Asian J Biol Life Sci., 2026; 15(2):266-276.
https://ajbls.com

Review Article

The Skin Microbiota: A Sentinel of Health and A New Frontier for Disease Indication

Sandhya Kuruba, Aparna Srikantam*

Department of Microbiology, School of Allied and Healthcare Sciences, Malla Reddy University, Maisammaguda, Dulapally, Hyderabad, Telangana, INDIA.

ABSTRACT

The skin microbiome contains a rich and complex ecosystem of microorganisms including bacteria, fungi as well as viruses which are essential in maintaining skin health and the homeostasis of the human. The skin microbiome changes with body site, and the atmosphere (temperature, humidity and sunlight), etc., contribute to its diversity. Imbalance of the skin microbiome is associated with different complexion disorders such atopic dermatitis, acne, psoriasis, rosacea. Moreover, modifications of the skin microbiome have been related to systemic diseases (e.g., diabetes, obesity and inflammatory bowel disease) via the gut-skin axis. The skin microbiome also plays a critical role in the regulation of immune homeostasis and pathogen defense. The skin microbiota type can be used as a biomarker of the health of the skin, and has potential applications in early identification and personalized treatment. The current review deals with the information pertaining to the composition and dynamics of skin microflora, contribution of skin microbiota to systemic health status, the value of skin microbiome as a marker of human health, some perspectives new research avenues in psychodermatology, environmental and lifestyle influences on host-microbe interactions occurring on the skin (skinomic studies) and gut-skin cross-talk.

Keywords: Biomarker, Dysbiosis, Human skin, Microbiome, Skin-brain axis, Skinomic studies, Systemic human health.

Correspondence:
Dr. Aparna Srikantam
Department of Microbiology, School of Allied and Healthcare Sciences, Malla Reddy University, Maisammaguda, Dulapally, Hyderabad-500100, Telangana, INDIA.
Email: aparnasb4@gmail.com

Received: 11-05-2026;
Revised: 05-06-2026;
Accepted: 29-07-2026.

INTRODUCTION

The skin is the initial defence of the body against the environment. "Skin microbiome" describes the diverse and numerous microbial system that comprises skin. The skin microbiome comprises a diversity of commensals that coexistence with homeostatic processes (Khan and Koh, 2024). The skin, our body's largest organ, is the home of countless microbial communities, determined by topographical areas such as sebaceous, moist and dry regions. The skin microbiota is responsible for health homeostasis and represents the general physiological state of human beings as well as, environmental health (Prescott 2017).

Like the gut, cutaneous microbiome has a crucial role in maintaining homeostasis. Colonization resistance is the process through which the skin microbiota protects host from infections (Boxberger *et al*., 2021). Maintenance of skin homeostasis and performance of functions such as immunomodulation, pathogen defense, and nutrient acquisition are associated with variations in the composition of the skin microbiome (Khan and Koh, 2024). As the skin microbiome is an indicator for human health, this even affects systemic diseases as changes in skin microbial community play a role to immune response (Zhu *et al*., 2023).

Numerous skin diseases, ranging from Atopic Dermatitis (AD) and acne to psoriasis and rosacea are associated with perturbations in the microbial diversity where imbalances occur, resulting in decreased or overgrowth of specific pathogenic microbial species. Additionally, emerging studies suggest that alterations of the skin microbiota can impact gut-skin axis and systemic diseases including diabetes, obesity, and Inflammatory Bowel Disease (IBD) (Khan and Koh, 2024). It also considers the skin-gut axis with variations in gut microbiota reported in various skin dysbiosis that implies a link between these microorganisms (Polkowska-Pruszyńska *et al*., 2019) (Figure 1).

The present review covers the composition and dynamics of skin microbiota, interplay between skin microbiome and human health, the importance of skin microbiota as a biomarker of human systemic health, aspects pertaining to new research areas in psychodermatology, influence of environment and lifestyle on host-microbe associations prevailing on the skin (skinomics) and skin and gut cross talk.

OPEN ACCESS

Manuscript TECHNOMEDIA

DOI: 10.5530/ajbls.20260164

Publishing Partner : Manuscript Technomedia. [www.mstechnomedia.com]

Search Strategy

A comprehensive literature search was conducted using databases such as PubMed, Scopus, and Web of Science. The search strategy utilized the following keywords and their combinations: "skin microbiome," "dysbiosis," "gut-skin axis," and "biomarkers." Articles published up to 2025 were reviewed, focusing on the composition of skin microflora, its systemic implications, and emerging psychodermatological research.

REVIEW OF LITERATURE

Composition and dynamics of skin microflora

Approximately 1,000 species of bacteria on human skin are members of four major phyla: Actinobacteria, Firmicutes, Proteobacteria, and *Bacteroidetes* (Niemeyer-van *et al*., 2018). These microbes are distributed differently on different areas of the skin, with sebaceous (oily) patches being richer in *Propionibacterium and Staphylococci*, moist areas containing *Corynebacteria and Staphylococci*, and dry patches occupied by *Betaproteobacteria* as well as *Flavobacteriales.* The microbiota composition is dependent on factors that belong to the host (including age, sex, and genetics) besides environmental variables and lifestyle habits (Mun *et al*., 2025; Niemeyer-Van *et al*., 2018) (Table 1).

Skin microbiota is critical for immune responses from very young age; the divergence of skin microbiome development may underlie the differences seen in human skin physiology or propensity to a disease. The epidermal and dermal microbiomes may also help to track skin conditions, predict development of disease from them as well as treatment efficacy and assist in choosing the best intervention type and therapy. It is possible to manipulate the composition of the microbiome throughout to support skin health (Luna, 2020). The interaction of the host natural system and the skin microbiota is important for health of the skin. Commensals modulate immunological responses. via interactions with host Pattern Recognition Receptors (PRRs), such as Nucleotide-binding Oligomerization Domain (NOD)-like receptors, and Toll-Like Receptors (TLRs). This reciprocal interaction maintains resistance to commensals and activation on invasive pathogens. For instance, *S. epidermidis* can induce ATP synthesis through the TLR2 in keratinocytes and enhances the activity of regulatory T cells (Treg) to suppress inflammation. The microbiota plays a crucial role in maintaining consistent immune status of skin. and lowering the risk of autoimmune and inflammatory diseases (Zheng *et al*., 2020).

Certain commensal bacteria present on the surface of the skin metabolize amino acids, steroids, fatty acids, and sugars (Melnyk *et al*., 2024). therefore, changing the microenvironment of the skin, which leads to dysbiosis. Through antimicrobial peptide synthesis (e.g., bacteriocins) and immunomodulation, a few commensal bacteria, including *Staphylococcus epidermidis* and *Cutibacterium acnes, improve* skin health (Costello *et al*., 2009). *S. epidermidis* activates TLR4 signalling to attract immune cells: *C. acnes* metabolites manage T cell reaction through the Aryl hydrocarbon Receptor (AhR) pathway (Melnyk *et al*., 2024; Zhang *et al*., 2021). By regulating the host immune system, the skin microbiome also improves and helps in resistance towards pathogens. The skin health depends on this symbiotic equilibrium, whose disturbance might cause skin conditions like eczema and psoriasis (Timm *et al*., 2020).

The skin microbiome's role in skin inflammation has recently undergone a significant change. The skin microbiome and gut microbiome play a vital role in regulating the immune response and maintaining homeostasis. An alteration in the microbiome diversity or hyperproliferation of any microbial community (skin and gut microbiome) contributes to disrupted epithelial integrity and immune dysregulation, resulting in cutaneous inflammation (Kreouzi *et al*., 2025).

Role of skin microbiota in systemic health

Skin microbiota in the maintenance of barrier integrity and immune homeostasis

The extrinsic microbiota plays an important role in skin regeneration and healing by activating Interleukin (IL)-1 signalling and activating keratinocytes by the IL-1R/myeloid differentiation.

The aryl hydrocarbon receptors in keratinocytes play a crucial role both in controlling epidermal differentiation and maintaining barrier integrity. The production of sphingomyelinase by *Staphylococcus epidermidis*, a commensal bacterium, is believed to aid in maintaining homeostasis of the skin barrier (Wu and Yao, 2024).

The chemical barrier and the skin microbiome have a mutually beneficial relationship, which is capable of synthesizing amino acids, proteins, and diverse Free Fatty Acids (FFAs) from dead keratinocytes, sweat, sebum, and other waste products. *C. acnes* and *Corynebacterium* produce lipases that convert triglycerides from sebum FFAs, which have antibacterial properties against various Gram-positive bacteria. On the other hand, isotretinoin (13-cis-retinoic acid) significantly reduces acne by increasing the protein neutrophil gelatinase-associated lipocalin, leading to sebocyte apoptosis (Wu and Yao, 2024).

The skin microbiota and microbial barriers play a key role in controlling the pathogenic bacterial infections. *Staphylococcus* species like *S. epidermidis* and *S. hominis* produce strain-specific antibiotics that selectively inhibit *Staphylococcus aureus. S. epidermidis* produces Pseudo Soluble Modulins (PSMs) that can break down lipid membranes, while certain Coagulase-negative *Staphylococci* (CoNS) like *Staphylococcus caprae* release autoinducing peptides to counteract *Staphylococcus aureus. Cutibacterium* species inhibit *Staphylococcus aureus* from

settling in by competing for space in hair follicles and oil glands. *Malassezia globosa* secretes an aspartyl protease that has an impact on *Staphylococcus aureus* biofilms, preventing them from forming, which indicates its anti-biofilm properties (Wu and Yao, 2024).

The skin microbiota serves as an endogenous adjuvant, moulding local T cell function through the production of IL-1 to contain inflammation that guides innate immune receptors toward protecting against infections from resident commensals. *C. acnes*, a principal commensal species of the normal skin microflora, modifies acne severity and the diversity of *C. acnes* but not proliferation positively correlated to disease establishment, the reduced diversity of *C. acnes* can induce the innate immune system and cause skin inflammation. T cells recirculate through skin to acquire immune tolerance. The epithelium functions as immune protection against the tissue damage and microorganisms sensed by all Anti-Microbial Proteins (AMPs) on the skin surface; a commensal organism like *S. epidermidis* may increase the production of AMPs and trigger inhibition of the nuclear factor pathway initiators (Wu and Yao, 2024).

Skin microbiome imbalance (dysbiosis) and skin conditions

Dysbiosis has been linked to various conditions, including Atopic Dermatitis (AD), Acne Vulgaris (AV), psoriasis, Hidradenitis Suppurativa (HS), and chronic wounds (Afshari *et al*., 2024; Niemeyer-van *et al*., 2018; Olunoiki *et al*., 2022). In the case of AD, higher levels of *S. aureus* and a decrease in commensal diversity are associated with the severity of the disease and tend to improve during remission (Afshari *et al*., 2024) (Table 2).

AD mostly affects the antecubital and popliteal fossae, which have different consistent and high numbers of microbial occupations compared to other areas. The skin barrier dysfunction helps to define Alzheimer's disease by the Th-2-dominated immune response. The skin barrier disruption is related to the expression of claudin-1, which is a component protein of Tight Junctions (TJs) that helps to cause AD development. *Staphylococcus aureus* generates a significant virulence factor (α-toxin), a membrane pore-forming toxin that causes the Nod-like receptor containing three inflammasomes to be activated. The pyrin domain also promotes the release of proinflammatory cytokines IL-1β and IL-18, which are linked to tissue degradation and inflammation (Lou *et al*., 2025). Majority of AD patients show hyperproliferation of *S. aureus* on the skin (Kreouzi *et al*., 2025).

The skin bacterial flora of psoriasis patient is very distinct from that of healthy humans, exhibiting low diversity and increased bacterial number and loss of balance between *Corynebacterium* and *Cutibacterium* particularly in patients suffering from psoriasis, there is increase in *S. aureus and S. pyogenes.* Pathogenic *streptococci* induce psoriasis by the release of M protein (Super antigen). The microbial changes can be characterized by an increase of Th17-mediated inflammatory reactions. Acne vulgaris also results from the alterations, prevalence, and activity of *C. acnes,* whereby particular strains can produce excess amount of inflammatory lipids and intensify the follicular inflammation (Lou *et al*., 2025).

Rosacea is a chronic inflammatory skin disorder that presents itself papules, pustules, and telangiectasia in connection with imbalances of skin microbiome. It has found that lesions of rosacea have high numbers of *Demodex folliculorum, Bacillus oleronius*, and *S. epidermidis* as well as lower numbers of *Cutibacterium acnes.* Exposure of the innate immune system to these organisms causes neutrophils to be activated and helps in the release of inflammatory cytokines, which stimulates angiogenesis, a vital process considered in the pathogenesis of rosacea (Lou *et al*., 2025).

Wound healing is relied on the skin bacterial diversity; hence, changes in microbial composition significantly impact the rate and quality of wound healing. Gram-positive and Gram-negative bacteria, including *Staphylococcus aureus, Streptococcus* sp., *Pseudomonas aeruginosa, and Enterobacteriaceae*, make up most of the microbial population of Diabetic Foot Ulcers (DFU) (Maity *et al*., 2024). These organisms slow down the recovery of ulcers by creating biofilms and enhancing antibiotic resistance (Dinić *et al*., 2024). In DFUs, dysbiosis of skin flora exacerbates inflammation by altering the host immunological response as well as wound repair. *Staphylococcus aureus* in DFUs may express enzymes, which discompose the skin barrier and produce biofilms that act against host immunity and antibiotics. The decrease in diversity of the skin microbiome and increase in pathogenic bacteria were found to be confirmed in patients with DFU, which may create obstacles for wound healing (MacDonald *et al*., 2019). Associated with chronicity of ulcers have greater susceptibility to risk of infection are *Staphylococcus* and *Pseudomonas.*

Obesity has been linked to changes in the skin microbiome, with differences in diversity and community composition between underweight, normal weight, and overweight/obese individuals. *Corynebacterium* relative abundance is correlated with Body Mass Index (BMI), which suggests obesity and metabolic syndrome manifestations. Skin commensals such as *Staphylococcus epidermidis* and *Staphylococcus hominis* are diminished in hidradenitis suppurativa, which affects skin homeostasis and immune response (Frasca and Strbo, 2022).

Skin microbiome linked to metabolic disorders and aging

Alterations in skin microbiota are noted in metabolic disorders and aging. In cases of diabetes, there is a noticeable increase in diversity along with the proliferation of *S. epidermidis*. Meanwhile, skin cancers are marked by a reduction in *Cutibacterium acnes* and an increase in *S. aureus*, indicating dysbiosis (Nurkolis *et al*., 2024) (Table 3).

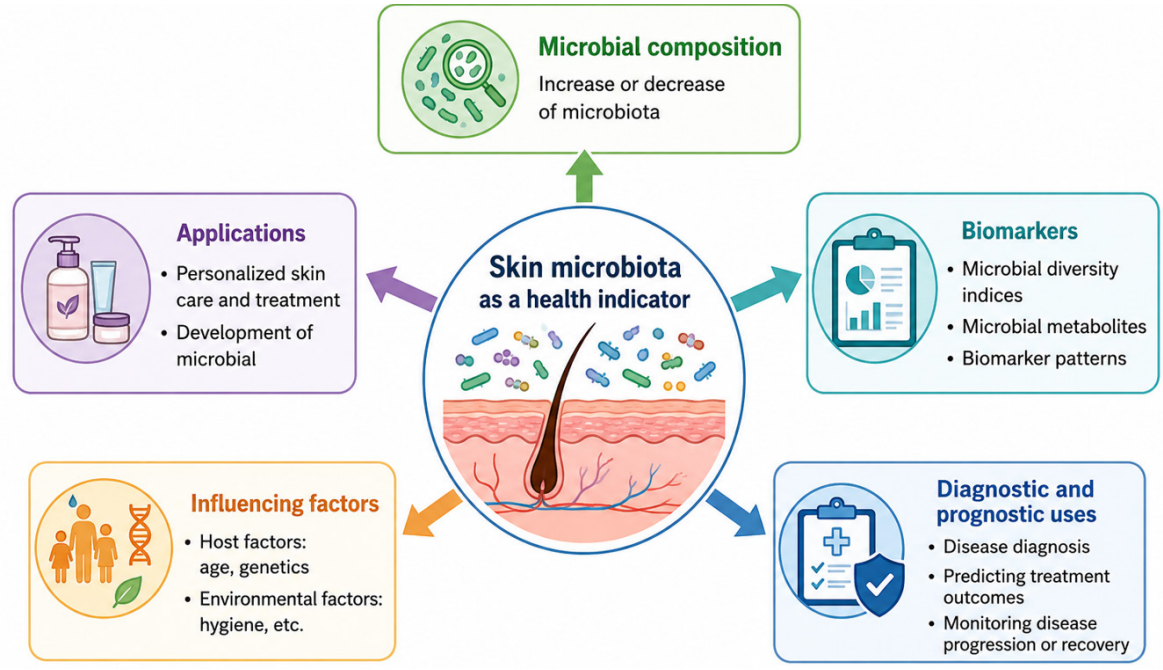

Figure 1: Skin microbiota as a health indicator.

C. acnes-derived Short-Chain Fatty Acids (SCFAs) inhibit Histone Deacetylases (HDAC)-8 and -9 and promote the activation of fatty acid receptors, which induce activation of cytokines via the TLR-2 or TLR-3 signalling pathway. Additionally, SCFAs can prevent *S. epidermidis* from forming biofilms. Hence, microbial metabolic and inflammatory backgrounds can trigger the unique characteristics of immune responses (Lee and Kim, 2022).

A specific class of adaptive immunity is potentially induced by *S. epidermis*. A major problem is to anaylze how receptors of specific host cells determine the molecular characteristics of *S. epidermis*. *Staphylococci* release a wide range of immune modulatory compounds, such as teichoic acids, capsular polysaccharides, and dipeptide aldehydes. Future studies of how, *S. aureus* and *S. epidermidis* differ from each other on molecular basis, will guide to analyse how both these important skin bacteria are differentiated by the immune system and will emphasize key host targets for much significant and specific methods of therapy (Erin *et al*., 2018).

Skin microbiome as an indicator of health

Skin health indicators

Skin microbiota may be used as biomarkers in early-stage clinical trials for AD and AV, according to some systematic reviews, although there is little information available for diseases like psoriasis, HS, and seborrheic dermatitis (Niemeyer-van *et al*., 2018) (Table 4).

The change in the microbiota of skin, metabolism and oxidative stress is caused by certain Volatile Organic Compounds (VOC) profiles evaluate the important pathophysiological processes in Parkinson's Disease (PD) helps in the identification of reliable VOC biomarkers for the early identification of disease and evaluation of therapy (Mitra *et al*., 2022).

The psoriatic microbiome has been shown to harbour increased pathogen species, and decreased members of the microbiome resulting in a dysbiosis characterized by decreased microbial diversity. In psoriatic lesions, *Streptococcus pyogenes* and *S. aureus* are excessive and possess the ability to stimulate T cells acting as superantigens. The commensal bacteria *Cutibacterium* and *Corynebacterium* are lowered, and this status of the microbiome results in an inability to mount an effective immune response. This dysbiosis enhances the inflammatory process via PRR presented on keratinocytes (TLR2, TLR4, and NOD-like receptors), constituting a positive feedback loop promoting inflammation and further interfering with the microbiome (Radaschin *et al*., 2024). The microbiota may promote more rapid healing, according to some theories. Correlations were obtained between 16 disparate metabolites and bacterial species, which may provide an indication of the various ties between the microbiome and metabolic profile (Bianchi *et al*., 2025).

Patients with existing metabolic diseases exhibit an increased severity and greater extent of lesions due to Atopic Dermatitis (AD), and the associated systemic inflammation, oxidative stress and dysbiosis inherent in metabolic disease greatly aggravate the activity of disease and reduce the responses to standard therapies such as topical corticosteroids and calcineurin inhibitors. However, the improved metabolic control can impose significantly lessened effects. Weight loss and control of blood sugar levels reduce inflammation and *S. aureus* colonization through the restoration of AMP production, improvement of barrier integrity, and reduction of systemic inflammation. Newly emerging microbiome-targeting therapies have captured

increased attention in the management of AD. Probiotics, encompassing *lactobacilli* and species of *Bifidobacterium*, increase microbial diversity, probiotic immune responses through enhanced Treg activity, and reduction of Th2 polarization. SCFAs and other postbiotics improve the epidermal barrier and reduce the virulence of *S. aureus* (Kumar *et al*., 2024).

The anaerobic commensal *C acnes* is believed to be important in the pathogenesis of *acne* because it lives within the lipid-rich microhabitat of sebaceous follicles. It hydrolyses triglycerides to FFAs via the action of lipase and thereby influences keratinocyte proliferation while increasing follicular permeability. Some *C. acnes* strains are quite pro-inflammatory, generate porphyrins that create Reactive Oxygen Species (ROS) and activate the Nucleotide Binding Oligomerization, Leucine-Rich Repeat, and Pyrin Domain-Containing Protein 3 (NLRP3) inflammasome leading to neutrophilic infiltrate and pustules/nodules. Metabolic disorders that alter sebaceous lipid production and raise follicular pH contribute to this dysbiosis, favouring expansion of virulent *C. acnes* strains. These strains create a biofilm that protect against AMPs and including cathelicidins defensins, used as antimicrobial countermeasures and the control of chronic inflammation (Kreouzi *et al*., 2025).

Seborrheic Dermatitis (SD) is a long-term inflammatory skin disease. It affects 1-3% of people. SD appears as red scaly patches in places on the body that have lots of oil glands-like your face, scalp and chest. SD is caused by a complicated interplay of oil gland activity, skin microbe (*Malassezia* species) changes and immune system problems. These local factors also play a close relationship with systemic metabolic diseases, including abnormal blood fats and Metabolic Syndrome (MetS). This demonstrates how not only metabolic well-being, but also cutaneous microbial communities collaborate in the development of SD (Kreouzi *et al*., 2025).

Table 1: Composition, function and dynamics of the skin microbiome.

Reference	Aspect	Key findings / Insights	Implications
Mun *et al*., 2025; Niemeyer - van der kolk *et al*., 2018,	Microbial Diversity and Distribution	Skin hosts approx. 1000 species from four major phyla: *Actinobactria, Firmicutes, Proteobacteria*, *Bacteroidetes*. Distribution varies: Sebaceous: *Propionibacterium, Staphylococci* Moist: *Corynebacteria, Staphylococci* Dry: *Betaproteobacteria, Flavobacteriales*.	Microbial distribution is site specific and influenced by age, sex, genetics and environment
Luna, 2020	Microbiota and immune development	Early microbiome development influences immune response and skin physiology. Alterations affect disease predisposition and treatment outcomes.	Monitoring microbiome can aid disease prediction and therapy effectiveness across lifespan.
Zheng *et al*.,2020	Immune interaction and Tolerance	Commensals interact with PRRs (e.g., TLRs, NOD - like receptors) to balance immune activation and tolerance. S.*epidermidis* activates TLR2 and enhances Treg activity, reducing inflammation.	Maintains immune homeostasis, reduces risk of autoimmune / inflammatory skin conditions
Melnyk *et al*., 2022	Commensal Metabolism and Microenvironment	Commensals metabolize amino acids, steroids, fatty acids, sugars, changing the skin's microenvironment. Dysbiosis may occur when balance is disrupted.	Commensal metabolism can both benefit and disrupt skin health depending on the balance.
Costello *et al*., 2009; Zhang *et al*., 2021; Melnyk *et al*., 2022	Antimicrobial and Immunomodulatory roles	Certain microbes produce antimicrobial peptides (e.g., bacteriocins) and modulate the immune system. *S.epidermidis* activates TLR4; *C.acnes* modulates T-cell response via Aryl hydrocarbon Receptor (AhR) pathway.	These commensals protect against pathogens and support immune balance.
Timm *et al*., 2020	Homeostasis and Disease prevention	A symbiotic microbiome is essential for immune resistance and skin health. Disruption (e.g., via dysbiosis) is linked to conditions like eczema and psoriasis.	Microbiome maintenance is vital for preventing inflammatory skin diseases
Kreouzi *et al*., 2025	Skin - Gut Microbiome and Inflammation	Both skin and gut microbiomes regulate immunity and homeostasis. Dysbiosis in either can compromise epithelial integrity and trigger inflammation.	Highlights the systemic role of microbiota in controlling skin inflammation and disease.

Table 2: Dysbiosis and skin conditions with reference.

Reference	Skin disorder	Dysbiosis	Effects
Olunoiki *et al*.,2022; Lou *et al*., 2025; Kreouzi *et al*., 2025	Atopic Dermatitis (AD)	Increase of *S. aureus, cutibacterium, corynebacterium, prevotella, Malassezia* Gut dysbiosis: Increase of *Clostridium,* Decrease of *Escherichia; Akkermansia, Bacteroidetes, bifidobacterium*	AD severity correlates with S. *aureus* load *S. aureus* α - toxin activates Inflammasomes (IL-1β, IL-18) Barrier dysfunction (claudin -1 down regulation).
Niemeyer-van der Kol *et al*., 2018; Lou *et al*., 2025	Psoriasis	Decrease of Microbial diversity, Increase of bacterial load Increase of *S. aureus, S. pyogenes* Imbalance between *Cutibacterium* and *Corynebacterium*.	Streptococcal M protein triggers Th17 inflammation Superantigens from *S. pyogenes* stimulates T-cell response.
Kreouzi *et al*., 2025; Lou *et al*., 2025	Acne Vulgaris (AV)	Dysbiosis of *C. acnes* strains - some are highly pro - inflammatory Gut dysbiois: Decrease of *Firmicutes,* Increase of *Bacteroides,* Decrease of *Clostridium, Clostridiales, Lachnospiraceae, Ruminococcaceae*.	Pro- inflammatory *C. acnes* strains increase lipid metabolism and ROS Gut- skin axis potentially contributes to acne inflammation.
Lou *et al*., 2025	Rosacea	Increase of *Demodex folliculorum, Bacillus oleronius*, *S. epidermidis* Decrease of *Cutibacterium acnes*.	Microbes stimulate neutrophils and cytokine release Induce angiogenesis and chronic inflammation in facial skin.
Maity *et al*., 2024; Dinic *et al*.,2024; MacDonald *et al*., 2019	Chronic wounds / DFUs	Decrease of *S. aureus, Streptococcus, Pseudomonas aeruginosa*, Enterobacteriaceae Decrease of Overall microbial diversity.	Biofilm formation impairs healing and antibiotic penetration Pathogens disrupt barrier and immune defense.
Frasca and strbo, 2022	Obesity/ Metabolic Syndrome	Decrease of *S. epidermidis, S. hominis* Increase of *Corynebacterium* in obese individuals.	Altered skin microbiota affects immune responses and inflammation BMI correlates with *corynebacterium* abundance.
Frasca and strbo, 2022	Hidradenitis Suppurativa (HS)	Skin commensal (e.g., *S. epidermidis, S. hominis)* Imbalanced microbiota favors pro-inflammatory species.	Disrupted skin homeostasis Impaired immune modulation and chronic inflammation.

In Hidradenitis Suppurativa (HS), there is not a diversity of bacteria like there should be, and the harmful ones prevail. These bacterial changes are associated with the inflammation in HS sores. *C. acnes*, a bacterium that can thrive in the presence or absence of air, metabolizes skin oils into fatty acids. These acids attack skin cells and create irritation via TLR2. The protective layers built by *C. acnes* and other dangerous bacteria protect them from the body's defense as well as from drugs. This results in persistent swelling and tissue destruction. The imbalanced bacteria also produce compounds such as SCFAs and ROS. These make skin cells work even more poorly and maintain the inflammation (Kreouzi *et al*., 2025). Burn Injuries (BIs) can modulate the skin bacterial flora makes healing of the wounds difficult. Burn wounds possess less diversified bacteria which shows decreases in normal flora of skin like *S. epidermidis* and *C. acnes*. A study found that higher levels of *Corynebacterium* were linked to more infections in burn patients, while *Propionibacterium* and *Staphylococcus* were associated with fewer infections. *S. aureus* is a common pathogen in burn wounds. Severe burns also lead to changes in gut bacteria and increased intestinal permeability (Madaan *et al*., 2024).

Indicators of allergic disorders

Research using Mendelian randomization indicates causal relationships between skin genera (*S. aureus, P. acnes, Corynebacterium*, and *Proteobacteria*) and allergic conditions, advancing the idea of microbiota as diagnostic indicators (Zhang *et al*., 2025) (Table 5).

Epidemiologic studies reveal that an association exists between environmental exposures, which alter the microbiota, and developing atopic dermatitis, food allergy, and/or asthma. When compared to healthy controls, skin, gastrointestinal, and

respiratory tract samples actually show different microbiotas, with microbial alterations (dysbiosis) frequently occurring before allergic disease manifests. Mechanistic research has demonstrated that microbes can either change the integrity of the skin and harm the gut and airway epithelium, or they can strengthen the barrier and improve the health of the skin, gut, and airways (Aguilera *et al*., 2020).

Quality of Life (QoL) in Patients with Nonmelanoma Cervicofacial Skin Cancer, one study provides an interesting perspective that there's some other things about engaging in sun-protective behaviours that can actually enhance quality of life. The study supports the value of testing measures about the disease-specific aspects (Rhee *et al*.,2003).

The Chronic Skin Diseases and Daily Life (ISDL) is a self-assessment tool that measures the impact of chronic skin disorders, such as psoriasis and atopic dermatitis, on patients. This instrument also addresses different dimensions including physical and physiological health; thus, it can be a useful tool to explore the multifaceted impact of chronic skin diseases on patients (Evers *et al*., 2007).

New studies of the skin microbiome, which show that what's on our skin is just as important for its health and for how good or bad it looks. The research highlights the importance of supporting the microbiome - particularly in older adults - to help improve skin health and address age-related skincare concerns (Haykal *et al*., 2024).

Epidemiologic study: people with skin problems had decreased quality of life. Since those using topical prescription drugs had even more deterioration of life quality, this suggests a strong influence of cutaneous diseases on the daily life situation (Bingefors *et al*., 2022). Studies on postbiotics of *M. luteus* have shown efforts against skin barrier improvement, immune response modulation and recovery from environmental damage. These results revealed new medical treatments for skin health (Heo *et al*., 2023).

Development in thermal sensing tools has led to non-invasive assessment of skin health. These approaches can have a future perspective to be used in diagnosis, either by clinical practitioners or at home based on thermophysiological properties which validate skin health (Madhvapathy *et al*., 2022).

Omics and volatile biomarkers

Volatile Organic Compounds (VOC) produced by skin microbes and metabolism are currently been evaluated as non-invasive biomarkers of human body status and skin cancer in present studies (Duffy and Morrin, 2019).

The skin and the microflora on it release a set of substances, more than 600 Volatile Organic Compounds (VOCs) have been determined. According to Mitra *et al*. (2022), sensing techniques capable of identifying concrete compounds associated with physiological relevance, such as isoprene, 2-nonenal, ammonia, acetone and ethanol from breath and skin have been developed. Volatile saturated and aromatic aldehydes, the terminal products

Table 3: Skin microbiome, Metabolic Disorders, Aging and Immune Modulation.

References	Aspect	Insights	Implications
Nurkolis *et al*., 2024	Diabetes and Skin Microbiome	Proliferation of *S. epidermidis* observed in diabetic skin.	Suggests metabolic Dysfunction alters skin microbiota, potentially influencing wound healing and immune function.
Nurkolis *et al*., 2024	Skin cancer and Microbiome	*Cutibacterium acnes*, *S. aureus* noted in skin cancers.	Indicates dysbiosis; microbial shifts may contribute to local immune dysregulation and tumor progression.
Lee and Kim, 2022	Oxygen Gradient and Microbiome	Skin area oxygenation affects microbial distribution (e.g., anaerobes Vs. aerobes).	Local oxygen level shapes microbiome structure and immune interaction potential.
Lee and Kim, 2022	*C. acnes* Metabolism (SCFAs)	*C.acnes* produces SCFs via fermentation; SCFAs inhibit HDAC8/9, activate TLR2/3, and modulate immune responses. Also, SCFAs reduce biofilm formation by *S. epidermidis*.	SCFAs act as a immune modulating metabolites, influencing inflammation, pathogen resistance, and microbial balance.
Y. Erin *et al*., 2018	*S.epidermidis* and immunity	Activates adaptive immunity via unique molecular feature. Produces teichoic acids, capsular polysaccharides, dipeptide aldehydes. Shares features with *S. aureus* but immune system can distinguish between them.	Understanding specific immune recognition may lead to more targeted therapies differentiating between commensals and pathogens.
Y. Erin *et al*., 2018	Host-Microbe Interaction	Host receptors recognize unique features of commensals vs. pathogens (e.g., *S. epidermidis* vs. *S. aureus*, despite molecular similarities.	Highlights need to define how immune system distinguishes commensal from pathogenic Staphylococci to prevent inappropriate inflammatory responses.

Table 4: Skin health indicators, Microbiota and Related conditions.

References	Aspect	Insights	Implications
Niemeyer-van *et al.*,2018	Skin Microbiota as Biomarkers	Microbiota may serve as early-stage biomarkers in AD (atopic dermatitis) and AV (Acne vulgaris); limited data for psoriasis, HS, and seborrheic dermatitis.	Potential diagnostic use in early clinical trials.
Mitra A *et al.*, 2022	VOC Biomarkers in Parkinson's Disease (PD)	VOC profiles may reflect microbiome changes, oxidative stress and metabolic dysfunction in Parkinson's Disease.	Could lead to non-invasive diagnostic tools for early PD detection.
Radaschnin *et al.*, 2024	Psoriasis and Microbiota	Dysbiosis with reduced diversity; *S. aureus* and *S. pyogenes* increase inflammation via T-cell activation and PRRs like TLR2/4 and NLRs. Commensals like *Cutibacterium* and *Corynebacterium* are reduced.	Inflammation perpetuates microbiome imbalance; supports need for microbial targeted therapies.
Binachi *et al.*, 2025	Microbiota and metabolites	Correlations between 16 metabolites and microbial species suggest links between metabolic profiles and wound healing.	Indicates microbiome's role in recovery and healing.
Kumar A. *et al.*, 2024	Atopic Dermatitis (AD) with Metabolic Disorders	Increased severity of AD with metabolic dysfunction; systemic inflammation worsens disease; improved metabolic control (e.g. Weight loss, glycemic control) restores AMPs and improves outcomes. Probiotics (e.g., *Lactobacillus, Bifidobacterium*) and Postbiotics (e.g., SCFAs) show therapeutic promise.	Microbiome-targeted interventions can enhance treatment response
Kreouzi *et al.*, 2025	Acne and *C.acnes*	*C.acnes* metabolizes lipids into FFAs disrupting skin barrier; pathogenic strains form ROS, activate inflammasome, and resist AMPs via biofilm formation. Metabolic disorders worsen dysbiosis.	Treatment resistance and chronic inflammation linked to microbiome imbalance; requires targeted therapy.
Kreouzi *et al.*, 2025	Seborrheic Dermatitis (SD)	SD involves *Malassezia* species and is connected to sebum production, immune dysfunction, and systemic metabolic conditions like MetS.	Suggests link between systemic health and localized skin conditions.
Kreouzi *et al.*, 2025	Hidradenitis Suppurativa (HS)	Dysbiosis with reduced diversity; pathogenic bacteria like *C. acnes* promote inflammation via TLR2, produce SCFAs/ROS, and resist treatments due to biofilms.	Ongoing inflammation and damage sustained by microbiome imbalance; highlights need for microbiota-based interventions
Madaan *et al.*,2024	Burn Injuries (Bis)	Burn wounds show reduced bacterial diversity; high *Corynebacterium* linked to infections; *S. epidermidis* and *C. acnes* linked to fewer infections. Gut microbiota also affected post-burn.	Bacterial composition influences wound healing and infection risk; suggests need for microbiota- informed burn care.

of both local and systemic lipid peroxidation are being currently studied as putative biomarkers. These skin emissions of volatile organic compounds are influenced by sweat and sebum, provided by several glands acting in synergy with the skin microbiota and they have been implicated to give information related to metabolic processes connected to an individual's health.

The Research by Angioi *et al.* (2025) suggests that the diagnostic capabilities of skin VOCs, when paired with advanced wearable sensor technologies to track these emissions, can fluctuate with changes in ambient ozone levels and may act as indicators of human activity.

Crucial biomarkers like SFAs were high lightened through the current research progress in metabolomics and microbiome sequencing. Recent progress in metabolomics and microbiome sequencing has highlighted crucial biomarkers, such as short-chain fatty acids, and distinct microbial patterns that can forecast treatment results. For example, elevated butyrate levels in psoriasis to reduction of Th17-driven inflammation, while specific *Lactobacillus* strains contribute to managing immune tolerance associated with atopic dermatitis.

FUTURE DIRECTIONS

Psychodermatology

Psychodermatology is defined as an intersection of psychiatry and dermatology, which investigates the influence of neurological stress on the aggravation or chronic nature of skin diseases. Further, it is viewed as a discipline that explores the interrelationship between neurological comorbidities and dermatological

conditions. The gut and skin are considered as key components of the nervous, endocrine, and immune systems (Munoli, 2020). Further, the signalling compounds (neurohormones, cytokines, etc.) play a key role in cellular signalling within the gut-brain-skin axis (Tyson-Carr *et al*., 2025; Munoli, 2020). Additionally, research continues to investigate the interrelationship between human skin microbiota in various regions of the body (such as the scalp, axilla, forearm, face, etc.) and mental wellness. *Cutibacterium* abundance is linked to reduced stress and better mood, according to recent research on the "skin-brain axis," which may be mediated by microbial metabolites and neuroendocrine signalling (Tyson-Carr *et al*., 2025).

Impact of environment and lifestyle

Since our skin's epithelial surface is in close proximity to the outside world (environment), our living conditions have a significant influence on the skin microbiome. More particularly, there will be a notable difference in skin microbial populations between humans who live in rural and urban settings. Since the skin acts as body's primary defense to outside threats, experts are currently concentrating on how growing urbanization affects the skin ecosystem and, consequently, human health. Microbes that may act as innovative probiotics or postbiotics and offer therapeutic remedies for human illnesses such as dermatological disorders are still being investigated (Callewaert *et al*., 2020).

Omics technology

To determine the indicators of microbes for the diagnosis and therapy of skin dysbiosis, omics technologies can provide the interplay between skin microbiome and skin issues. The identification of the relation between skin microbiota and skin dysbiosis will become clearer with clinical isolation of pathogens and probiotics (Yang *et al*., 2022).

The term "Skinomics" refers to the comprehensive knowledge of the metabolic states of different skin types under varied settings, which also makes it possible to identify potential biomarkers of distinct skin types. Indeed, multi-omics integration may allow for the analysis of the network of their eventual interactions as well as the metabolic pathways specific to genes, proteins, metabolites, and the microbiome (Dessì *et al*., 2024).

Gut and skin axis

The gut-skin axis, in which our microbiota plays a pivotal role, presents a fascinating area of study with potential medical and

Table 5: Skin allergic Indicators.

Reference	Focus	Insights	Implications
Zhang *et al*., 2025	Mendelian randomization in microbiota and allergy.	Identified causal links between specific skin genera (e.g., *S. aureus, P. acnes, Corynebacterium*, Proteobacteria) and allergic diseases.	Supports use of microbiota as diagnostic indicators for allergic conditions.
Aguilera *et al*., 2020	Environmental exposure, microbiota, and allergic disease.	Dysbiosis observed in skin, gut, and respiratory tract microbiotas of allergic individuals; changes often precede disease.	Suggests microbes influence barrier integrity and contribute to disease development.
Rhee *et al*., 2003	Quality of life in nonmelanoma cervicofacial skin cancer patients.	Sun-protective behaviours improve quality of life.	Highlights the need for tailored QoL assessment tools in skin cancer patients.
Evers *et al*., 2007	Chronic Skin Diseases and Daily life (ISDL) instrument.	ISDL assesses physical and psychological impacts of chronic skin conditions like psoriasis and atopic dermatitis.	Useful tool for evaluating QoL in chronic dermatological diseases.
Haykal *et al*., 2024	Skin microbiome in aging.	Skin microbiome is essential for maintaining healthy skin; support needed especially in older adults.	Promotes microbiome targeted strategies for aging skin care.
Bingefors *et al*., 2002	QoL in Individuals with Skin Conditions.	Lower QoL scores in patients with skin problem; further decrease with topical drug use.	Emphasizes significant burden of skin disorders on daily life.
Heo *et al*., 2023	Postbiotics from *Micrococcus luteus*.	Improve skin barrier, modulate immune response, aid in recovery from environmental stress	Potential for novel dermatological therapies based on postbiotics.
Madhvapathy *et al*., 2022	Thermal sensing for dermatological assessment.	Non-invasive techniques assess skin health via thermal properties.	Could be developed into clinical or home-use diagnostic tools for skin monitoring.

cosmetic uses. Understanding the relationship between the microbiome and the host tissues will improve our knowledge of health and illness and open up new possibilities. Currently, interdisciplinary teams are working together to put up well-designed trails that mimic the interrelationship between microorganisms and our own bodies (De Pessemier *et al*., 2021).

Depends on the skin and gut microbiota, the prebiotic and probiotic products can be developed for various skin disorders that can be treated. Recent studies revealed that probiotics derived from *S. epidermidis* can help restore the naturally balanced microbiota and regulate the host's AMP mediators (Yang *et al*., 2022).

CHALLENGES

Biomarker validation is complicated by environmental factors and high intra- and inter-individual variability. Moving from correlation to causation requires standardized sampling and analysis procedures as well as longitudinal, well-powered studies (Rosenthal *et al*., 2011).

CONCLUSION

The skin microbiota serves as dynamic and significant marker of human health, playing a key role in host defence, immune regulation, and upkeep the skin homeostasis. The present review highlights the change of our perception from analyzing the skin microbial communities as mere commensals to determine them as vital physiological allies. The composition and functional abilities of the skin microbiota are greatly affected by intrinsic factors such as genetics, age and sex and extrinsic factors like hygiene, environmental factors and therapeutic agents administered, resulting in a distinct microbiological profile for every human.

The most intriguing frontier is characterized by the mounting evidence that dysbiosis, an imbalance in microbial profile, is not just a consequence but my also serve as a key driver of strong indicator of disease. In addition to the well-documented associations with skin disorders like atopic dermatitis and acene, emerging research is linking skin microbiome profile to systemic illness, including metabolic, neurological and autoimmune disorders. This positions the dermatological microbial profile as a key and non-invasive source of biomarkers for the early identification and monitoring of disorders.

Future research integrating with advanced techniques to understand about the biomarkers, it is important to conduct interventional and longitudinal research that confirms their real word value. Using advanced techniques like multi-omics including metabolomics, metagenomics, and Volatile Organic Compound (VOC) profiling, to develop biomarkers in comprehensive manner. The research should focus on microbiome - targeted treatments, such as probiotics, prebiotics, and engineered consortiums. Further incorporating neurocosmetic research that influence insights of skin - brain axis which can provide valuable evaluations of psychological outcomes, helps in understating the interplay between microbiome and psychological well-being. Understanding and mobilizing the skin microbiome along with its systemic connections represent a promising frontier for improving dermatological and overall human health

ACKNOWLEDGEMENT

The Authors acknowledge the Management and Vice-Chancellor of Malla Reddy University for their support and encouragement.

ABBREVIATIONS

AD: Atopic Dermatitis; **AMPs:** Anti-microbial proteins; **Ahr:** Aryl hydrocarbon receptor; **AV:** Acne Vulgaris; **BMI:** Body mass index; **CoNS:** Coagulase-negative Staphylococci; **DFU:** Diabetic Foot Ulcers; **FFAs:** Free Fatty Acids; **HDAC:** Histone Deacetylases; **HS:** Hidradenitis Suppurativa; **IBD:** Inflammatory Bowel Disease; **IL:** Interleukin; **ISDL:** Impact of Chronic Skin Disease on Daily Life; **MetS:** Metabolic Syndrome; **NOD:** Nucleotide-binding oligomerization domain; **PD:** Parkinson's Disease; **PRRs:** Pattern Recognition Receptors; **PSMs:** Phenol-Soluble Modulins; **QoL:** Quality of Life; **ROS:** Reactive Oxygen Species; **SCFAs:** Short-Chain Fatty Acids; **SD:** Seborrheic Dermatitis; **TJs:** Tight Junctions; **TLR:** Toll-like Receptors; **Treg:** Regulatory T cells; **VOC:** Volatile Organic Compounds.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest.

AUTHOR CONTRIBUTIONS

Sandhya K. conducted the literature review and drafted the manuscript. Aparna Srikantam conceptualized the review, supervised and critically revised the manuscript. Both authors read and approved the final manuscript.

SUMMARY

This review highlights the skin microbiome as a critical sentinel for both localized and systemic human health. Commensal microorganisms play a pivotal role in pathogen defense, immune regulation, and barrier maintenance. Dysbiosis is not only linked to dermatological conditions like atopic dermatitis, acne, and psoriasis, but also to systemic issues such as diabetes, obesity, and gastrointestinal disorders via the gut-skin axis. Advancements in omics technologies and Volatile Organic Compound (VOC) profiling offer promising non-invasive biomarkers for early disease detection. Ultimately, understanding host-microbe interactions and the skin-brain axis paves the way for novel, microbiome-targeted therapeutic interventions.

REFERENCES

Afshari, M., Kolackova, M., Rosecka, M. C., Čelakovska, J., and Krejsek, J. (2024). Unraveling the skin: A comprehensive review of atopic dermatitis, current understanding, and approaches. *Frontiers in Immunology, 15*, 1361005.

Aguilera, A. C., Dagher, I. A., and Kloepfer, K. M. (2020). Role of the microbiome in allergic disease development. *Current Allergy and Asthma Reports, 20*, 44.

Aimon Khan, and Koh, Y.-S. (2024). The role of skin microbiome in human health and diseases. *Journal of Bacteriology and Virology, 54*(3), 191-202.

Angioi, R., Thamatam, N., Agah, M., and Morrin, A. (2025). Monitoring skin volatile emissions using wearable sensors. *Annual Review of Analytical Chemistry, 18*(1), 285-305.

Bianchi, P., Jacques, C., Jamin, E. L., Orlandi, L., Cauhape, S., Alvarez-Georges, A., Alves, A., Simcic-Mori, C., Lauze, C., Gravier, E., Carballido, F., Ribet, V., Bessou-Touya, S., and Duplan, H. (2025). Clinical profiling of skin microbiome and metabolome during re-epithelialization. *Scientific Reports, 15*, 22282.

Bingefors, K., Isacson, D., and Lindberg, M. (2002). Self-reported dermatological problems and use of prescribed topical drugs correlate with decreased quality of life: An epidemiological survey. *British Journal of Dermatology, 147*(2), 285-290.

Boxberger, M., Cenizo, V., Cassir, N., and La Scola, B. (2021). Challenges in exploring and manipulating the human skin microbiome. *Microbiome, 9*, 125.

Callewaert, C., Ravard Helffer, K., and Lebaron, P. (2020). Skin microbiome and its interplay with the environment. *American Journal of Clinical Dermatology, 21*(Suppl 1), 4-11.

Chen, Y. E., Fischbach, M. A., and Belkaid, Y. (2018). Skin microbiota-host interactions. *Nature, 553*(7689), 427-436.

Costello, E. K., Lauber, C. L., Hamady, M., Fierer, N., Gordon, J. I., and Knight, R. (2009). Bacterial community variation in human body habitats across space and time. *Science, 326*(5960), 1694-1697.

De Pessemier, B., Grine, L., Debaer, M., Maes, A., Paetzold, B., and Callewaert, C. (2021). Gut-skin axis: Current knowledge of the interrelationship between microbial dysbiosis and skin conditions. *Microorganisms, 9*, 353.

Dessì, A., Pintus, R., Fanos, V., and Bosco, A. (2024). Integrative multiomics approach to skin: The synergy between individualized medicine and futuristic precision skin care. *Metabolites, 14*, 157.

Dinić, M., Burgess, J. L., Lukić, J., Catanuto, P., Radojević, D., Marjanović, J., Verpile, R., Thaller, S. R., Gonzalez, T., Golić, N., Strahinić, I., and Tomic-Canic, M. (2024). Postbiotic lactobacilli induce cutaneous antimicrobial response and restore the barrier to inhibit the intracellular invasion of *Staphylococcus aureus in vitro* and *ex vivo*. *The FASEB Journal, 38*, e23801.

Duffy, E., and Morrin, A. (2019). Endogenous and microbial volatile organic compounds in cutaneous health and disease. *TrAC Trends in Analytical Chemistry, 111*, 163-172.

Evers, A. W. M., Kraaimaat, F. W., Van de Kerkhof, P. C. M., Gerritsen, M. J. P., Duller, P., De Jong, E. M. G. J., Verhaak, C. M., Verhoeven, E. W. M., Van der Valk, P. G. M., and Otero, E. (2007). The impact of chronic skin disease on daily life (ISDL): A generic and dermatology-specific health instrument. *British Journal of Dermatology, 158*(1), 101-108.

Frasca, D., and Strbo, N. (2022). Effects of obesity on infections with emphasis on skin infections and wound healing. *Journal of Dermatology and Skin Science, 4*(3), 5-10.

Haykal, D., Cartier, H., and Dréno, B. (2024). Dermatological health in the light of skin microbiome evolution. *Journal of Cosmetic Dermatology, 23*(12), 3836-3846.

Heo, Y. M., Lee, D.-G., Lee, H., Mun, S., Kang, S., Han, K., Yun, S. K., Baek, C., and Kim, M. (2023). Skin benefits of postbiotics derived from *Micrococcus luteus* derived from human skin: An untapped potential for dermatological health. *Genes and Genomics, 46*(1), 13-25.

Kreouzi, M., Theodorakis, N., Nikolaou, M., Feretzakis, G., Anastasiou, A., Kalodanis, K., and Sakagianni, A. (2025). Skin microbiota: Mediator of interactions between metabolic disorders and cutaneous health and disease. *Microorganisms, 13*(1), 161.

Kumar, A., Green, K. M., and Rawat, M. A. (2024). Comprehensive overview of postbiotics with a special focus on discovery techniques and clinical applications. *Foods, 13*, 2937.

Lee, H. J., and Kim, M. (2022). Skin barrier function and the microbiome. *International Journal of Molecular Sciences, 23*, 13071.

Lou, J., Xiang, Z., Zhu, X., Li, J., Jin, G., Cui, S., Huang, N., Le, X., Fan, Y., and Sun, Q. (2025). Skin microbiota and diabetic foot ulcers. *Frontiers in Microbiology, 16*, 1575081.

Luna, P. C. (2020). Skin microbiome as years go by. *American Journal of Clinical Dermatology, 21*(Suppl 1), 12-17.

MacDonald, A., Brodell, J. D., Jr., Daiss, J. L., Schwarz, E. M., and Oh, I. (2019). Evidence of differential microbiomes in healing versus non-healing diabetic foot ulcers prior to and following foot salvage therapy. *Journal of Orthopaedic Research, 37*, 1596-1603.

Madaan, T., Doan, K., Hartman, A., Gherardini, D., Ventrola, A., Zhang, Y., and Kotagiri, N. (2024). Advances in microbiome-based therapeutics for dermatological disorders: Current insights and future directions. *Experimental Dermatology, 33*.

Madhvapathy, S. R., Arafa, H. M., Patel, M., Winograd, J., Kong, J., Zhu, J., Xu, S., and Rogers, J. A. (2022). Advanced thermal sensing techniques for characterizing the physical properties of skin. *Applied Physics Reviews, 9*(4), 041307.

Maity, S., Leton, N., Nayak, N., Jha, A., Anand, N., Thompson, K., Boothe, D., Cromer, A., Garcia, Y., Al-Islam, A., and Nauhria, S. (2024). A systematic review of diabetic foot infections: Pathogenesis, diagnosis, and management strategies. *Frontiers in Clinical Diabetes and Healthcare, 5*, 1393309.

Melnyk, N., Popowski, D., Strawa, J. W., Przygodzińska, K., Tomczyk, M., Piwowarski, J. P., and Granica, S. (2024). Skin microbiota metabolism of natural products from comfrey root (*Symphytum officinale* L.). *Journal of Ethnopharmacology, 318*(Part B), 116968.

Mitra, A., Choi, S., Boshier, P. R., Razumovskaya-Hough, A., Belluomo, I., *et al.* (2022). The human skin volatolome: A systematic review of untargeted mass spectrometry analysis. *Metabolites, 12*(9), 824.

Mun, S., Jo, H., Heo, Y. M., Baek, C., Kim, H.-B., Lee, H., Yun, K., Jeong, J., Lee, W., Jeon, D., Kang, S. M., Kang, S., Choi, Y.-B., Han, S., Kim, G., Ahn, K., Lee, D. H., Ahn, Y. J., Lee, D.-G., and Han, K. (2025). Skin microbiome-biophysical association: A first integrative approach to classifying Korean skin types and aging groups. *Frontiers in Cellular and Infection Microbiology, 15*, 1561590.

Munoli, R. N. (2020). Psychodermatology: An overview of history, concept, classification, and current status. *Indian Journal of Private Psychiatry, 14*(2), 85-91.

Niemeyer-van der Kolk, T., van der Wall, H. E. C., Balmforth, C., Van Doorn, M. B. A., and Rissmann, R. (2018). A systematic literature review of the human skin microbiome as biomarker for dermatological drug development. *British Journal of Clinical Pharmacology, 84*(10), 2178-2193.

Nurkolis, F., Utami, T. W., Alatas, A. I., Wicaksono, D., Kurniawan, R., Ratmandhika, S. R., Sukarno, K. T., Pahu, Y. G. P., Kim, B., Tallei, T. E., Tjandrawinata, R. R., Alhasyimi, A. A., Surya, R., Helen, H., Halim, P., Muhar, A. M., and Syahputra, R. A. (2024). Can salivary and skin microbiome become a biodetector for aging-associated diseases? Current insights and future perspectives. *Frontiers in Aging, 5*, 1462569.

Olunoiki, E., Rehner, J., Bischoff, M., Koshel, E., Vogt, T., Reichrath, J., and Becker, S. L. (2022). Characteristics of the skin microbiome in selected dermatological conditions: A narrative review. *Life, 12*(9), 1420.

Polkowska-Pruszyńska, B., Krasowska, D., and Gerkowicz, A. (2019). The gut microbiome alterations in allergic and inflammatory skin diseases-An update. *Journal of the European Academy of Dermatology and Venereology, 34*(3), 455-464.

Prescott, S. L., Larcombe, D. L., Logan, A. C., *et al.* (2017). The skin microbiome: Impact of modern environments on skin ecology, barrier integrity, and systemic immune programming. *World Allergy Organization Journal, 10*, 29.

Radaschin, D. S., Tatu, A., Iancu, A. V., Beiu, C., and Popa, L. G. (2024). The contribution of the skin microbiome to psoriasis pathogenesis and its implications for therapeutic strategies. *Medicina, 60*, 1619.

Rhee, J. S., Loberiza, F. R., Burzynski, M., Matthews, B. A., Smith, T. L., and Neuburg, M. (2003). Quality of life assessment in nonmelanoma cervicofacial skin cancer. *The Laryngoscope, 113*(2), 215-220.

Rosenthal, M., Goldberg, D., Aiello, A., Larson, E., and Foxman, B. (2011). Skin microbiota: Microbial community structure and its potential association with health and disease. *Infection, Genetics and Evolution, 11*(5), 839-848.

Timm, C. M., Loomis, K., Stone, W., Mehoke, T., Brensinger, B., Pellicore, M., Staniczenko, P. P. A., Charles, C., Nayak, S., and Karig, D. K. (2020). Isolation and characterization of diverse microbial representatives from the human skin microbiome. *Microbiome, 8*(1), 58.

Tyson-Carr, J., Leng, J., Scott, M., Adams, S., Hoptroff, M., Murphy, B., Fallon, N., Paterson, S., Thomas, A., Giesbrecht, T., and Roberts, C. (2025). Body-site specific associations between human skin microbiome composition and psychological wellbeing. *British Journal of Dermatology, 193*(Suppl 2), ii6-ii14.

Wu, M.-Y., and Yao, X. (2024). Skin microbiota and the skin barrier. *International Journal of Dermatology and Venereology, 7*(1), 18-26.

Yang, Y., Qu, L., Mijakovic, I., and Wei, Y. (2022). Advances in the human skin microbiota and its roles in cutaneous diseases. *Microbial Cell Factories, 21*(1), 176.

Zhang, K., Huang, Q., Deng, S., Yang, Y., Li, J., and Wang, S. (2021). Mechanisms of TLR4-mediated autophagy and nitroxidative stress. *Frontiers in Cellular and Infection Microbiology, 11*, 766590.

Zhang, Y., Wu, Y., Su, X., Gan, Q., Ding, Y., Wang, J., Wang, X., Zhang, N., and Wu, K. (2025). Inflammation biomarkers mediate causal inference of the effect of skin microbiota on the risk of allergic diseases. *AMB Express, 15*, 116.

Zheng, D., Liwinski, T., and Elinav, E. (2020). Interaction between microbiota and immunity in health and disease. *Cell Research, 30*, 492-506.

Zhu, Y., Yu, X., and Cheng, G. (2023). Human skin bacterial microbiota homeostasis: A delicate balance between health and disease. *mLife, 2*(2), 107-120.

Cite this article: Kuruba S, Srikantam A. The Skin Microbiota: A Sentinel of Health and A New Frontier for Disease Indication. Asian J Biol Life Sci. 2026;15(2):266-76.