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Isolation and Identification of *Staphylococcus aureus* Isolated from Mobile Phone Using 16S rRNA

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Structured Abstract

Background: *Staphylococcus aureus* is a major opportunistic pathogen that causes skin infections, pneumonia, and sepsis. *S. aureus* lives on often touched objects like mobile phones. Molecular techniques like 16S ribosomal RNA (rRNA) gene sequencing have made bacterial identification much easier. This study uses 16S rRNA gene sequencing to identify *S. aureus* bacteria from mobile phone surfaces.

Methods: After sterilisation with 70% alcohol, the phones were placed against human cheeks for contact with human skin. The phones were then sampled by moistening a sterile cotton bud with distilled water and swabbing it onto Mannitol Salt Agar (MSA) to obtain single colonies. To get pure colonies, the single colonies were isolated in Brain Heart Infusion agar (BHI). Pure colonies then were streak onto MSA, BHI, and Baird Parker Agar, (BPA). *S. aureus'* structure and features were then tested by catalase and Gram staining. Finally, PCR and gel electrophoresis to were conducted to amplify the targeted gene before DNA sequencing.

Results: The results show *Staphylococcus* grows selectively on MSA and BPA. *S. aureus* ferments mannitol and acidifies. The pH indicator phenol red turns MSA medium yellow below 6.9. The media around the bacterial colony remains pink because CONS cannot ferment mannitol and the formation of black or grey colonies on Baird Parker agar, indicating tellurite reduction. Gram stain showed *Staphylococcus* bacteria, which are small spherical (cocci) and form grape-like clusters. *S. aureus* and *S. epidermidis* were Gram-positive and should have been purple or blue. However, the bacteria were pink, indicating Gram stain troubleshooting difficulties. A catalase-positive result could be seen in the bubbles that were produced due to the production of oxygen gas. Gel electrophoresis showed bands solely for samples 1, 3, and 6, indicating positive DNA amplification. The absence of bands in samples 2, 4, and 5 shows no gene amplification.

Conclusion: In conclusion, *S. aureus* was identified by its growth patterns and metabolic reactions on selective and differential media. PCR and gel electrophoresis can determine species conformation in some samples. PCR results must be sequenced to identify bacteria species.

Keywords: *S. aureus,* catalase test, Gram stain, 16S rRNA, PCR

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