



(REVIEW ARTICLE)



Current approaches to maintaining the facial skin microbiome in professional procedures

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World Journal of Advanced Research and Reviews, 2025, 27(01), 2029-2034

Publication history: Received on 02 June 2025; revised on 08 July 2025; accepted on 11 July 2025

Article DOI: <https://doi.org/10.30574/wjarr.2025.27.1.2613>

Abstract

The article presents a comprehensive analysis of current approaches to assessing the impact of professional dermatological procedures on the facial skin microbiome. The study is conducted within an interdisciplinary framework that integrates dermatology, microbiology, molecular medicine, and bioengineering. Particular attention is given to content and visual analysis of both domestic and international sources describing microbiome shifts resulting from invasive and non-invasive interventions, as well as the composition of professional skincare formulations. Key mechanisms of post-procedural dysbiosis are examined, including decreased taxonomic diversity, growth of opportunistic microorganisms, and disruption of the skin barrier. Procedures are classified by degree of microbiome-related aggressiveness: from damaging (peelings, laser treatments) to modulatory and physiological (phototherapy, mildly acidic pH care, and prebiotic-based treatments). Summarized data on the effects of skincare ingredients (lactic acid, zinc, polysaccharides) on skin microorganisms are presented, along with visualized overlapping zones of active component action. Theoretical and laboratory models reproducing interactions between microbiota and epithelium are also discussed, including stable ex vivo assessment systems. The article addresses the limitations of current in vivo studies, the need for standardized microbiome-compatibility assessment models, and the prospects for incorporating postbiotic technologies into individualized skincare strategies. This article is intended for professionals in aesthetic medicine and dermatology, cosmetic product developers, and researchers focused on the skin microbiome.

Keywords: Skin Microbiome; Dysbiosis; Dermatological Procedures; Prebiotics; Postbiotics; pH Acidity; Cutibacterium Acnes; *Staphylococcus Aureus*; Phototherapy; Microbiome Compatibility

1. Introduction

Contemporary dermatology is progressively integrating insights into the skin microbiome within both diagnostic and therapeutic frameworks. The skin microbiota—a complex ecosystem of bacteria, fungi, viruses and microscopic arthropods—maintains epidermal homeostasis, modulates immune responses and inhibits pathogen colonization [2]. Disruption of this balance, or dysbiosis, is associated with a broad spectrum of dermatoses, including acne, atopic dermatitis, psoriasis, seborrheic dermatitis and rosacea [6].

Recent advances in high-sensitivity amplicon and metagenomic sequencing have substantially deepened our understanding of the microbiome's role in disease pathogenesis and in the mechanisms of action of cosmetic formulations [4]. At the same time, interest is growing in how dermatological interventions influence microbial composition and function. Ellis's systematic review emphasizes that phototherapy remains the most extensively studied modality for its effects on skin microbiota, demonstrating increased microbial diversity and enhanced barrier restoration following treatment [1].

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In contrast, the impact of procedures such as micropigmentation, chemical peels, laser ablation, dermabrasion and cryotherapy has been scarcely investigated or entirely overlooked in current literature. Some clinical studies suggest that even topical products with particular acidity parameters can exert statistically significant shifts in dominant microbial populations—for instance, suppressing *Staphylococcus Aureus* while promoting proliferation of *Cutibacterium acnes* [5].

Investigations into microbiome effects gain further importance in conditions where dysbiosis is a key pathogenic driver. In atopic dermatitis, Kim et al. report pronounced overgrowth of *S. aureus* accompanied by a sharp decline in bacterial diversity, a situation that may be exacerbated by inadequately selected skincare regimens or overly aggressive treatments [4]. Similar dysbiotic mechanisms have been identified in acne, where loss of *C. acnes* phylotype diversity contributes to chronic inflammation [9]. Moving from empirical application of cosmetic and therapeutic interventions toward microbiome-informed strategies requires interdisciplinary collaboration among dermatologists, microbiologists, immunologists and pharmacologists. Ex vivo laboratory models that replicate microbial interactions—such as those described by Wang et al.—are instrumental in this endeavor [10].

The aim of this study is to perform a comprehensive analysis of scientific data on the effects of dermatological procedures on the skin microbiome, to classify these interventions by the strength of evidence supporting their impact, and to determine the risks of post-procedural dysbiosis.

2. Materials and Methods

The methodological framework for this study lies at the intersection of dermatology, microbiology, molecular medicine and bioengineering, reflecting the interdisciplinary nature of the topic. The primary analytical tool was qualitative content analysis of scientific publications addressing the impact of dermatological interventions on the skin microbiome and microbiome-based skincare in the post-procedural period.

Key sources included the analytical review by Ferdaous Mim et al. [3], which elucidated how the acidity of skincare products alters bacterial composition and highlighted the dermatological potential of postbiotics, and the work of Podwojniak [7], which examined microbial imbalances in conditions such as acne and atopic dermatitis.

Content analysis was structured according to the following scheme

- Classification of interventions (invasive, non-invasive, hygienic, therapeutic);
- Description of documented changes in microbial communities for each intervention;
- Identification of recurring patterns of dysbiosis and subsequent restoration;
- Delineation of methodological approaches to modeling microbiome effects both ex vivo and in vivo;
- Comparison of microbiome outcomes by intervention type (phototherapy, chemical peels, antibiotics, cosmetic care products, etc.).

This methodological strategy, based on juxtaposing clinical and experimental findings with theoretical models of microbiome dynamics, enabled the identification of consistent trends and risks associated with post-procedural dysbiosis. It further allowed categorization of dermatological interventions according to their relative impact on the stability of the skin microbiome.

3. Results

Analysis of the available literature indicates that professional dermatocosmetic interventions significantly alter the composition and stability of the facial skin microbiome, inducing both transient and persistent shifts in bacterial populations. The overall trend is a reduction in taxonomic diversity and a shift toward opportunistic taxa, particularly following aggressive or poorly adapted procedures [6].

As demonstrated by Ellis et al. [1], interventions that cause marked epidermal-barrier disruption—such as chemical peels, aggressive laser resurfacing or injectable techniques—lead to decreased overall species diversity and altered ratios of key symbionts, notably *Cutibacterium acnes* and *Staphylococcus epidermidis*. Concurrently, there is an increase in opportunistic taxa, chiefly *Staphylococcus Aureus*, which is associated with inflammatory responses and post-procedural complications. Clinical observations by Rocha et al. [9] further confirm this pattern, recording *Staphylococcus Aureus* overgrowth in acne patients with compromised skin homeostasis following inadequate aftercare.

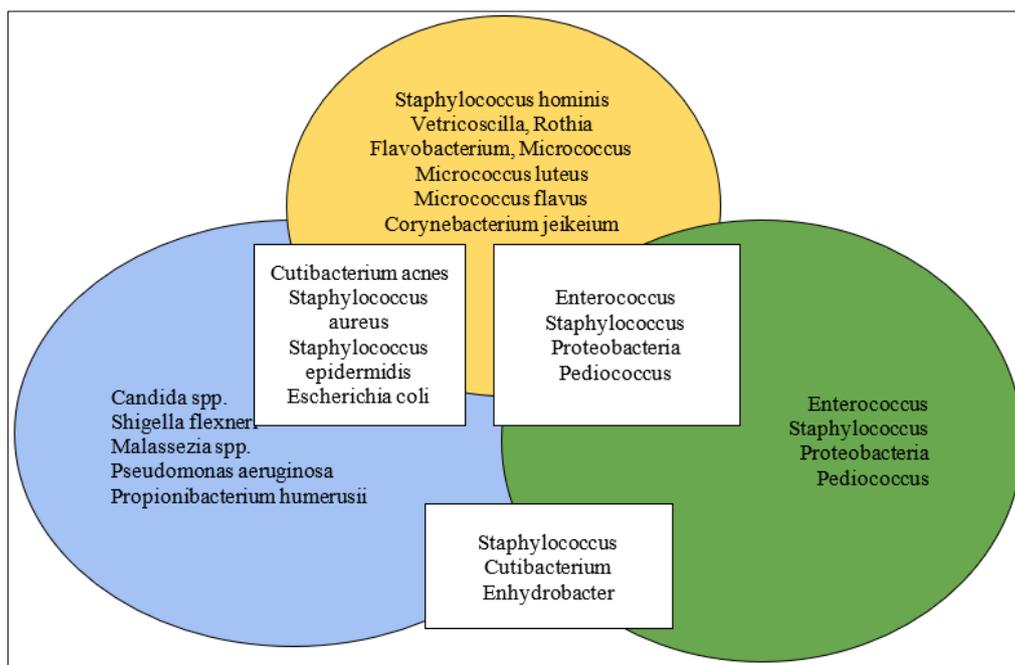
Conversely, gentle skincare protocols—employing formulations at physiological or mildly acidic pH and enriched with prebiotic and postbiotic ingredients (e.g., lactic acid, zinc, plant polysaccharides)—help preserve microbial balance. Ferdaous Mim et al. [3] and Janssens-Böcker et al. [5] report that such formulations foster growth of *C. acnes* and *S. epidermidis* while suppressing undesirable organisms, including *Pseudomonas aeruginosa* and *Candida* spp. These findings align with Al-Smadi et al. [8], who emphasize the role of prebiotic environments in reducing dysbiosis risk among individuals with sensitive skin.

Theoretical models give special attention to photodynamic therapy and LED treatments, which do not inflict direct barrier damage. These modalities exert a modulatory rather than suppressive effect on the microbiota. According to Ellis [1], phototherapy reduces the density of inflammatory taxa without depleting commensal populations. Table 1 summarizes key interventions and their documented effects on dominant facial-skin microorganisms.

Table 1 Comparison of professional interventions and their effects on key microorganisms of the facial skin microbiome (Compiled by the author based on sources: [1], [4], [6])

Type of Procedure	Main Acting Factors	Observed Microbiota Changes
Chemical peeling	Acid exposure, pH reduction	Decrease in <i>C. acnes</i> , increase in <i>S. aureus</i>
Microneedling	Microdamage to the epidermis	Temporary increase in microbial diversity
Professional skincare (pH < 5)	Prebiotic and acidic stimulation	Increase in <i>S. epidermidis</i> , reduction in pathogens
Phototherapy (LED)	Inflammation modulation	Stabilization of microbial composition

The results in Table 1 reveal a direct correlation between procedural invasiveness and the magnitude of microbiome perturbation: the more aggressive the barrier insult, the greater the risk of dysbiosis and *S. aureus* dominance. In contrast, physiologically compatible interventions (e.g., phototherapy or pH-balanced care) demonstrate potential to restore microbial equilibrium and prevent inflammatory dermatoses. These insights underscore the importance of accounting for microbiome compatibility when selecting professional facial-care strategies, especially for patients with sensitivity, chronic inflammation or dermatological conditions.



(Source: [3])

Figure 1 The impact of various professional skincare components on the structure of the facial skin microbiota

According to the analysis by Ferdaous et al. [3], professional cosmetic formulations exert a selective influence on the facial skin microbiota, promoting the growth of specific commensals while suppressing pathogens. In particular, active ingredients such as lactic acid and retinoids stimulate proliferation of *Staphylococcus epidermidis* and *Cutibacterium*

acnes while reducing counts of *Staphylococcus Aureus*, *Candida* spp. and other potentially undesirable organisms. Preservatives, by contrast, tend to act broadly, affecting both pathogenic and neutral strains. Serums containing prebiotic components support restoration of microbial diversity and maintenance of a stable microbiome. Figure 1 illustrates both unique and overlapping zones of activity among these component groups—for example, suppression of *Pseudomonas aeruginosa* is seen with both preservatives and active ingredients, whereas enhancement of *Cutibacterium acnes* occurs primarily with specialized serum formulations.

This visual summary provides an analytical foundation for organizing empirical observations and designing skincare strategies that respect each individual's microbiome profile. Such an approach enables personalized cosmetic interventions and minimizes the risk of dysbiotic shifts.

4. Discussion

One of the primary factors determining how cosmetic formulations affect the facial skin microbiome is pH. According to Janssens-Böcker et al. [5], products with a pH below physiological levels (under 5.0) promote the growth of commensal bacteria while inhibiting pathogens such as *Staphylococcus Aureus* and *Candida* spp. Table 2 organizes the principal ingredients found in professional skincare formulations that have been shown to modulate the microbiome.

Table 2 Key components of professional skincare products and their microbiome-modulating properties (Compiled by the author based on sources: [3], [8])

Component	Effect on Microbiome	Target Microorganisms
Lactic acid	pH reduction, stimulation of commensal growth	<i>Cutibacterium acnes</i> , <i>Staphylococcus epidermidis</i>
Polysaccharides	Prebiotic effect	<i>Staphylococcus hominis</i> , <i>Micrococcus luteus</i>
Zinc PCA	Anti-inflammatory, antiseptic effect	<i>Staphylococcus Aureus</i> , <i>Propionibacterium acnes</i>
Preservatives (phenoxyethanol)	Reduction of overall microbial diversity	–

As shown in Table 2, each ingredient exerts a distinct effect on the microbiome—from creating an environment favorable to commensals to modulating inflammation and reducing pathogenic load. Lactic acid, for example, adjusts skin pH and encourages proliferation of *C. acnes*, which supports the epidermal barrier's physiological defenses. Polysaccharides demonstrate pronounced prebiotic activity, fostering growth of organisms associated with healthy skin flora [3].

Antiseptic actives such as zinc PCA deserve particular attention, as they selectively target *S. aureus* without substantially diminishing overall microbial diversity [8]. However, overuse of broad-spectrum preservatives—including phenoxyethanol—can disrupt microbial balance and weaken the skin ecosystem's resilience to external stressors [5].

Despite the growing interest in the skin microbiome's role in dermatological and aesthetic practice, several significant limitations impede the development of unified protocols and the broad adoption of microbiome-focused strategies. Chief among these are issues of study quality and design.

As Santiago-Rodriguez [2] observes, many existing investigations suffer from restricted sample diversity, short follow-up periods and a lack of control over confounding variables (age, skin type, concurrent dermatoses). This is particularly evident in aesthetic procedures—peels, injections and laser treatments—where emphasis is often placed on visual or subjective outcomes rather than on microbiome safety. Carmona-Cruz [6] similarly highlights poor reproducibility of data obtained in salon settings. Against this backdrop, standardization of microbiome-compatibility assessments becomes paramount. Protocols described by Wang et al. [10] propose the use of stable in-vitro models and representative microbial panels for quantitative and qualitative evaluation of microbiota shifts following cosmetic exposure. However, these models must be adapted to the realities of aesthetic medicine, which relies on multi-component formulations and complex treatment sequences.

A promising emerging field deserving separate attention is that of postbiotics—metabolites produced by beneficial bacteria. Prajapati [4] demonstrates that postbiotic application can be a key tool for modulating the skin's microbial environment without risk of pathogen overgrowth or antibiotic resistance. Moreover, researchers advocate for development of personalized skincare formulations tailored to each patient's unique microbial profile.

Accordingly, future research should prioritize the creation of validated, in-vivo assessment protocols, establishment of microbiome "reference" databases for different skin types and integration of postbiotic technologies into professional treatment regimens. Such advances would enhance procedural safety and secure lasting efficacy by supporting the skin ecosystem's symbiotic equilibrium.

5. Conclusion

This study has systematically characterized the impact of professional dermatological procedures on the facial skin microbiome and classified interventions by their degree of microbiome compatibility. It was shown that aggressive or invasive techniques—specifically chemical peels, injectable treatments and laser therapies—significantly reduce bacterial diversity and provoke dominance of opportunistic organisms such as *Staphylococcus Aureus*, thereby increasing the risk of post-procedural dysbiosis. Conversely, physiological and modulatory interventions—including phototherapy, LED treatments and skincare with postbiotic or prebiotic formulations—demonstrated strong efficacy. These methods support restoration of microbial balance and reduce inflammatory burden without disrupting the epidermal barrier, making them preferable for skin exhibiting sensitivity, chronic inflammation or dermatological conditions.

The pivotal role of product pH emerged as a key parameter directing microbiome shifts. Formulations with pH < 5 and enriched with active ingredients (lactic acid, zinc, plant polysaccharides) foster commensal proliferation while limiting pathogen spread. It was also determined that preservatives must be applied with precise dosing due to their potential to diminish overall microbial diversity.

Methodological challenges remain, notably limited reproducibility of in vivo data and the absence of standardized protocols for assessing microbiome effects. A promising avenue involves development of robust ex vivo models of skin-microbiome interaction and implementation of personalized care strategies based on each patient's microbial profile.

Overall, the findings highlight the necessity of integrating microbiome-oriented principles into professional dermatological practice. Such an approach will enhance procedural safety and long-term effectiveness, ensure resilient restoration of the skin ecosystem and build an evidence base for further personalization of cosmetic interventions. Future research should focus on validating experimental models, establishing microbiome reference databases for different skin types and standardizing criteria of microbiome compatibility in aesthetic medicine.

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