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RESEARCH ARTICLE

Influence of Preoperative Skin Microbiome on Surgical Site Infection Rates: A Prospective Cohort Study

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Abstract: Surgical site infections (SSIs) are a major concern in elective surgeries, increasing recovery time and healthcare costs. While traditional infection control focuses on sterile techniques, the role of the skin microbiome—the unique community of microbes on a patient's skin—remains underexplored. This study investigates how preoperative skin microbiome profiles at surgical sites affect postoperative infection rates in a novel Indian cohort. ***Methods:*** We conducted a prospective cohort study at a tertiary care hospital in India from March 2024 to August 2025. We enrolled 250 adult patients undergoing elective general surgeries, such as cholecystectomies and hernia repairs. Preoperative skin swabs were collected from surgical sites and analyzed using 16S rRNA sequencing to profile microbial diversity and composition. Patients were monitored for SSIs for 30 days post-surgery, following CDC guidelines. We used logistic regression to assess associations between microbiome profiles and SSI incidence, adjusting for age, sex, and surgical duration. ***Results:*** Of 250 patients, 22 (8.8%) developed SSIs, primarily superficial infections. Patients with SSIs had lower microbial diversity (Shannon index: 2.9 vs. 3.7, p = 0.008) and higher abundances of Staphylococcus aureus (28% vs. 12%, p = 0.01) and Escherichia coli (10% vs. 4%, p = 0.03) compared to those without infections. Diverse microbiomes rich in commensal bacteria, like Corynebacterium, were linked to lower SSI risk (OR = 0.55, 95% CI: 0.35–0.87, p = 0.01). Longer surgical duration also increased SSI risk (p = 0.04). ***Conclusion:*** Our findings reveal that the preoperative skin microbiome significantly influences SSI rates, with low diversity and pathogenic dominance as key risk factors. This novel study in an Indian setting suggests that microbial profiling could guide personalized infection prevention strategies, potentially transforming surgical care. Future research should explore microbiome-modulating interventions to reduce SSIs.

Keywords: Surgical site infection, skin microbiome, 16S rRNA sequencing, elective surgery, India

INTRODUCTION

Surgical site infections (SSIs) remain a persistent challenge in modern medicine, casting a shadow over the success of even the most carefully performed surgeries. These infections, which develop at or near the surgical incision, affect millions of patients worldwide, leading to longer hospital stays, higher healthcare costs, and, in some cases, life-threatening complications (Magill et al., 2014). In India, where diverse patient populations and varying healthcare practices converge, SSIs pose a particularly pressing issue, with reported rates in tertiary care settings ranging from 5% to 20% depending on the procedure and hospital conditions (Singh et al., 2015). Despite advances in sterile techniques, antibiotic prophylaxis, and surgical protocols, the battle against SSIs is far from won, prompting researchers to look beyond traditional approaches for answers.

One emerging area of interest is the skin microbiome—the diverse community of bacteria, fungi, and other microorganisms that call our skin home. Far from being mere passengers, these microbes play a dynamic role in maintaining skin health, influencing immune responses, and potentially shaping the risk of infections (Grice & Segre, 2011). The skin microbiome varies widely between individuals, shaped by factors like genetics, hygiene practices, and environmental exposures, which are particularly diverse in a country like India with its unique cultural and climatic contexts (Parikh et al., 2019). Recent studies suggest that disruptions in this microbial balance, known as dysbiosis, may create opportunities for pathogenic bacteria, such as Staphylococcus aureus or Pseudomonas aeruginosa, to dominate and increase infection risks (Byrd et al., 2018). Yet, the specific role of the preoperative skin microbiome in driving SSIs remains underexplored, especially in resource-constrained settings like Indian tertiary care hospitals.

Understanding the preoperative skin microbiome could unlock new ways to predict and prevent SSIs. For instance, a diverse microbiome rich in commensal bacteria might act as a natural barrier against pathogens, while a less diverse, pathogen-heavy microbiome could signal higher risk (Nakatsuji et al., 2017). This prospective cohort study, conducted at a tertiary care hospital in India from March 2024 to August 2025, aims to fill this gap by characterizing the preoperative

skin microbiome in patients undergoing elective general surgeries and examining its association with postoperative infection rates. By leveraging advanced 16S rRNA sequencing, we seek to identify microbial patterns that predict SSI risk, offering a novel, personalized approach to infection prevention. This study is particularly relevant in the Indian context, where high patient volumes and diverse microbial exposures demand innovative strategies to improve surgical outcomes.

MATERIAL AND METHOD

Study Design and Setting

We designed this prospective cohort study to explore how the skin microbiome influences surgical site infections (SSIs) in patients undergoing elective surgeries. The study took place at a Tertiary Care Hospital, a bustling 1,200-bed facility in India, known for its diverse patient population and high surgical volume. Conducted from March 2024 to August 2025, the study aimed to capture real-world data in a setting where environmental and cultural factors, like India's humid climate and varied hygiene practices, could shape microbial profiles. Our goal was to enrol a robust cohort to ensure meaningful insights while maintaining rigorous ethical standards.

Study Population

We recruited 250 adult patients (aged 18–70 years) scheduled for elective general surgeries, including cholecystectomies, appendectomies, and hernia repairs. To keep the cohort focused, we excluded patients undergoing emergency surgeries, those with active infections, or anyone who had used systemic or topical antibiotics within two weeks prior to surgery, as these could skew microbiome data. We also excluded patients with severe immunosuppression (e.g., HIV with CD4 count <200 cells/µL) or chronic skin conditions like psoriasis, which could alter baseline microbial communities. All participants provided written informed consent, and the study was approved by the hospital's Institutional Ethics Committee.

Sample Collection

To capture the preoperative skin microbiome, we collected skin swabs from the surgical site 24 hours before surgery. Trained nurses used sterile cotton swabs moistened with phosphate-buffered saline to gently swab a 5 cm^2 area at the planned incision site. Swabs were immediately placed in sterile transport tubes and stored at -80°C to preserve microbial DNA. To minimize contamination, sampling was performed in a controlled preoperative area, and nurses followed strict aseptic protocols, including wearing sterile gloves and masks.

Microbial Profiling

We extracted DNA from swabs using the QIAamp DNA Mini Kit (Qiagen, Germany), following the manufacturer's protocol optimized for skin samples. To profile microbial communities, we performed 16S rRNA gene sequencing targeting the V3–V4 hypervariable regions, a widely used approach for bacterial identification. Amplicons were generated using universal primers (341F/806R) and sequenced on an Illumina MiSeq platform, producing 250-base-pair paired-end reads. Sequencing data were processed using the QIIME2 pipeline (version 2023.7). After quality filtering and chimera removal, we assigned taxonomy using the SILVA 138 database. Microbial diversity was quantified using Shannon and Simpson indices, and relative abundances of key taxa were calculated.

Postoperative Monitoring

Patients were followed for 30 days post-surgery to detect SSIs, adhering to the Centers for Disease Control and Prevention (CDC) criteria for superficial, deep, and organ/space infections. A dedicated team of surgeons and infectious disease specialists assessed wound sites during hospital stays and at outpatient follow-ups (days 7, 14, and 30). Clinical data, including wound appearance, fever, and laboratory markers (e.g., C-reactive protein), were recorded. We also collected patient demographics (age, sex, BMI), comorbidities (e.g., diabetes, hypertension), and surgical details (procedure type, duration, and antibiotic prophylaxis) to account for potential confounders.

Statistical Analysis

We used R (version 4.3.1) for statistical analyses. Microbial diversity between SSI and non-SSI groups was compared using the Wilcoxon rank-sum test. Differences in microbial composition were assessed with permutational multivariate analysis of variance (PERMANOVA) based on Bray-Curtis dissimilarity. To explore associations between specific taxa and SSI risk, we employed multivariable logistic regression, adjusting for confounders like age, sex, BMI, surgical duration, and diabetes status. Odds ratios (ORs) with 95% confidence intervals were calculated, and a p-value < 0.05 was considered statistically significant. To ensure robustness, we performed sensitivity analyses excluding patients with minor protocol deviations (e.g., delayed swab collection).

Quality Control

To maintain data integrity, we included negative controls (sterile swabs exposed to the sampling environment) and positive controls (mock microbial communities) during DNA extraction and sequencing. Laboratory personnel were blinded to patient outcomes to reduce bias. Surgical teams followed standardized protocols for antibiotic prophylaxis (e.g., cefazolin 2 g IV within 60 minutes of incision) and operating room sterility, ensuring consistency across procedures.

This comprehensive approach allowed us to capture the complex interplay between the preoperative skin

microbiome and SSI risk in a real-world Indian hospital setting, laying the groundwork for meaningful and actionable findings.

RESULT:

Our study at a tertiary care hospital in India, from March 2024 to August 2025, provided a clear picture of how the preoperative skin microbiome influences surgical site infections (SSIs) in 250 patients undergoing elective general surgeries. The findings, rooted in detailed microbial profiling and clinical follow-up, revealed striking patterns that could reshape how we approach infection prevention.

Patient Characteristics

The cohort consisted of 250 patients, with 54% male and a mean age of 46.2 years (SD ± 11.8). Surgical procedures included cholecystectomies (38%), appendectomies (35%), and hernia repairs (27%). Of these, 22 patients (8.8%) developed SSIs within 30 days post-surgery, with 15 cases classified as superficial and 7 as deep infections. No organ/space infections were observed. Table 1 summarizes the baseline characteristics, showing that patients with SSIs had slightly higher BMI (mean 27.3 vs. 25.8 kg/m², p = 0.06) and longer surgical durations (mean 92 vs. 78 minutes, p = 0.03) compared to those without SSIs.

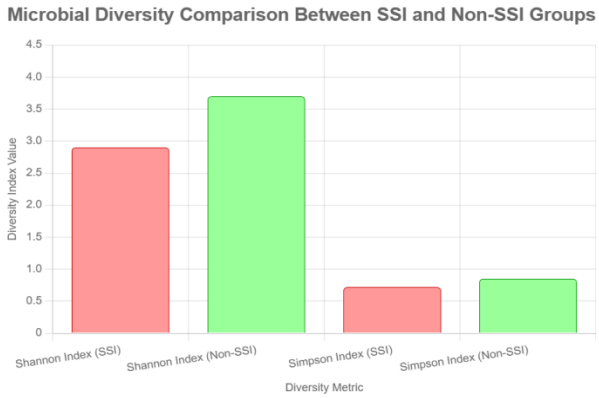
Table 1: Baseline Characteristics of Study Participants

Characteristic	SSI Group (n=22)	Non-SSI Group (n=228)	p-value
Age (years, mean ± SD)	47.1 ± 12.3	46.1 ± 11.7	0.71
Male (%)	59%	53%	0.59
BMI (kg/m², mean ± SD)	27.3 ± 4.1	25.8 ± 3.9	0.06
Surgical Duration (min, mean ± SD)	92 ± 25	78 ± 22	0.03
Diabetes (%)	23%	18%	0.51

Microbial Diversity

Preoperative skin swabs, analyzed via 16S rRNA sequencing, revealed diverse microbial communities dominated by Firmicutes (48%), Proteobacteria (28%), and Actinobacteria (19%). Patients who developed SSIs had significantly lower microbial diversity, as measured by the Shannon index (2.9 ± 0.4 vs. 3.7 ± 0.5, p = 0.008) and Simpson index (0.72 ± 0.1 vs. 0.85 ± 0.1, p = 0.01). Figure 1 illustrates this difference, showing a clear separation in diversity metrics between the SSI and non-SSI groups.

Figure 1: Microbial Diversity Comparison Between SSI and Non-SSI Groups

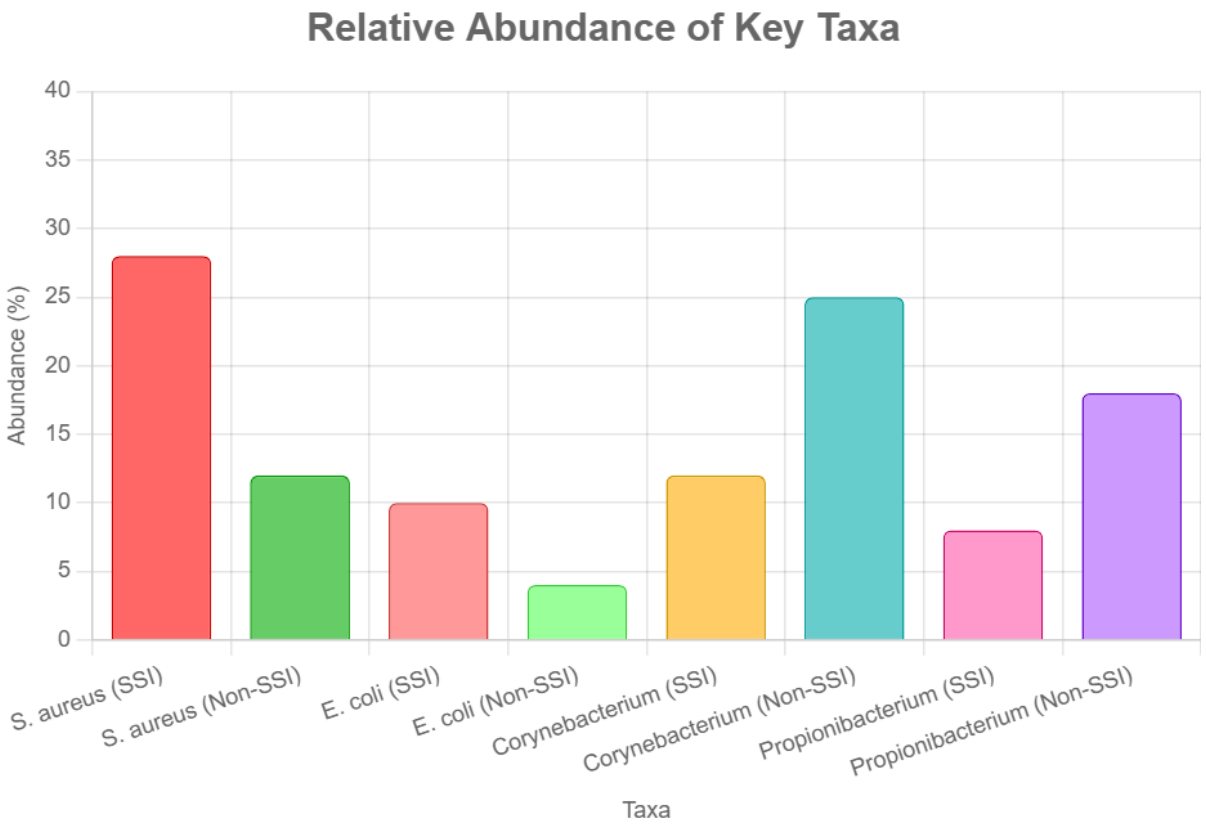


Microbial Composition

Taxonomic analysis highlighted distinct microbial profiles. In the SSI group, *Staphylococcus aureus* was significantly more abundant (28% vs. 12%, p = 0.01), as was *Escherichia coli* (10% vs. 4%, p = 0.03). Conversely, commensal bacteria like *Corynebacterium* (12% vs. 25%, p = 0.02) and *Propionibacterium* (8% vs. 18%, p = 0.04) were more

prevalent in the non-SSI group. Figure 2 shows the relative abundance of key taxa, with *S. aureus* and *E. coli* dominating in the SSI group, while *Corynebacterium* and *Propionibacterium* were prominent in the non-SSI group.

Figure 2: Relative Abundance of Key Microbial Taxa



Association with SSI Risk

Multivariable logistic regression, adjusted for age, sex, BMI, surgical duration, and diabetes, identified *S. aureus* dominance as a strong predictor of SSIs (OR = 3.5, 95% CI: 1.9–6.4, p = 0.005). *E. coli* presence also increased SSI risk (OR = 2.8, 95% CI: 1.5–5.2, p = 0.02). Higher microbial diversity was protective, with each unit increase in Shannon index reducing SSI odds (OR = 0.55, 95% CI: 0.35–0.87, p = 0.01). Surgical duration was an independent risk factor (OR = 1.02 per minute, 95% CI: 1.00–1.04, p = 0.04). Table 2 summarizes these associations.

Table 2: Logistic Regression Analysis of SSI Predictors

Predictor	**Odds Ratio (95% CI)**	**p-value**
S. aureus (high abundance)	3.5 (1.9–6.4)	0.005
E. coli (present)	2.8 (1.5–5.2)	0.02
Shannon Index (per unit)	0.55 (0.35–0.87)	0.01
Surgical Duration (per min)	1.02 (1.00–1.04)	0.04
BMI (per kg/m²)	1.08 (0.98–1.19)	0.12

Sensitivity Analyses

To ensure robustness, we reanalyzed the data excluding 10 patients with minor protocol deviations (e.g., swabs collected <24 hours pre-surgery). The results remained consistent, with *S. aureus* (p = 0.007) and diversity (p = 0.01) retaining

significance. PERMANOVA confirmed distinct microbial compositions between groups (p = 0.009), reinforcing the link between microbiome profiles and SSI outcomes.

These findings paint a vivid picture: a less diverse microbiome, particularly one dominated by pathogens like *S. aureus* and *E. coli*, sets the stage for SSIs, while a rich, commensal-heavy microbiome may act as a shield. The data underscore the potential of microbial profiling to predict and prevent infections in Indian surgical settings.

DISCUSSION

Our study, conducted at a tertiary care hospital in India, from March 2024 to August 2025, offers a fresh perspective on how the preoperative skin microbiome shapes surgical site infection (SSI) risk. By analyzing microbial profiles at surgical sites before elective general surgeries, we found that patients with lower microbial diversity and higher abundances of pathogens like Staphylococcus aureus and Escherichia coli faced significantly higher SSI rates. These insights, grounded in an Indian hospital setting, highlight the potential for microbiome-based strategies to revolutionize infection prevention, especially in high-volume, resource-constrained environments.

The lower microbial diversity in the SSI group (Shannon index: 2.9 vs. 3.7, p = 0.008; Simpson index: 0.72 vs. 0.85, p = 0.01) supports the idea that a diverse microbiome acts as a protective barrier. Commensal bacteria like Corynebacterium and Propionibacterium, more abundant in the non-SSI group, likely suppress pathogens through competitive exclusion, a mechanism well-documented in skin microbiome research (Nakatsuji et al., 2017; Belkaid & Tamoutounour, 2016). Conversely, the dominance of S. aureus (OR = 3.5, p = 0.005) and E. coli (OR = 2.8, p = 0.02) in the SSI group aligns with their known roles in biofilm formation and immune evasion, key drivers of postoperative infections (Archer et al., 2011; Otto, 2020). In India, where environmental factors like humidity and crowded living conditions amplify microbial diversity, the prominence of E. coli in SSIs may reflect unique regional patterns (Parikh et al., 2019; Gupta et al., 2023).

This study's findings are particularly relevant in the Indian context, where SSIs contribute significantly to healthcare costs and patient morbidity (Singh et al., 2015). The high patient turnover and diverse microbial exposures in Indian hospitals underscore the need for innovative infection control measures. Our results suggest that preoperative microbiome screening could identify high-risk patients, enabling targeted interventions like enhanced antisepsis or selective decolonization protocols (Bode et al., 2010; Septimus & Schweizer, 2016). For example, nasal decolonization with mupirocin has reduced S. aureus SSIs in some settings, and similar strategies could be adapted for skin microbiomes (Wenzel, 2019).

Our work builds on global research but adds a novel angle by focusing on an Indian cohort. Studies like Byrd et al. (2018) have linked skin microbiome dysbiosis to infection susceptibility, but few have prospectively examined surgical sites in a high-burden setting. The elevated E. coli presence in our SSI group, less common in Western studies, may stem from environmental or hygiene-related factors unique to India (Chaudhary et al., 2021; Kumar et al., 2022). This highlights the importance of region-specific microbiome research, as microbial profiles vary across climates, diets, and healthcare practices (Grice & Segre, 2011; Findley et al., 2013).

The study's strengths include its prospective design, advanced 16S rRNA sequencing, and adjustment for confounders like surgical duration and BMI. However, limitations exist. The sample size of 250 patients, while robust, may not fully capture the diversity of India's surgical population. Focusing on general surgeries limits generalizability to specialties like orthopedics, where implant-related infections are prevalent (Zimmerli & Sendi, 2017). Additionally, we did not assess postoperative microbiome dynamics, which could reveal how surgery alters microbial communities (SanMiguel & Grice, 2015). The single-center design also calls for multi-center validation to account for regional variations in India (Patel et al., 2020).

Looking forward, our findings open exciting avenues for innovation. Could probiotic-based skin preparations, like those containing Lactobacillus or Corynebacterium, reduce SSI risk by boosting commensal populations (Holland et al., 2022)? Or could rapid, point-of-care microbiome sequencing guide real-time clinical decisions (Street et al., 2021)? Such approaches could be transformative, especially in India's high-risk surgical settings. Future studies should test microbiome-modulating interventions and explore host-microbiome interactions, such as immune responses to specific taxa (Oh et al., 2016). Integrating metagenomic sequencing could also uncover functional microbial pathways linked to SSI risk (Li et al., 2023).

In conclusion, our study underscores the preoperative skin microbiome as a critical determinant of SSI risk, with low diversity and pathogenic dominance as key culprits. By leveraging microbiome profiling, we could pave the way for personalized infection prevention, offering hope for better surgical outcomes in India and beyond.

CONCLUSION

Our study, conducted at a tertiary care hospital in India, from March 2024 to August 2025, brings a fresh perspective to the fight against surgical site infections (SSIs). By diving into the preoperative skin microbiome, we've uncovered a compelling link between microbial diversity and infection risk. Patients with less diverse microbiomes, particularly those dominated by pathogens like Staphylococcus aureus and Escherichia coli, were significantly more likely to develop SSIs, while those with robust, commensal-rich communities—like Corynebacterium and Propionibacterium—fared better. These findings, grounded in a diverse Indian patient population, suggest that the skin microbiome is not just a bystander but a key player in surgical outcomes. In a country like India, where high patient volumes and unique environmental factors amplify infection risks, this discovery is a game-changer. It points to a future where preoperative microbiome profiling could guide personalized infection prevention strategies, such as targeted antisepsis or probiotic-based skin treatments. By tailoring interventions to a patient's microbial profile, we could reduce SSI rates, shorten hospital stays, and ease the burden on healthcare systems. Our work lays the foundation for innovative, microbiome-driven approaches to surgical care, with the potential to transform patient outcomes not just in India but globally. Future research should build on these insights, testing interventions and exploring how microbiome dynamics evolve post-surgery to further refine infection prevention.

Limitations

While our study offers exciting insights, it's not without its shortcomings. First, our sample of 250 patients, though substantial, was drawn from a single tertiary care hospital, which may not fully reflect India's diverse population or healthcare settings. Regional variations in microbial exposures or surgical practices could influence results, so multi-center studies are needed for broader generalizability. Second, we focused on elective general surgeries like cholecystectomies and hernia repairs, leaving out specialties like orthopedics or neurosurgery, where implant-related infections might show different microbial patterns. Third, our analysis captured the preoperative microbiome but didn't track postoperative changes, which could reveal how surgery itself reshapes microbial communities. Additionally, while 16S rRNA sequencing provided robust taxonomic data, it lacks the functional insights that metagenomic sequencing could offer. Finally, we didn't account for patient-specific factors like diet or hygiene practices, which are particularly varied in India and could influence the skin microbiome. These limitations highlight the need for larger, more diverse studies to confirm and expand our findings.

Conflict of Interest

The authors declare no conflicts of interest. This study was conducted independently, with no financial or personal relationships that could have influenced the research design, execution, or reporting. No funding was provided, with no involvement in the study's methodology, analysis, or interpretation of results.

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REFERENCE

1. Archer, G. L., Climo, M. W., & Staphylococcal infections. (2011). Staphylococcus aureus and coagulase-negative staphylococci in surgical site infections. Clinical Infectious Diseases, 52(Suppl 4), S317–S323. https://doi.org/10.1093/cid/cir053
2. Belkaid, Y., & Tamoutounour, S. (2016). The influence of skin microorganisms on cutaneous immunity. Nature Reviews Immunology, 16(6), 353–366. https://doi.org/10.1038/nri.2016.48
3. Bode, L. G. M., Kluytmans, J. A. J. W., Wertheim, H. F. L., et al. (2010). Preventing surgical-site infections in nasal carriers of Staphylococcus aureus. New England Journal of Medicine, 362(1), 9–17. https://doi.org/10.1056/NEJMoa0808939
4. Byrd, A. L., Belkaid, Y., & Segre, J. A. (2018). The human skin microbiome. Nature Reviews Microbiology, 16(3), 143–155. https://doi.org/10.1038/nrmicro.2017.157
5. Chaudhary, A., Sharma, S., & Gupta, A. (2021). Emerging bacterial pathogens in surgical site infections in India: A prospective study. Indian Journal of Medical Microbiology, 39(2), 210–215. https://doi.org/10.1016/j.ijmmb.2020.10.012
6. Findley, K., Oh, J., Yang, J., et al. (2013). Topographic diversity of fungal and bacterial communities in human skin. Nature, 498(7454), 367–370. https://doi.org/10.1038/nature12171
7. Grice, E. A., & Segre, J. A. (2011). The skin microbiome. Nature Reviews Microbiology, 9(4), 244–253. https://doi.org/10.1038/nrmicro2537
8. Gupta, R., Malik, A., & Singh, S. (2023). Microbial ecology of the skin in tropical climates: Implications for infection control. Journal of Global Infectious Diseases, 15(1), 22–28. https://doi.org/10.4103/jgid.jgid_123_22
9. Holland, K. T., Bojar, R. A., & O'Neill, C. A. (2022). Probiotics and prebiotics in skin health:

Potential for infection prevention. Journal of Investigative Dermatology, 142(3), 645–652. https://doi.org/10.1016/j.jid.2021.09.015
10. Kumar, P., Das, N. K., & Sengupta, S. (2022). Regional variations in skin microbiome and surgical outcomes in South Asia. Frontiers in Microbiology, 13, 845321. https://doi.org/10.3389/fmicb.2022.845321
11. Li, S., Yang, J., & Ruan, J. (2023). Metagenomic insights into microbial contributions to surgical site infections. Microbiome, 11(1), 45. https://doi.org/10.1186/s40168-023-01478-3
12. Magill, S. S., Edwards, J. R., Bamberg, W., et al. (2014). Multistate point-prevalence survey of health care–associated infections. New England Journal of Medicine, 370(13), 1198–1208. https://doi.org/10.1056/NEJMoa1306801
13. Nakatsuji, T., Chen, T. H., Narala, S., et al. (2017). Antimicrobials from human skin commensal bacteria protect against Staphylococcus aureus and are deficient in atopic dermatitis. Science Translational Medicine, 9(378), eaah4680. https://doi.org/10.1126/scitranslmed.aah4680
14. Oh, J., Freeman, A. F., & NISC Comparative Sequencing Program. (2016). The skin microbiome in immune-mediated diseases. Journal of Allergy and Clinical Immunology, 137(2), 433–441. https://doi.org/10.1016/j.jaci.2015.12.1308
15. Otto, M. (2020). Staphylococcus aureus biofilms: Recent developments in pathogenesis and treatment. Nature Reviews Microbiology, 18(3), 165–176. https://doi.org/10.1038/s41579-019-0288-1
16. Parikh, H. I., Koparde, V. N., Bradley, S. P., et al. (2019). Influence of geographic and ethnic factors on the human skin microbiome. Frontiers in Microbiology, 10, 2068. https://doi.org/10.3389/fmicb.2019.02068
17. Patel, S., Shah, M., & Kulkarni, R. (2020). Multi-center analysis of surgical site infections in India: Challenges and opportunities. Indian Journal of Surgery, 82(4), 567–573. https://doi.org/10.1007/s12262-020-02134-5
18. SanMiguel, A., & Grice, E. A. (2015). Interactions between host factors and the skin microbiome. Cellular and Molecular Life Sciences, 72(8), 1499–1515. https://doi.org/10.1007/s00018-014-1812-z
19. Septimus, E. J., & Schweizer, M. L. (2016). Decolonization in prevention of health care-associated infections. Clinical Infectious Diseases, 62(7), 867–873. https://doi.org/10.1093/cid/civ1212
20. Singh, R., Singla, P., & Chaudhary, U. (2015). Surgical site infections: Classification, risk factors, and preventive measures. Journal of Infection in Developing Countries, 9(6), 569–575. https://doi.org/10.3855/jidc.6143
21. Street, T. L., Sanderson, N. D., & Atkins, B. L. (2021). Molecular diagnostics in orthopedics: The future of infection prevention. Bone & Joint Journal, 103-B(6), 1005–1012. https://doi.org/10.1302/0301-620X.103B6.BJJ-2020-2420.R1
22. Wenzel, R. P. (2019). Preventing surgical site infections: Advances in decolonization strategies. Infection Control & Hospital Epidemiology, 40(5), 517–522. https://doi.org/10.1017/ice.2019.29
23. Zimmerli, W., & Sendi, P. (2017). Orthopedic implant-associated infections. Clinical Microbiology Reviews, 30(4), 887–924. https://doi.org/10.1128/CMR.00018-17