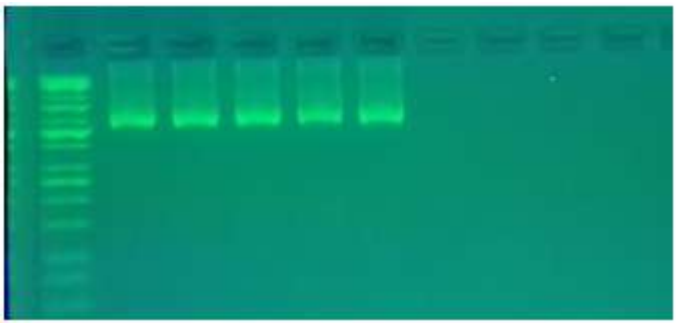

**Figure 1:** PCR product the band size 1250 bp. The product was electrophoresis on 1.7% agarose at 5volt/cm$^2$. 1x TBE buffer for 1:30 hours. N: DNA ladder (100)

**Table 1:** Sequencing ID in GenBank, score, Expect and compatibility of sequences for *S.aureus* partial 16S rRNA gene.

| | ACCESSION | strain | country | Source | Compatibility | expect | score | Range |
|---|---|---|---|---|---|---|---|---|
| 1 | ID: JF431908.1 | strain B3 | Colombia | *Staphylococcus aureus* | 99% | 0 | 2071 | 1 to 1130 |
| 2 | ID: X68417.1 | strain="ATCC 12600 | FRG | *S.aureus* | 98% | 0 | 1977 | 62 to 1191 |
| 3 | ID: KU354461.1 | strain SY3 | Malaysia | *Staphylococcus aureus* | 98% | 0 | 1971 | 42 to 1171 |
| 4 | ID: KY007579.1 | --------- | USA | *Staphylococcus aureus* | 98% | 0 | 1965 | 54 to 1183 |
| 5 | ID: MF144449.1 | strain FQIV | Peru | *Staphylococcus aureus* | 98% | 0 | 1965 | 38 to 1167 |
| 6 | ID: NR_118997.2 | strain ATCC 12600 | FRG | *Staphylococcus aureus* | 98% | 0 | 1977 | 61 to 1190 |
| 7 | ID: MF784283.1 | strain="s1266-9 | China | *Staphylococcus aureus* | 98% | 0 | 1965 | 18 to 1147 |
| 8 | ID: CP017682.1 | strain CFSAN007850 | USA | *Staphylococcus aureus* | 98% | 0 | 1971 | 516671 to 517800 |
| 9 | ID: CP014420.1 | strain USA300-SUR16 | Suriname: Paramaribo | *Staphylococcus aureus* | 98% | 0 | 1965 | 557060 to 558189 |
| 10 | ID: CP019117.1 | strain SJTUF_J27 | China: Shanghai | *Staphylococcus aureus* | 98% | 0 | 1965 | 510847 to 511976 |
| 11 | ID: CP014397.1 | strain USA300-SUR10 | Suriname: Paramaribo | *Staphylococcus aureus* | 98% | 0 | 1965 | 556971 to 558100 |

***Staphylococcus aureus*** strain B3 16S ribosomal RNA gene, partial sequence
Sequence ID: JF431908.1Length: 1384Number of Matches: 1
Related Information

Range 1: 1 to 1130GenBankGraphicsNext MatchPrevious Match

Alignment statistics for match #1

| Score | Expect | Identities | Gaps | Strand |
|---|---|---|---|---|
| 2071 bits(1121) | 0.0 | 1127/1130(99%) | 0/1130(0%) | Plus/Plus |

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Query 1 GTCGAGCGAACAGATAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAACA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1 GTCGAGCGAACAGATAAGGAGCTTGCTCCTTTGACGTTAGCGGCGGACGGGTGAGTAACA 60

Query 61 CGTGGGTAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATACCGGATA 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 61 CGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCTAATACCGGATA 120

Query 121 ACATATTGAACCGCATGGTTCAATAGTGAAAGGCGGCTTTGCTGTCACTTATAGATGGAT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 121 ACATATTGAACCGCATGGTTCAATAGTGAAAGGCGGCTTTGCTGTCACTTATAGATGGAT 180

Query 181 CCGCGCCGTATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATACGTAGCCGA 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 181 CCGCGCCGTATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATACGTAGCCGA 240
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Query 241 CCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCA 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 241 CCTGAGAGGGTGATCGGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCA 300

Query 301 GCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATG 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 301 GCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGAGTGATG 360

Query 361 AAGGTCTTCGGATCGTAAAACTCTGTTATCAGGGAAGAACATATGTGTAAGTAACTGTGC 420
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 361 AAGGTCTTCGGATCGTAAAACTCTGTTATCAGGGAAGAACAAATGTGTAAGTAACTGTGC 420

Query 421 ACATCTTGACGGTACCTGATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAA 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 421 ACATCTTGACGGTACCTGATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAA 480

Query 481 TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTT 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 481 TACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTTTT 540

Query 541 TAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTT 600
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 541 TAAGTCTGATGTGAAAGCCCACGGCTCAACCGTGGAGGGTCATTGGAAACTGGAAAACTT 600

Query 601 GAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAG 660
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 601 GAGTGCAGAAGAGGAAAGTGGAATTCCATGTGTAGCGGTGAAATGCGCAGAGATATGGAG 660

Query 661 GAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTG 720
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 661 GAACACCAGTGGCGAAGGCGACTTTCTGGTCTGTAACTGACGCTGATGTGCGAAAGCGTG 720

Query 721 GGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGT 780
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 721 GGGATCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGT 780

Query 781 TAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTA 840
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 781 TAGGGGGTTTCCGCCCCTTAGTGCTGCAGCTAACGCATTAAGCACTCCGCCTGGGGAGTA 840

Query 841 CGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGT 900
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 841 CGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGT 900

Query 901 GGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTGACAGCTCTA 960
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 901 GGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCTTTGACCGCTCTA 960

Query 961 GAGATAGAGTCTTCCCCTTCGGGGGACAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCT 1020
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 961 GAGATAGAGTCTTCCCCTTCGGGGGACAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCT 1020

Query 1021 CGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCA 1080
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1021 CGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCA 1080

Query 1081 TCATTAAGTTGGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAG 1130
 ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 1081 TCATTAAGTTGGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAG 1130
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**Figure 2:** The similarity value of query with subject sequence of Staphylococcus aureus strain B3 16S ribosomal RNA gene, partial sequence Sequence ID: JF431908.1

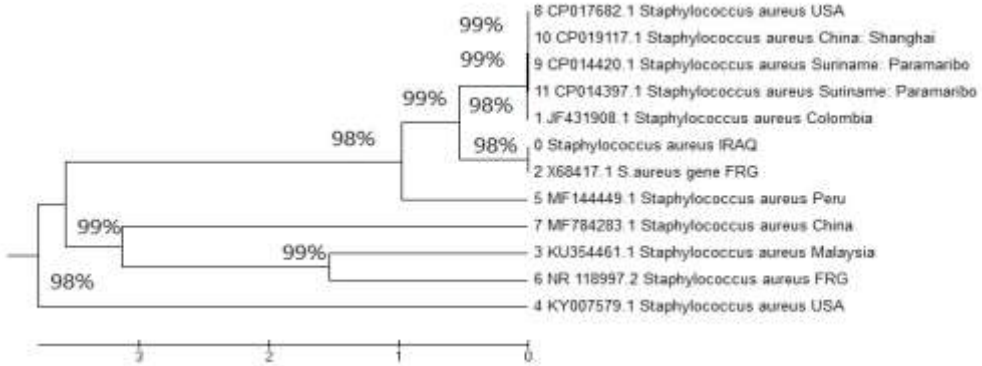


**Figure 3:** Evolutionary relationships of local strains of *S. aureus*as demonstrated asPhylogenetic tree

The sequence results of the isolate of *S. aureus*in this study show high similarity to deferent strains in different countries with relationship up to 98% with most of them and it closely releatedto*S. aureus*FRG. The similarity value of our isolate with comparative strains all above 97% that mean it belong to the same species ,***Staphylococcusaureus*** , but it may represent as another strain .

## 4. Conclusion

*Staphylococcus* is the dominant genus that cause mobile contamination in both Galaxy phone and I phone ,Galaxy devices had lower percentage of contamination than I phone. Ogmintin have the lowest effect on *Staphylococcus* isolated from both type of devices while cefitriaxone have the highest effect. Isolate with highest resistance was sequenced and it reveals that is *Staphylococcus aureus* and it closely resemble with *Staphylococcus aureus*FRG. (X68417.1).

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