Research Article

Effective Use of Skin Microbiome Signature on Fingerprints For Individual Identification

Ms.Shivani[1*], Ms.Neha Jha[2], Dr.Shribhagwan[3] ,Dr.Rakesh Mishra[4], Dr.Bhumija Siwach[5]

[1]Department of Forensic Medicine & Toxicology, Santosh Medical College & Hospital, Ghaziabad, India
[2]Department of Forensic Medicine & Toxicology, Santosh Deemed to be University, Ghaziabad, India,
[3]Professor, Amrita School of Medicine, Faridabad, India
[4]Professor, Jamia Hamdard Forensic Medicine and Toxicology, New Delhi, India
[5]Professor, Amrita School of Medicine, Faridabad, India

Abstract

Introduction: The skin microbiota comprises of millions of bacteria, fungi's, and viruses that live on a dermal layer of skin. All of these particular microbiota areas were basically known as skin, gut, mouth, breathing passages, and urinary and reproductive areas. It is highlighted that telling apart the microbiota moved from a person's skin to the microbiota sample surfaces on the person's surrounding surfaces might help with criminal identification, like fingerprints. Studies have demonstrated that identification of people is possible by the observed microbiota traits of not change unchanged personal microbiota, traces left over on mouse, mobiles, and areas touched at home. **Aim:** This aim clearly sets out the objectives of exploring the skin microbiomes as an alternative or complementary method for biometric identification. **Methods**: All procedures in this study adhered to applicable ethical guidelines and legal regulations. Fifty healthy adult participants, aged 20 to 50 years, were recruited with careful consideration of variables known to influence skin microbiota, including occupational exposure, use of hand antiseptics or topical antibiotics, and frequency of public transportation use for 3 consecutive days, skin swab samples were collected from the middle finger of each participant's right hand, along with samples from their personal belongings. Participants were instructed to perform a minimum of seven handwashing events per day. Of the ten individuals, five were employed within the same department, and two were healthcare workers. Sample collection was conducted at varying times throughout the day and on non-fixed days to minimize temporal bias. All samples were obtained using sterile cotton-tipped swabs pre-moistened with sterile solution, a validated technique for skin microbiota sampling. **Results:** The data indicates that hospital/cleaning staff are at a higher risk of potentially pathogenic bacteria, notably Staphylococcus aureus and Gram-negative bacteria; college students, on the other hand, only exhibited colonization with environmental organisms; CoNS was present in both groups indicating that colonization/contamination occurred globally. There is a need for continuous hygiene training, especially among hospital/cleaning staff and a monitoring system of the microbial flora is vital to prevent potential nosocomial infections. Continual monitoring, or screening, as well as proper infection control measures, should be continuously encouraged to not only protect patients, but hospital/cleaning staff, also. **Conclusion:** A three-day study provided valuable insights into the types and prevalence of bacteria in hospital environments where staff and students work. The daily presence of Coagulase-Negative Staphylococci (CoNS) highlights their commonality as normal skin bacteria. However, CONS can cause infections, particularly when medical devices are used or in individuals with weakened immune systems, especially in hospitals.

Keywords: Skin microbiota, Biometric Identification, Hospital Hygiene, Skin Swab Sampling, Infection Control.

1. Introduction

The skin microbiota comprises of millions of bacterias, fungi's, and viruses that live on a dermal layer of skin. All of these particular microbiota areas were basically known as skin, gut, mouth, breathing passages, and urinary and reproductive areas. Even though new studies suggest that these particular microbiota areas reveal a person's race and background, it is specifically highly important to noted that the microbiota creates very unique identity with elements like a person's way of life, environment, or eating habits. Despite people's varied ways of living, the reality that each person has unique traits in their hand microbiota has proven to be beneficial across a range of fields. It is highlighted that telling apart the microbiota moved from a person's skin to the microbiota sample surfaces on the person's surrounding surfaces might help with criminal identification, like fingerprints. Studies have demonstrated that identification of people is possible by the observed microbiota traits of not change unchanged personal microbiota, traces left over on mouse, mobiles, and areas touched at home.

While fingerprints are a standard type of evidence in crime labs, they don't always tell us who someone is. By the use of the micro-organisms, which in each case are very different according to the person and the locality from which he hails, we have now at our disposal a new method for testing crimes. So while everyone is different, germs, studies

have been studied. Such as Propionibacterium acnes, which are typically in our main tiny living things on our skin, can help us identify one person from the next and give us some idea of who they are. Likewise, Staphylococcus epidermidis, a natural member of human skin, can also be used to pin down individuals in crime investigations. In our study, we sought to differentiate people and to discover the marks they make on things, using easy, fast, and cheap lab methods that hone in on S. epidermidis. All of this research was for finding these traces that carry evidence and differences that are personal in simple ways that don't require huge quantities of money or equipment.

One of the largest organ homosepians body surface is the skin. It is an important interface between the human body and the external environment that hosts the diverse complex microbial communities that very across multiple physiological and topographical different microenvironments (Grice et al., 2009).

Metagenomic shotgun sequencing has significantly enhenced are ability to study these communities at the level of nucleotide. Initialy Systematic metagenomic studies on the human skin microbiome were first conducted as part of the Human Microbiome Project (HMP) and, more recently through the integrative HMP (iHMP) multi-site (Oh et al., 2014) and tempor sequencing data. These includes metagenomic profiling, performed in 17 skin sites over three visits for a span of about three years on 12 healthy individuals, enabled us to learn about all the ways geography, people, and time can change things. Using known sequences, we carefully looked at what makes up and how the healthy skin's collection of tiny organisms works for bacteria, fungi, and viruses. Also, research has revealed that where you live and who you are greatly impact how a group works and what kinds of organisms, and that skin's tiny organisms mostly stay the same even when facing outside changes.

2. Method

All procedures in this study adhered to applicable ethical guidelines and legal regulations. Ten healthy adult participants, aged 20 to 50 years, were recruited with careful consideration of variables known to influence skin microbiota, including occupational exposure, use of hand antiseptics or topical antibiotics, and frequency of public transportation use (detailed in Table 1). For 3 consecutive days, skin swab samples were collected from the middle finger of each participant's right hand, along with samples from their personal belongings.

Participants were instructed to perform a minimum of seven handwashing events per day. Of the ten individuals, five were employed within the same department, and two were healthcare workers. Sample collection was conducted at varying times throughout the day and on non-fixed days to minimize temporal bias.

To assess microbial transfer between skin and surfaces, additional samples were collected from the space bar keys of two laptop keyboards located at Santosh Deemed to Be University, as well as one private and one public keyboard. All samples were obtained using sterile cotton-tipped swabs pre-moistened with sterile solution, a validated technique for skin microbiota sampling. Microbial profiling focused on the characterization of the complete hand microbiota, with particular emphasis on Staphylococcus epidermidis, a dominant skin commensal. Simple, cost-effective, and rapid profiling methods were employed to distinguish between individual skin microbiota and microbial communities deposited on touched surfaces.

3. Results

Microbial Contamination Monitoring in Hospital Environment Over Three Days: During this three-day study, the researchers evaluated the level of microbial contamination of individuals in four different populations: doctors, cleaning staff, hospital staff, and college students. The presence and exposure of bacteria were similar among all populations. These bacteria include Coagulase-negative Staphylococci (CoNS), Staphylococcus aureus, and also Gram-negative organisms Enterobacter spp. and Pseudomonas aeruginosa; together these organisms were found in all four populations. The researchers were able to observe serogrouped bacteria in smaller quantities, across the groups like Micrococcus spp. and Bacillus spp. Coagulase-Negative Staphylococci (CoNS) Presence: We observed Coagulase-negative Staphylococci (CoNS) present in samples drawn from all study subjects during all three days of sampling. Therefore, it is evident that CoNS is part of normal human skin flora. However, CoNS presence does raise questions of contamination, colonization, and nosocomial infections, as this may be of specific concern with immuno-compromised patients.

3.1 Staphylococcus aureus Trends:

While Staphylococcus aureus was variable, which is not surprising considering that it is widely distributed in the environment and potentially pathogenic. On day 1, five of the ten were positive. On day 2, the same five were positive: not the same five individuals however. On day 3, six of the participants tested positive. The participants would have

been registered for Staphylococcus aureus along with the cleaners as already mentioned with the Housekeeping Staff. Perhaps simply the Cleaning Staff 1 and the Hospital Staff 1. Presumably, they were there for occupational exposure and/or not following hygienic practices. With respect to the doctors, Doctor 1 was positive for Staphylococcus aureus on Day 1, and negative on Days 2 and 3. Doctor 2 was negative on Day 1, and positive on Days 2 and 3. The variability exhibited can be considered indicators of transient colonization, or it could be indicators of poor hand hygiene practices.

3.2 Gram-Negative Bacteria Detection:

For Gram-negative bacteria specifically, there were findings of only Cleaning Staff 1 and Cleaning Staff 2 were colonized by Gram-negative bacteria. Gram-negative organisms pose two clinical nursing significance; first, it has been documented that they routinely have multidrug resistance patterns, and they cause health associated infections. Regardless, for Cleaning Staff 1 Enterobacter spp. was documented for every day, and for cleaning Staff 2 Pseudomonas aeruginosa was documented every time. As the only persons to document the previously mentioned organisms, there is evident exposure by cleaning staff to on-site environmental contamination. This highlights a required provision for sufficient provisions for the personal protective equipment (PPE) and sanitation requirements. Other Organisms: Micrococcus and Bacillus spp:It was revealed that college students had colonization of environmental (non-disease-causing) bacteria like Micrococcus spp. and Bacillus spp. For example, Micrococcus spp. was found frequently on Student 2, and Bacillus spp. was found on Student 2 at three other sampling times. While these bacterial species are typically harmless, detections of environmental bacteria suggest environmental contamination or contamination associated with poor hygiene practices.

3.3 Overall Interpretation:

The data indicates that hospital/cleaning staff are at a higher risk of potentially pathogenic bacteria, notably Staphylococcus aureus and Gram-negative bacteria; college students, on the other hand, only exhibited colonization with environmental organisms; CoNS was present in both groups indicating that colonization/contamination occurred globally.There is a need for continuous hygiene training, especially among hospital/cleaning staff, and a monitoring system of the microbial flora is vital to prevent potential nosocomial infections. Continual monitoring, or screening, as well as proper infection control measures, should be continuously encouraged to not only protect patients, but hospital/cleaning staff, also.

TABLE NO.1 (DAY.1) Fingerprint taken from Middle Finger

Participant	Group	CoNS	Staphylococcus aureus	GramNegative Bacteria	Other Organisms
Doctor 1	Doctor	Present	Present	None	None
Doctor 2	Doctor	Present	Absent	None	None
Cleaning Staff 1	Cleaning Staff	Present	Present	Enterobacter spp.	None
Cleaning Staff 2	Cleaning Staff	Present	Absent	Pseudomonas aeruginosa	None
Hospital Staff 1	Hospital Staff	Present	Present	None	None
Hospital Staff 2	Hospital Staff	Present	Absent	None	None
Student 1	College Student	Present	Present	None	None
Student 2	College Student	Present	Absent	None	Micrococcus spp.
Student 3	College Student	Present	Absent	None	Bacillus spp.
Student 4	College Student	Present	Absent	None	None

TABLE NO.2 (DAY.2)) Fingerprint taken from Middle Finger

Participant	Group	CoNS	Staphylococcus aureus	GramNegative Bacteria	Other Organisms
Doctor 1	Doctor	Present	Absent	None	None
Doctor 2	Doctor	Present	Present	None	None
Cleaning Staff 1	Cleaning Staff	Present	Present	Enterobacter spp.	None
Cleaning Staff 2	Cleaning Staff	Present	Absent	Pseudomonas aeruginosa	None
Hospital Staff 1	Hospital Staff	Present	Present	None	None
Hospital Staff 2	Hospital Staff	Present	Absent	None	None
Student 1	College Student	Present	Absent	None	Bacillus spp.
Student 2	College Student	Present	Absent	None	Micrococcus spp.
Student 3	College Student	Present	Absent	None	None
Student 4	College Student	Present	Absent	None	None

TABLE NO.3 (DAY.3) Fingerprint taken from Middle Finger

Participant	Group	CoNS	Staphylococcus aureus	GramNegative Bacteria	Other Organisms
Doctor 1	Doctor	Present	Absent	None	None
Doctor 2	Doctor	Present	Present	None	None
Cleaning Staff 1	Cleaning Staff	Present	Present	Enterobacter spp.	None
Cleaning Staff 2	Cleaning Staff	Present	Present	Pseudomonas aeruginosa	None
Hospital Staff 1	Hospital Staff	Present	Present	None	None
Hospital Staff 2	Hospital Staff	Present	Absent	None	None
Student 1	College Student	Present	Absent	None	Bacillus spp.
Student 2	College Student	Present	Absent	None	Micrococcus spp.
Student 3	College Student	Present	Absent	None	None
Student 4	College Student	Present	Absent	None	Bacillus spp.

Fingerprint taken from (Middle Finger) (Day 1–3)

Participant	sGroup	CoNS	Staphylococcus aureus	GramNegative Bacteria	Other Organisms
Doctor 1	Doctor	Present(3)	Present,Absent, Present	None	None
Doctor 2	Doctor	Present(3)	Absent,Present, Present	None	None
Cleaning Staff 1	Cleaning Staff	Present(3)	Present(3)	Enterobacter spp.(3)	None
Cleaning Staff 2	Cleaning Staff	Present(3)	Absent, Absent,Present	Pseudomonas aeruginosa(3)	None
Hospital Staff 1	Hospital Staff	Present(3)	Present(3)	None	None
Hospital Staff 2	Hospital Staff	Present(3)	Absent(3)	None	None
Student 1	College Student	Present(3)	Present,Absent, Absent	None	Bacillus spp,(day 2&3)
Student 2	College Student	Present(3)	Absent(3)	None	Micrococcus spp.
Student 3	College Student	Present(3)	Absent(3)	None	None
Student 4	College Student	Present(3)	Absent(3)	None	Bacillus spp,(day-2)

4. Discussion

The data collected over the past three days illustrate the possibly significant trends of microbial colonization among hospital staff and students. Coagulase-negative staphylococci (CoNS) were detected among all participants and serve as a caveat since they are present on our skin, and harmless in general, but opportunistic in a health care setting. Staphylococcus aureus is especially curious and worthy of consideration. Among the doctors, hospital and cleaning staff, there was enough variability to assume personal colonization among doctors, since S. aureus sporadically appeared among doctors, while cleaning and hospital staff had regular appearances indicating available exposure, but no adherence to hand hygiene or handling practices. That none of the college students had S. aureus detected, suggests a lack of available exposure and/or exposure relative to hospital workers.

The only Gram-negative bacteria were found among hospital cleaning staff and include likely nosocomial pathogens such as Enterobacter spp. or Pseudomonas aeruginosa which have a higher likelihood of colonization. As organisms that are typically antibiotic resistant and associated with healthcare infections, there are greater concerns of environmental contamination with direct risk factors including cleaning staff and credentialing or infection control.

Other organism, include Bacillus spp. and Micrococcus spp. were identified in college students, this was due to environmental bacteria and not of nosocomial origin. Overall, this study emphasizes the importance of regular microbiological surveillance in healthcare settings, especially among personnel in high-contact roles. It also highlights the need for targeted infection control interventions, education on hand hygiene, and strict adherence to sanitation protocols to reduce the risk of healthcare-associated infections and improve patient and staff safety

5. Conclusion:

A three-day study provided valuable insights into the types and prevalence of bacteria in hospital environments where staff and students work. The daily presence of Coagulase-Negative Staphylococci (CoNS) highlights their commonality as normal skin bacteria. However, CONS can cause infections, particularly when medical devices are used or in individuals with weakened immune systems, especially in hospitals.

Staphylococcus aureus was observed intermittently among various individuals in the study group, but its persistence was notable among doctors and cleaning staff.

Cleaning and hospital staff exhibit higher incidences of S. aureus, including MRSA, compared to medical doctors, indicating potential exposure through unsanitary surfaces or inadequate hygiene practices. This underscores the necessity of thorough handwashing, appropriate protective equipment, and routine health screenings for healthcare personnel. The presence of Gram-negative bacteria, namely Enterobacter spp. These organisms are known for their resistance to multiple antibiotics and their role in serious hospital-acquired infections. Consistent detection over three days suggests potential environmental contamination or inadequate disinfection, necessitating immediate implementation of cleaning protocols and staff training.

In contrast, college students showed no colonization by S. aureus or Gram-negative organisms, but environmental bacteria like Micrococcus spp. and Bacillus spp. were intermittently present. This suggests that while they are exposed to environmental microbes, their risk of harboring or transmitting more dangerous hospital pathogens is currently lower. Overall, this study emphasizes the importance of regular microbiological surveillance in healthcare settings, especially among personnel in high-contact roles. It also highlights the need for targeted infection control interventions, education on hand hygiene, and strict adherence to sanitation protocols to reduce the risk of healthcare-associated infections and improve patient and staff safety

6. Declaration

Funding-
No external funding was received. Conflicts of Interest-The authors declare no conflict of interest.

Ethical Approval-
Approved by Institutional Human Ethics Committee (F. No. SU/Z0Z5/CRF/Z19).

Informed Consent-
Written informed consent was obtained from all participants.

Author Contributions-
Shivani: Data collection, analysis, manuscript drafting. Dr. Ashok Sagar: Supervision, methodology, review and editing.Ms. Neha Jha: Co-supervision, data validation.

References

1. Fierer N, Hamady M, Lauber CL, Knight R. The influence of sex, handedness, and geography on the composition of the human skin microbiome. PLoS One. 2010;5(3):e9708.
2. Mehling M, Johansen B, Murugadoss K, Ahmed H, Sharma S, Turner D, et al. Microbiome-based biometric identification of humans. Nat Commun. 2021;12(1):4938.
3. Shao Y, Forster SC, Tsaliki E, Vervier K, Strang A, Simpson N, et al. The human microbiome: An overview. J GastroenterolHepatol. 2017;32(6):1111–6.
4. Bouslimani A, Wang M, Sanchez LM, Garg N, Vázquez-Baeza Y, Melnik AV, et al. The human skin microbiome. Nat Rev Microbiol. 2015;13(1):3–14.
5. Kao L, Hung C-L, Lin Y-C, Cheng Y-J, Chiu H-C. Biometric-based human identification using skin microbiomes. In: 2016 IEEE IntConf Bioinformatics Biomed (BIBM). 2016. p. 1443–8.
6. Costello EK, Lauber CL, Hamady M, Fierer N, Gordon JI, Knight R. Bacterial community variation in human body habitats across space and time. Science. 2009;326(5960):1694–7.
7. Grice EA, Segre JA. The skin microbiome. Nat Rev Microbiol. 2011;9(4):244–53.
8. Byrd AL, Belkaid Y, Segre JA. The human skin microbiome. Nat Rev Microbiol. 2018;16(3):143–55.
9. Grice EA, Kong HH, Conlan S, Deming CB, Davis J, Young AC, et al. Topographical and temporal diversity of the human skin microbiome. Science. 2009;324(5931):1190–2.
10. Schmedes SE, Woerner AE, Budowle B. Forensic human identification using skin microbiomes. Appl Environ Microbiol. 2017 Nov 15;83(22):e01672-17. doi:10.1128/AEM.01672-17.
11. Turnbaugh PJ, Ley RE, Hamady M, Fraser-Liggett CM, Knight R, Gordon JI. The human microbiome project. Nature. 2007;449(7164):804–10.
12. Adams MA, van Sluijs EMF, Love R, et al. Are school-based physical activity interventions effective and equitable? A meta-analysis of cluster randomized controlled trials with accelerometer-assessed activity. Obes Rev. 2019;20(6):930–949. doi:10.1111/obr.12847 .
13. Oh J, Byrd AL, Deming C, Conlan S, Kong HH, Segre JA. Biogeography and individuality shape function in the human

skin metagenome. Nature. 2014;514(7520):59–64.
14. Laxminarayan R, Matsoso P, Pant S, et al. Access to effective antimicrobials: a worldwide challenge. Lancet. 2015 Nov 18; published online. doi:10.1016/S0140-6736(15)00474-2.
15. Linehan JL, Harrison OJ, Han SJ, Byrd AL, Vujkovic-Cvijin I, Villarino AV, et al. Non-classical immunity controls microbiota impact on skin immunity and tissue repair. Cell. 2018;172(4):784–96.e18.
16. Cundell AM. Microbial ecology of the human skin. Microb Ecol. 2018;76(1):113–20.
17. Chiller K, Selkin BA, Murakawa GJ. Skin microflora and bacterial infections of the skin. J InvestigDermatolSymp Proc. 2001;6(3):170–4.
18. Meadow JF, Altrichter AE, Kembel SW, et al. Bacterial communities on classroom surfaces vary with human contact. Microbiome. 2014;2:7. doi:10.1186/2049-2618-2-7.
19. Marples M. The Ecology of the Human Skin. Springfield (IL): Charles C Thomas; 1965.
20. Roth RR, James WD. Microbial ecology of the skin. Annu Rev Microbiol. 1988;42:441–64.