RESEARCH PAPER

Role of the Skin Microbiome in Dermatological Conditions: A Narrative Review.

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ABSTRACT
Background:
The skin microbiome, comprising bacteria, fungi, viruses, and mites, plays a critical role in maintaining cutaneous homeostasis through immune modulation, barrier protection, and inhibition of pathogenic colonization. Emerging evidence suggests that alterations in microbial composition, termed dysbiosis, are strongly associated with the pathogenesis of various dermatological conditions, particularly acne vulgaris and inflammatory dermatoses. Understanding these interactions has become essential for developing novel therapeutic strategies.
Objective:
To comprehensively evaluate the role of the skin microbiome in dermatological conditions, focusing on its composition, ecological variability, host–microbe interactions, contribution to disease pathogenesis, and emerging microbiome-targeted therapies.
Methods:
This narrative review was conducted using a structured approach in accordance with established guidance for narrative synthesis. A comprehensive literature search was performed primarily using PubMed, supplemented by dermatology textbooks and authoritative organizational resources. Keywords included "skin microbiome," "cutaneous microbiota," "acne vulgaris," "dysbiosis," "biofilms," "antimicrobial resistance," "probiotics," and "phage therapy." Relevant studies, including reviews, randomized controlled trials, and mechanistic studies, were selected based on scientific quality and relevance. Data were synthesized qualitatively and organized into thematic domains.
Results:
The skin microbiome demonstrates significant spatial and temporal variability influenced by anatomical, environmental, and host-related factors. While a stable core microbiome exists, microenvironmental differences lead to distinct microbial niches. Dysbiosis, particularly involving strain-level variations in Cutibacterium acnes, plays a central role in acne pathogenesis through activation of inflammatory pathways such as IL-1β-mediated responses. Beyond bacteria, the virome and mycobiome contribute to microbial diversity and immune modulation. Antibiotic use disrupts microbial balance and promotes antimicrobial resistance, while biofilm formation contributes to chronicity and treatment resistance. Emerging therapies, including probiotics, bacteriophage therapy, and bacteriocins, demonstrate promising results in restoring microbial balance and improving clinical outcomes.
Conclusion:
The skin microbiome is a dynamic and integral component of dermatological health, with dysbiosis contributing to disease development and progression. Future therapeutic strategies should shift from broad-spectrum antimicrobial approaches to precision microbiome modulation, emphasizing restoration of microbial balance. Continued research is essential to translate microbiome-based interventions into effective clinical practice..

Keywords Skin microbiome, cutaneous microbiota, dysbiosis, acne vulgaris, Cutibacterium acnes, skin immunity, gut–skin axis, biofilms, antimicrobial resistance, probiotics, bacteriophage therapy, bacteriocins, Malassezia, virome, dermatological diseases
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INTRODUCTION

The skin, the largest organ of the human body, functions as a vital physical and immunological barrier that protects against environmental insults, microbial invasion, and transepidermal water loss. Its structural complexity, comprising the epidermis, dermis, and adnexal components, enables it to perform essential protective and regulatory roles [1]. In addition to its anatomical significance, the skin is increasingly recognized as a biologically active interface where host–microbe interactions play a crucial role in maintaining physiological balance [2].

Advances in microbiological research have led to the identification of the skin microbiome as a diverse and dynamic community of microorganisms, including bacteria, fungi, viruses, and mites, that inhabit the cutaneous surface [3]. These microbial communities are not merely passive colonizers but actively contribute to skin homeostasis by regulating immune responses, inhibiting pathogen colonization, and maintaining barrier integrity.

Dermatological conditions represent a substantial global health burden, affecting individuals across all age groups and geographic regions. Skin diseases are among the most common non-fatal conditions worldwide and are associated with significant morbidity, psychosocial impact, and economic costs, highlighting the need for improved understanding of their underlying mechanisms [4]. Emerging evidence suggests that disturbances in the skin microbiome, commonly referred to as dysbiosis, are implicated in the pathogenesis of several dermatological disorders.

The composition and function of the skin microbiome are influenced by multiple intrinsic and extrinsic factors, including host genetics, immune status, hygiene practices, environmental exposures, and the use of antimicrobial agents [5]. These factors can alter microbial diversity and stability, thereby predisposing individuals to inflammatory and infectious skin conditions.

Furthermore, the skin microbiome exhibits considerable heterogeneity across different anatomical sites, driven by variations in moisture, sebum production, and local environmental conditions. This spatial diversity contributes to the formation of distinct microbial niches, each with specific functional roles in maintaining skin health [6].

The expanding availability of biomedical literature through platforms such as PubMed has facilitated rapid advancements in microbiome research, enabling a deeper understanding of host–microbial interactions and their clinical implications [7]. Consequently, there is growing interest in exploring microbiome-targeted therapeutic strategies aimed at restoring microbial balance and improving outcomes in dermatological diseases.

In this context, the present narrative review aims to comprehensively examine the role of the skin microbiome in dermatological conditions, with a focus on its composition, functional significance, involvement in disease pathogenesis, and emerging therapeutic interventions.

METHODS

This narrative review was conducted using a structured and transparent approach in accordance with established methodological guidance for narrative synthesis [8]. The objective was to comprehensively explore the role of the skin microbiome in dermatological conditions, with emphasis on microbial composition, host–microbe interactions, disease associations, and emerging therapeutic strategies.

A comprehensive literature search was performed using electronic databases, primarily PubMed, to identify relevant studies published in English. Additional sources included authoritative dermatology textbooks and organizational resources to provide foundational context. Keywords used in the search strategy included “skin microbiome,” “cutaneous microbiota,” “acne vulgaris,” “dysbiosis,” “skin immunity,” “biofilms,” “antimicrobial resistance,” “probiotics,” and “phage therapy.” Boolean operators (AND, OR) were applied to refine search results and enhance retrieval specificity.

Studies were selected based on relevance to the topic, scientific quality, and contribution to understanding the microbiome–disease relationship. Priority was given to recent studies, high-impact reviews, randomized controlled trials, and mechanistic investigations. Both foundational and contemporary literature were included to ensure a balanced and comprehensive perspective.

The selected studies were thematically organized into key domains, including microbiome composition, ecological variability, immune interactions, dermatological disease associations, antimicrobial resistance, and microbiome-targeted therapeutic approaches. Data were synthesized qualitatively, with emphasis on identifying patterns, consistencies, and emerging trends across studies.

Unlike systematic reviews, formal risk-of-bias assessment and meta-analysis were not performed; however, efforts were made to critically appraise the evidence and avoid selective reporting. The narrative synthesis approach enabled integration of diverse study designs and facilitated a holistic understanding of the evolving role of the skin microbiome in dermatology.

Structural Organization and Topographical Diversity of the Skin Microbiome

The human skin microbiome is characterized by remarkable heterogeneity, both across individuals and within different anatomical sites of the same individual. Early landmark studies demonstrated that microbial communities are not uniformly distributed but instead form highly specialized ecological niches. Findley et al. reported that sebaceous regions such as the forehead and back are predominantly colonized by *Cutibacterium species*, whereas moist areas like the axilla and groin harbor higher proportions of *Staphylococcus* and *Corynebacterium* species [9]. In contrast, dry regions exhibit greater microbial diversity, reflecting the influence of local environmental conditions such as hydration, temperature, and lipid content.

This spatial heterogeneity is complemented by temporal stability. Oh et al., through longitudinal sampling, demonstrated that despite inter-individual variability, the core microbiome within an individual remains relatively

stable over time [10]. Their findings suggest that the skin microbiome operates as a resilient ecological system, capable of maintaining equilibrium despite environmental perturbations. However, this stability does not preclude localized variability, as microenvironmental differences within the same anatomical region can significantly alter microbial composition.

Microenvironmental Variability and Advanced Sequencing Insights

Recent advances in shotgun metagenomic sequencing have provided deeper insights into fine-scale microbial variability. Wei et al. demonstrated that even within facial regions, distinct microbial communities exist between sites such as the forehead, cheek, and chin, each characterized by unique microbial signatures [11]. Their study revealed differences not only in species composition but also in functional gene expression, indicating that microbial communities adapt to localized conditions.

Temporal studies further reinforce the dynamic nature of the microbiome. Hillebrand et al., in a 2-year longitudinal analysis, observed fluctuations in microbial abundance associated with seasonal changes, cosmetic use, and environmental exposure [12]. Although core taxa remained stable, relative abundance shifts were noted, suggesting that external factors can modulate microbial equilibrium without completely disrupting it.

Environmental exposures have also been shown to influence microbial diversity. Nielsen et al. reported that exposure to ocean water results in transient increases in microbial diversity, along with the introduction of marine-associated microorganisms onto the skin surface [13]. These changes, although temporary, highlight the sensitivity of the skin microbiome to external environmental factors and suggest potential implications for both protective and pathogenic processes.

Microbiome–Immune System Interactions

The skin microbiome plays a critical role in shaping host immune responses. The cutaneous immune system is constantly exposed to microbial signals and must maintain a balance between tolerance to commensals and defense against pathogens. Nguyen and Soulika described how innate immune mechanisms, including antimicrobial peptides and pattern recognition receptors, mediate this interaction, allowing the skin to respond selectively to microbial stimuli [14].

Beyond local interactions, systemic influences have also been recognized. The concept of the gut–skin axis suggests that intestinal microbiota can influence skin inflammation through immune modulation and metabolic signaling pathways. Sinha et al. highlighted that alterations in gut microbiota composition can lead to systemic inflammatory responses, which may manifest as dermatological conditions such as acne and psoriasis [15].

At the molecular level, microbial components can directly activate inflammatory pathways. Kistowska et al. demonstrated that *Cutibacterium acnes* induces IL-1β production through activation of the inflammasome pathway, providing a mechanistic link between microbial colonization and inflammatory skin disease [16]. This finding underscores the role of specific microbial triggers in initiating immune responses.

Microbiome Dysbiosis and Acne Pathogenesis

The traditional view of acne as a simple bacterial infection has been replaced by a more complex model involving microbial dysbiosis and host–microbe interactions. Niedźwiedzka et al. emphasized that acne is associated with alterations in microbial diversity and the dominance of specific pathogenic strains rather than the mere presence of *C. acnes* [17]. Their study highlighted that strain-level variation plays a critical role in determining whether *C. acnes* acts as a commensal or a pathogen.

Supporting this, Dréno et al. described how acne pathogenesis involves a multifactorial process, including increased sebum production, follicular hyperkeratinization, and microbial imbalance [18]. These factors interact synergistically to create an environment conducive to inflammation and lesion formation.

Moradi Tuchayi et al. further elaborated that acne involves complex immunological and microbial interactions, with inflammatory mediators playing a central role in disease progression [19]. This integrated model highlights the importance of considering both host and microbial factors in understanding dermatological diseases.

Interestingly, not all microbial activity is pathogenic. Rozas et al. demonstrated that certain strains of *C. acnes* contribute to skin homeostasis by producing antimicrobial peptides that inhibit pathogenic organisms [20]. This suggests that maintaining microbial balance, rather than eliminating bacteria, is essential for skin health.

Recent studies have also identified early inflammatory events in acne development. Huang et al. reported increased expression of cytokines and immune cell infiltration in early lesions, indicating that inflammation precedes visible clinical manifestations [21]. These findings reinforce the concept that dysbiosis initiates a cascade of immune responses leading to disease.

Expanding the Microbiome: Virome and Mycobiome

The skin microbiome extends beyond bacteria to include viral and fungal communities that contribute to its functional complexity. Lecuit and Eloit introduced the concept of the human virome, emphasizing its role in regulating microbial ecosystems and influencing host immunity [22]. Viruses may modulate bacterial populations through mechanisms such as bacteriophage activity, thereby shaping overall microbial balance.

Hannigan et al. further demonstrated that the skin virome exhibits both spatial and temporal diversity, with dynamic interactions between viral and bacterial communities [23]. Their findings suggest that viral components may influence microbial stability and contribute to disease processes.

High-throughput sequencing studies have revealed a wide diversity of DNA viruses present on the skin. Foulongne et al. identified numerous viral species, many of which were previously unrecognized, highlighting the complexity of the skin virome [24]. These findings suggest that viruses may play a previously underappreciated role in both health and disease.

Fungal Microbiome and Host Immune Responses

The skin microbiome is a multi-kingdom ecosystem in which fungal organisms play a significant yet often underappreciated role. Among these, *Malassezia* species are the predominant fungal inhabitants of human skin and are closely associated with sebaceous regions. Sparber and LeibundGut-Landmann demonstrated that host immune responses to *Malassezia* are mediated through innate and adaptive pathways, particularly involving Th17-mediated inflammation [25]. Their findings suggest that while *Malassezia* exists as a commensal organism under normal conditions, dysregulated immune responses can trigger inflammatory dermatoses such as seborrheic dermatitis and atopic dermatitis.

This dual role of fungi—as both commensals and potential pathogens—highlights the importance of microbial balance in maintaining skin homeostasis. Disruption of fungal equilibrium may therefore contribute to disease progression through immune activation and barrier dysfunction.

Antibiotic-Induced Dysbiosis and Antimicrobial Resistance

The increasing reliance on antibiotics in dermatology has significantly impacted the composition and function of the skin microbiome. Jo et al. demonstrated that systemic antibiotic therapy leads to a reduction in microbial diversity and an expansion of antibiotic resistance genes within the skin microbiota [26]. Their study provided compelling evidence that antibiotic exposure not only targets pathogenic organisms but also disrupts commensal microbial communities, thereby altering the ecological balance of the skin.

The emergence of antibiotic-resistant *Cutibacterium acnes* has been widely reported and poses a major challenge in acne management. Alkhawaja et al. observed high rates of resistance to commonly used antibiotics such as clindamycin and erythromycin among acne patients [30]. This resistance contributes to treatment failure, prolonged disease duration, and increased healthcare burden.

Importantly, antibiotic-induced dysbiosis may have broader implications beyond resistance. Disruption of commensal populations can impair protective functions such as pathogen inhibition and immune regulation, thereby predisposing individuals to secondary infections and chronic inflammatory conditions.

Biofilm Formation and Its Role in Disease Persistence

Biofilm formation represents a critical survival strategy for microorganisms within the skin environment. Coenye et al. demonstrated that *Cutibacterium acnes* forms biofilms within hair follicles, creating a protective matrix that shields bacteria from host immune responses and antimicrobial agents [27]. These biofilms contribute to persistent inflammation and reduced treatment efficacy, particularly in chronic and severe acne.

Further evidence from Abbott et al. revealed that biofilm-forming *C. acnes* strains can interact with other skin pathogens, including *Staphylococcus aureus*, leading to enhanced biofilm stability and increased resistance to antibiotics [28]. This interspecies interaction underscores the complexity of microbial ecosystems and highlights the limitations of targeting single organisms in dermatological therapy.

The presence of biofilms also explains the recurrence of acne following antibiotic treatment, as residual microbial communities within biofilms can rapidly repopulate the skin once therapy is discontinued.

Microbiome-Targeted Therapeutic Approaches

Given the limitations of conventional antibiotic therapy, there has been growing interest in microbiome-targeted interventions aimed at restoring microbial balance rather than eradicating bacteria.

Probiotics and Microbiome Modulation

Probiotics have emerged as a promising therapeutic strategy in dermatology. Chilicka et al. highlighted that probiotics can modulate the skin microbiome by enhancing beneficial microbial populations, reducing inflammation, and improving barrier function [31]. These effects are mediated through mechanisms such as competitive inhibition of pathogenic bacteria, production of antimicrobial substances, and modulation of immune responses.

Clinical evidence supports these findings. Sathikulpakdee et al. conducted a randomized controlled trial demonstrating that topical probiotic formulations significantly reduced acne lesion counts and improved skin condition [32]. Similarly, Kim et al. reported that administration of *Lactobacillus plantarum* resulted in significant reductions in inflammatory lesions and improved overall skin health, suggesting both local and systemic benefits [33].

More recently, Eguren et al. demonstrated that oral probiotic therapy leads to measurable clinical improvement in acne severity, further supporting the role of systemic microbiome modulation in dermatological conditions [34].

Bacteriophage Therapy: A Precision Approach

Bacteriophage therapy represents a novel and highly targeted strategy for microbiome modulation. Natarelli et al. described how bacteriophages selectively target pathogenic bacteria while preserving commensal microbial populations, thereby minimizing disruption to the overall microbiome [35].

Advanced Phage-Based Therapeutics

Further advancements in phage therapy have reinforced its therapeutic potential. Rimon et al. demonstrated that topical phage application significantly reduced acne-like lesions in experimental models, along with modulation of inflammatory responses [36]. These findings suggest that phage-based therapies may play a key role in the future management of dermatological conditions.

Experimental studies have provided promising results. Rimon et al. demonstrated that phage therapy significantly reduced bacterial load and inflammation in acne models, highlighting its potential as an effective therapeutic approach [36].

Additionally, clinical trials evaluating topical phage formulations have reported favorable outcomes, with reductions in lesion counts and minimal adverse effects [37].These findings suggest that phage therapy may serve as a viable alternative to antibiotics, particularly in the context of increasing antimicrobial resistance.

Commensal-Based Therapies and Host Defense Mechanisms

Recent research has focused on harnessing the protective properties of commensal bacteria. O'Neill et al. identified specific skin commensals capable of selectively inhibiting *Cutibacterium acnes*, thereby restoring microbial balance without disrupting beneficial populations [38]. This approach represents a shift toward precision microbiome modulation.

In addition to microbial interactions, host-derived antimicrobial mechanisms also play a crucial role. O'Neill et al. demonstrated that perifollicular dermal cells produce antimicrobial factors that regulate microbial populations and contribute to the pathophysiology of acne [39]. These findings highlight the importance of host–microbe interactions in maintaining skin health.

Bacteriocins and Novel Antimicrobial Compounds

Bacteriocins, antimicrobial peptides produced by commensal bacteria, have emerged as potential therapeutic agents. Jang et al. demonstrated that bacteriocins derived from *Staphylococcus epidermidis* selectively target pathogenic bacteria, including methicillin-resistant *Staphylococcus aureus* (MRSA), without affecting beneficial microbes [40]. This selective activity offers a significant advantage over conventional antibiotics.

TABLE 1: Key Evidence on Skin Microbiome in Dermatological Conditions

Author & Year	Study Type	Sample / Model	Key Findings (with Data)	Clinical / Public Health Implication
Findley et al., 2013	Observational (metagenomic)	Multiple skin sites	Sebaceous areas dominated by *Cutibacterium*; moist areas by *Staphylococcus* and *Corynebacterium*	Site-specific microbiome influences disease patterns
Oh et al., 2016	Longitudinal study	Healthy individuals	Core microbiome remains stable over time despite inter-individual variation	Stability supports targeted microbiome therapies
Wei et al., 2022	Shotgun metagenomics	Facial regions	Significant variation between forehead, cheek, and chin microbiota	Microenvironment-specific treatment strategies required
Hillebrand et al., 2021	Longitudinal (2-year)	Healthy adults	Seasonal variation alters microbial abundance without disrupting core flora	Environmental factors influence microbiome dynamics
Nielsen et al., 2019	Experimental exposure	Ocean water exposure	Increased microbial diversity after exposure	External environment impacts skin microbiome
Nguyen et al., 2019	Review	—	Skin immunity regulated through microbial interactions and innate pathways	Microbiome essential for immune homeostasis
Sinha et al., 2021	Review	—	Gut–skin axis influences inflammatory skin conditions	Systemic microbiome contributes to dermatological diseases
Kistowska et al., 2014	Experimental (in vitro/in vivo)	Cellular models	*Cutibacterium acnes* induces IL-1β via inflammasome activation	Mechanistic basis of acne inflammation
Niedźwiedzka et al., 2024	Review	—	Acne linked to strain-specific dysbiosis rather than bacterial presence alone	Shift toward precision microbiome therapy
Dréno et al., 2018	Review	—	Acne involves microbiome imbalance, sebum production, and	Multifactorial disease model

			immune activation	
Moradi et al., 2015	Review	—	Acne pathogenesis includes keratinization, inflammation, and microbial changes	Integrated understanding of disease
Rozas et al., 2021	Experimental	Microbial analysis	Commensal *C. acnes* produces antimicrobial peptides	Protective role of microbiome
Huang et al., 2024	Molecular study	Acne lesions	Increased cytokine expression and immune cell infiltration	Inflammation precedes clinical lesions
Lecuit et al., 2013	Review	—	Virome contributes to microbial balance and host interaction	Expands microbiome concept beyond bacteria
Hannigan et al., 2015	Metagenomic study	Skin samples	High diversity of DNA viruses with temporal variability	Viral–bacterial interaction important
Foulongne et al., 2012	Sequencing study	Skin samples	Identification of multiple novel DNA viruses	Virome role in skin ecology
Sparber et al., 2017	Experimental	Immune models	*Malassezia* triggers Th17-mediated inflammation	Fungal contribution to dermatological diseases
Jo et al., 2021	Translational study	Human subjects	Antibiotics reduce microbial diversity and increase resistance genes	AMR is a major concern in dermatology
Coenye et al., 2022	Experimental	Biofilm models	*C. acnes* forms protective biofilms	Biofilms lead to treatment resistance
Abbott et al., 2022	Experimental	Mixed biofilms	Inter-species biofilm interactions increase resistance	Polymicrobial complexity affects therapy
Alkhawaja et al., 2020	Cross-sectional	Acne patients	High resistance to clindamycin and erythromycin	Limits effectiveness of antibiotics
Chilicka et al., 2022	Review	—	Probiotics reduce inflammation and restore microbiome balance	Alternative therapeutic strategy
Sathikulpakdee et al., 2022	Randomized controlled trial	Acne patients	Significant reduction in lesion count with probiotic lotion	Clinical evidence for topical probiotics
Kim et al., 2021	Randomized controlled trial	Acne patients	*Lactobacillus plantarum* improved skin condition and reduced inflammation	Systemic probiotic benefits
Eguren et al., 2024	Randomized clinical trial	Acne patients	Oral probiotics improved acne severity scores	Supports systemic microbiome therapy
Natarelli et al., 2023	Review	—	Bacteriophages selectively target pathogenic bacteria	Precision microbiome therapy

Rimon et al., 2023	Experimental study	Acne model	Phage therapy reduced bacterial load and inflammation	Promising alternative to antibiotics
Golembo et al., 2022	Clinical trial	Human subjects	Topical phage gel reduced acne lesions	Safe and effective therapeutic option
O'Neill et al., 2020	Experimental	Microbial interaction	Commensal bacteria selectively inhibit *C. acnes*	Protective microbiome modulation
O'Neill et al., 2022	Translational study	Human skin model	Dermal cells produce antimicrobial factors regulating microbiome	Host–microbe interaction critical
Jang et al., 2020	Experimental	Microbial compounds	Bacteriocins selectively kill pathogenic bacteria including MRSA	Novel antimicrobial strategy
Rimon et al., 2023	Experimental	Animal model	Topical phage therapy reduces acne-like lesions and inflammation	Future dermatological therapy

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