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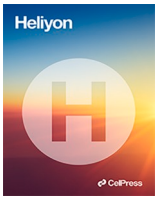

Review article

The dynamic relationship between skin microbiomes and personal care products: A comprehensive review

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ABSTRACT

Healthy skin reflects a healthy microbiome and vice versa. The contemporary society, marked by a sharp increase in skin irritation cases, has compelled researchers, dermatologists, and the cosmetics industry to investigate the correlation between skin microbiomes and the use of skincare products. Different cosmetics can change skin's normal flora to a varying degree –some changes can be detrimental, there are also instances where these alterations aid in restoring the skin microbiome. Previous studies using artificial skin models, metagenomic analysis, and culture-based approaches have suggested that skincare products play an important role in skin microbial alteration. This article assessed current knowledge on microbial shifts from daily use of various personal and skincare products. We have also introduced a readily applicable framework, synthesized from various observations, which can be employed to identify the normal skin microbiome and evaluate the impact of personal care and skincare products on it. We also discussed how lifestyle choice remake skin microbial makeup. Future studies are warranted to examine the effect of personal and skincare product usage on skin microbiome across various age groups, genders, and body sites with a multi-study approach.

1. Introduction

Beauty is a cherished aspect for everyone, recognizing inner intelligence and external beauty propels toward motivation and refinement. Opting for cosmetics or skincare products regularly—daily, weekly, or monthly—instead of pills or supplements is a convenient, hassle-free way to enhance our appearance. This preference contributes to the exponential growth of the global cosmetics market, expected to reach $463.5 billion by 2027 with a 5.3 % CAGR (compound annual growth rate) [1]. So, skin, the most versatile interface organ, comprising an average 30 m^2 surface area in adults, is the center of interest here [2]. Along with diversified chemicals and structural regimes, one thing that boosts skin's anisotropic heterogeneous nature is the composition of skin-dwelling microbiota. This is an absolute habitat for a diverse group of microorganisms, including bacteria, fungi, micro-eukaryotes (dust mites, Demodex mites), archaea, viruses, and phages [3]. A newborn baby gets colonized hugely after birth [4]. Gradually, due to topographical and site-specific diversity, the skin microbiota turns into a highly variable composition of an extremely versatile community depending on

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the areas of the body, between individuals, and over time. Contrary to a popular myth, not all skin microorganisms are inherently dangerous; pathogenicity only happens when the ecosystem's equilibrium is interrupted and variety is diminished. This issue of disruption has stirred the curiosity of health-conscious individuals.

Over the past 5–10 years, there has been a significant rise in skin damage rates. While there could be multiple environmental factors contributing to this issue, researchers have identified the increased usage of synthetic chemical components in modern-day cosmetics as the primary culprit posing a significant threat [5]. Skin care products are highly appreciated until they attract some uninvited guests. Within the personal care industry, the skin microbiota represents a promising yet often overlooked area, as evidenced by the increasing use of formulations that may impact the balance of the skin microbiota. Numerous instances of skin diseases have been linked to this dysbiosis or perturbation of the skin microbiome [6]. The imbalance can often be traced back to excessive product usage. Understanding the intricate relationship between skin chemistry, microbes, and their variations due to cosmetic application is essential. Gaining a better understanding of the correlation between microorganisms and skin care routines could significantly expand our knowledge of the relationship between the skin microbiome, skin diseases, and overall skin health. This, in turn, might pave the way for a more sustainable and healthier human existence. This review aims to highlight the latest findings on how different skin care products affect the skin's microbiome, as well as the potential consequences associated with these alterations. It also provides insights into various methods for assessing the skin microbiome and screening the effects of skin care products on skin inhabitants.

2. Conducting literature review

The literature search strategy entailed a comprehensive review of scholarly articles published up to November 2023, focusing on the contemporary discussion surrounding microbial shifts arising from the habitual use of various personal and skincare products. Here we reviewed more than 100 research articles to compile regarding the whole knowledge. We searched online databases including Web of Science, Science Direct, Scopus, and Google Scholar. Keyword selection was guided by the thematic structures and content of the review that included skin microbiome, cosmetics impacts, microbial dysbiosis, dermatological research, microbial alteration, active ingredients of skin care products and so on. Moreover, the search criteria were strictly limited to English-language publications.

3. Skin microbiome: composition and diversity

Skin microbiota, also known as skin flora, refers to microorganisms that live on the skin. It is the second-largest microbiota of the human body in mass [7]. Skin provides vital nutrients for the development of this microbiota through sweat or stratum corneum, which is composed of 75–80 % proteins (primarily keratins and membrane proteins), 5–15 % lipids (ceramides, cholesterol mainly), 5–10 % unknown compounds, and water (15–20 % of the total tissue dry weight) [8]. Within 2- and 3-mm thickness of the skin, microbiome has the most variation over time than the gut's and the mouth's microbiomes [9]. The skin harbors a vast array of bacterial species, with over 1200 identified. Among them, more than 90 % belong to four phyla: Actinobacteria (52 %), including *Micrococcus*, *Propionibacteria*, and *Corynebacteria* genera; Firmicutes (24 %), comprising *Staphylococcus*, *Lactobacillus*, and *Streptococcus* genera; Proteobacteria (16 %), which includes *Paracoccus*, *Haematobacter*, and *Sphingomonas* genera; and Bacteroidetes (6 %), represented by the genera *Porphyromonas*, *Prevotella*, and *Flavobacterium* [10,11]. Estimates suggest that *Cutibacterium*, *Staphylococcus*, and *Corynebacterium* genera, found throughout various sites on the skin, constitute approximately 45–80 % of the skin microbiome [12]. Additionally, up to 4.2 % of the prokaryotic skin microbiome is composed of archaea, with the dominant group being Thaumarchaeota phyla [13].

Various fungi have been notably found on different body regions, including *Malassezia* spp., *Aspergillus*, *Cladosporium*, *Epicoccum, Phoma, Cryptococcus, Rhodotorula, Microsporum, Trichophyton, Saccharomyces, Candida,* and *Epidermophyton* [14].

Regarding viruses or phages, the skin can harbor Molluscum contagiosum virus, Merkel cell polyomavirus (MCPyV), Alphapapillomavirus, Simian virus, Acheta domestica densovirus (AdDNV), Actinomyces phage, Propionibacterium phage, Polyomavirus HPyV7, Streptococcus phage, Stenotrophomonas phage, Enterobacteria phage, and more [7].

The resident microflora plays an advantageous role in modulating the immune system, occupying niches, and preventing the entry of harmful and contagious microorganisms into the skin. While skin microorganisms have been broadly identified and categorized [15], quantitative measurements are still necessary to compare investigations carried out by different researchers using various methodologies to consolidate their findings.

4. Interplay between cosmetics and skin microbiome

A vast array of skin care products, including body washes, gels, lotions, exfoliants, moisturizers, toners, and sunscreens, is available to address various beauty conditions, with a primary focus on nourishing the skin from within. However, researchers must acknowledge that cosmetic components can have both positive and negative impacts on the skin's microbiota [16]. Additionally, under specific physiochemical conditions, cosmetic compounds can serve as nutrient sources, promoting the growth of opportunistic pathogenic microorganisms that may lead to significant infections and diseases [17].

Certain research points to "microbiome resilience," suggesting that there may be no negative effects on microorganisms due to the use of skin wash products. According to these studies, the concentrations of microorganisms are dramatically reduced by 5–10 times during product application [18]. However, the durability of these products varies depending on the application site, and their effects can last for weeks with highly individual reactions. These reactions may include changes in steroid and pheromone levels, as well as alterations in the structure and dynamics of bacterial and archaeal ecosystems, leading to a modified scenario [18].

As richness in microbial diversity has been proven to be linked with healthy skin [19], any kind of effect upon them destines changes leading to threats. But due to the broader range, studying their variations over skin has always been a challenge. These effects are not only occupied in the applied sites, but also other parts of the body [20]. For launching cosmetics, in depth studies are needed in context of microbiome. It is a fact of optimism that such practices are being encouraged nowadays in modern cosmetics. The first "Microbiome-friendly" certification for a cosmetic product was premiered in 2019 and was established by 'MyMicrobiome'. Here the product's purity, the targeted area's specific bacteria's safety, the preservation of the microbiome diversity, and the preservation of the skin's natural balance are all confirmed (neither through the induction of harmful microorganisms nor by the repression of commensals) [21].

5. Assessing skin microbiome and screening the response of cosmetics

There is a need to explore effective approaches for comparing the skin microbiome after using skin care products to determine any deviations from normal skin conditions. This initial step is crucial in establishing a connection between the amount of synthetic ingredients in a product and its impact on skin health. In the 1950s, American dermatologist Albert Kligman pioneered human microbiota research in dermatology, employing advanced cell culture methods [22,23]. Today, modern research techniques allow us to identify non-culturable, newer forms of microbes residing in the surface and deeper layers of human skin. Overcoming the limitations of culture-dependent studies, molecular methods, such as multi-omics approach integration [20], 18S and 16S rRNA gene sequencing, DNA barcoding, PCR-denaturing gradient gel electrophoresis sequencing [24], enable the detection of microbes present in low quantities. Additionally, studying the chemicals produced by microbes through mass spectrometry visualization and molecular networking provides a wide range of microbial studies [16]. To identify the microbes, various methods like swabbing, biopsy, or tape stripping [25] are used, with the selection depending on the categories of microbes to be identified [26]. For assessing the ultimate outcomes resulting from the application of different products, the use of artificial 3D skin models and leather skin models has become popular [27,28]. Other methods for screening include the duel culture method, Mass spectrophotometry, FTIR spectro microscopy (Fourier-transform infrared spectroscopy), or magnetic resonance imaging [29,30]. Incorporating bioinformatics studies can also shed light on the effects of chemicals and bioactive products from microbes. Fig. 1 illustrates a workflow for identifying skin microbes and outlines possible approaches for screening cosmetics in relation to changes in the skin microbiome. Molecular approaches are commendable, but they do raise some counter-thoughts, such as their inability to differentiate between the genes of living and dead organisms, which can lead to confusing results. Therefore, to gain a comprehensive understanding of skin microbes, it is essential to combine whole genome sequencing with skin models and cultural approaches.

6. Effect of cosmetics on the skin's microbiome

6.1. *Effect of common cosmetic preservatives on skin microbe dynamics*

In cosmetics, ingredients such as water, oils, peptides, and carbohydrates create an environment conducive to the growth of microorganisms. To prevent contamination, preservatives are commonly added, which remain active on the skin upon application.

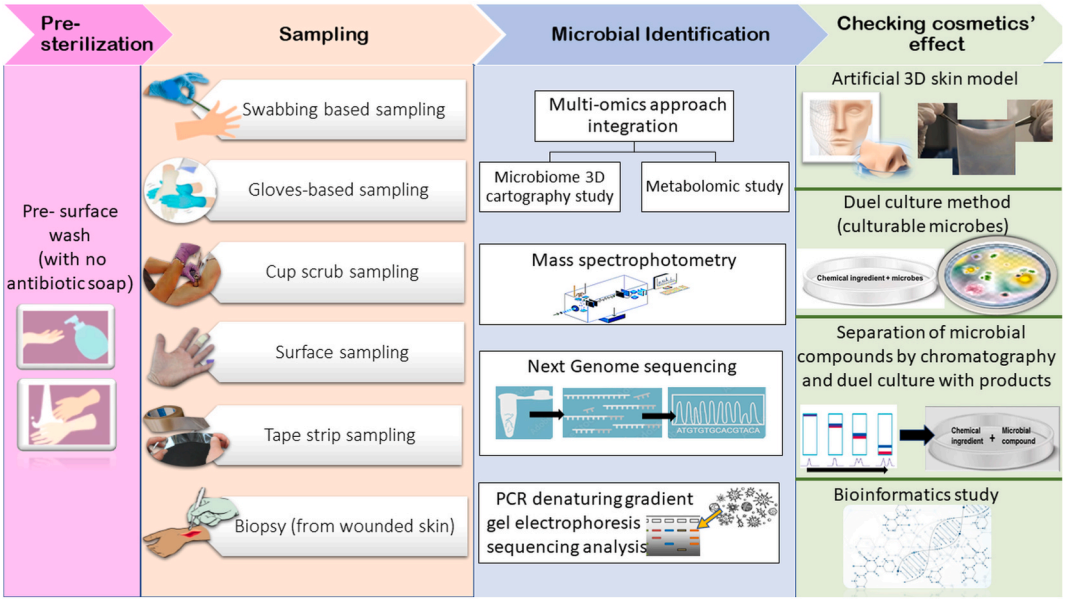

Fig. 1. A workflow of assessing skin microbe and cosmetics' response.

However, their blind use solely for preservation with antimicrobial properties might not serve their intended purpose [31].

A study conducted by Pinto, Ciardiello [32] revealed that various tested preservatives had an impact on the dynamics of targeted bacteria, including *Cutibacterium acnes* (previously known as *Propionibacterium acnes*), *Staphylococcus epidermidis*, and *Staphylococcus aureus*. While the combination of different preservatives in one bacterial strain (*S. aureus*) showed somewhat positive results, it proved to be both beneficial and harmful for the other two bacteria.

The most effective mixtures for reestablishing a pre-existing dysbiosis were found to contain hydroxyacetophenone, phenylpropanol, propanediol, caprylyl glycol, tocopherol, and tetrasodium glutamate diacetate because they act to moderately inhibit *C. acnes* and strongly inhibit *S. aureus* without simultaneously inhibiting *S. aureus* growth. The finest combinations to use in topical solutions for the skin and scalp where it is vital to maintain the eubiosis of the microbiota were proposed to be C1 (Sodium benzoate phenoxyethanol, ethylhexylglycerin), C4 (Sodium anisate, 1,2-hexanediol, ammonium acryloyldimethyltaurate/vp copolymer), C6 (Hydroxyacetophenone, phenylpropanol, propanediol, caprylyl glycol, tocopherol, disodium EDTA), and C7 (Benzyl alcohol, benzoic acid, dehydroacetic acid, ammonium acryloyldimethyltaurate/vp copolymer).

Toner, emulsion, cream, and baby cream contain common preservatives like parabens, 1, 2-hexanediol, phenoxyethanol. They exhibited potent antibacterial effects against *S. aureus*, *Escherichia coli*, *Pseudomonas aeruginosa* as well as other skin-resident bacteria such as *S. epidermidis, Shigella flexneri, Enterobacter aerogenes* and so on that are not the target at all [33]. Paraben, used in common cream had shown to have robust effects against skin filamentous fungi and yeasts like *Candida* spp. and *Malassezia* spp. [34]. *C. acnes* and *S. epidermis* were significantly inhibited by the short-term usage of 0.5–5 % methylparaben in cosmetics [35]. Methylisothiazolinone was seen to inhibit *S. epidermidis* [36]. The use of phenoxyethanol disturbed the skin microbiota conferring the change both at the phylum level (Proteobacteria increased) and at species level (*Propionibacterium humerusii, S. epidermidis* decreased) [33,36]. The influence of preservatives may go beyond the parameters of the product composition and may have a potentially negative impact on the skin microbiota, according to a theory put up in light of the expanding understanding of the significance of the human microbiome. The specified and some common microbes changed by basic ingredients that are used in skin care products are illustrated in Fig. 2.

6.2. Changes in hand and palm microbiome by cosmetics

Hand and palm microbiome seems quite interesting with 83 % difference between the left and right hands of same individual, 87 % differences in difference in individuals and a greater overall diversity in female hands than males [37]. The amount of exposure to environmental elements, how often hands are washed all likely play a role in the variation in the skin microbiota of the hands. It is obviously affirmative to have a health care setting strategies for cleaning hands in but chronic washing is potential for dysbiosis in some individuals [38]. Healthcare personnel who routinely washed their hands have more pathogenic bacteria on them than those who didn't [39] indicating less microbial diversity led to the potentiality to increase pathogenic species including *S. aureus*,

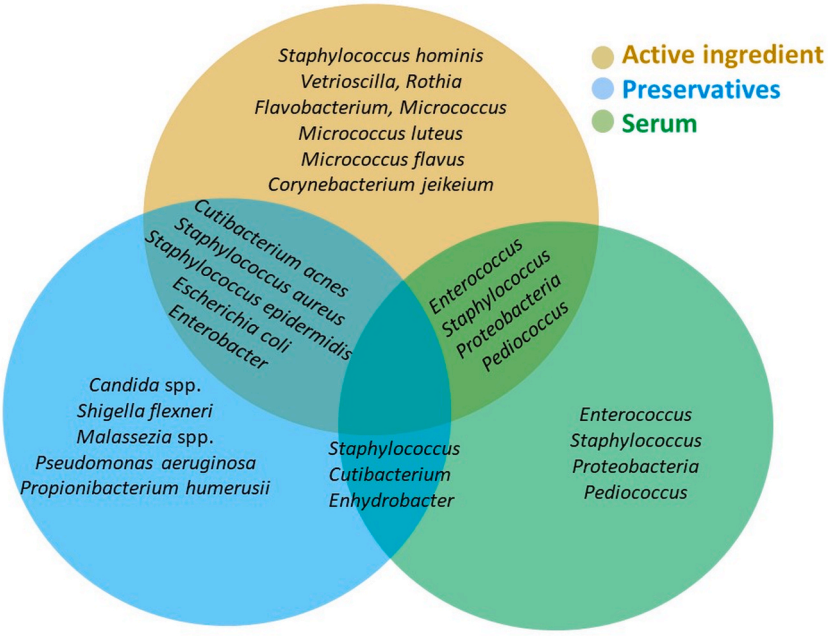

Fig. 2. A Venn diagram showing the specified and some common microbes changed by basic ingredients that are used in skin care products. Different color code represents different groups (Bronze- Active ingredient (eg.Kojic Acid, Isotretinoin etc.); Blue- Preservative (eg.Parabens, Methylparaben, Ethylparaben, Phenoxyethanol, Methylisothiazolinone etc.); Green- Serum (Galacto-oligosaccharide, Hyaluronic Acid etc.).

Table 1
The Alteration in skin microbes caused by the active ingredients used in cosmetics.

Active ingredients/A mixture of active ingredients	Alteration in skin microbes	References
Maltodextrin, *Zymomonas* ferment extract, honey extract, aqua	*Corynebacterium jeikeium* ⬆ *Micrococcus luteus* ⬆ *Staphylococcus aureus* ⬆ *Micrococci* ⬇ *Staphylococcus epidermidis* ⬇ *Staphylococcus hominis* ⬇ *Micrococcus flavus* ⬇ *Cutibacterium avidum* ⬇	[58]
Glycerin, *Laminaria digitata* extract, *Chlorella vulgaris* extract, saccharide isomerate, phenoxyethanol, ethylhexylglycerin, aqua, seawater	*Staphylococcus aureus* ⬆ *Staphylococcus hominis Micrococcus luteus* ⬆ *Cutibacterium avidum* ⬆ *S. epidermidis* ⬇ *Micrococcus flavus* ⬇	[58]
Fermented oil	*Staphylococcus* ⬆ *Proteobacteria* ⬇	[59]
ExpoZenfi by GREENTECH	Bacterial diversity ⬆ *Staphylococcus epidermidi* ⬆	[60]
Isotretinoin	Rothia ⬆ Flavobacterium Enterobacter Micrococcus *Cutibacterium acnes* ⬇	[61]
Halymenia durvillei (red algae) extract	Proteobacteria phyla ⬆	[60]

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Table 1 (*continued*)

Active ingredients/A mixture of active ingredients	Alteration in skin microbes	References
	Bacteriodetes phyla ⬆ Actinobacteria phyla ⬇ Firmicutes phyla ⬇ *Corynebacterium kroppendenstedtii* ⬇	

⬆ indicates increase, ⬇indicates decrease.

Enterococcus spp., *Candida albicans* [40]. The alteration is most in the prominent skin taxa than others in antiseptic treatments [41]. The alcohol-based hand sanitizer and ethanol showed a reduction of the levels of viable aerobic-anaerobic bacteria [42]. Antimicrobial soap had impacts on epidermal antibacterial defense system and upon skin microbes alike Streptococcus [43]. Antibacterial wipes resulted in a decrease in the number of *S. aureus* [44].

Many cleansers use surfactants that not only take away the key defensive components of our protective skin barrier exposing it to outside aggressors, but also misbalances the pH of skin [42]. Skin pH is fundamental to maintaining a healthy microbial community. Higher concentration of NaOH in cleansers, soaps, makeup, creams or lotions leads to higher pH level, causing *Candida albicans*, a commensal microbe turning into a fungal infection [45]. Extreme amount of citric acid and lactic acid in cleanser or exfoliants lowered normal skin pH causing decreased *C. acnes.* Similarly, with the increase in pH, the activity and population had been seen to be boosted for *C. acnes* and *S. aureus* [46].

6.3. Microbiome alterations induced by the active ingredients in cosmetics

Active ingredients in skin care products are specifically formulated for various purposes such as brightening, addressing dryness, combating aging, treating sunburn, and managing acne. In addition to different extracts and chemicals, pre-pro-postbiotics are also included in this list. Collectively, all these groups can have both positive and negative impacts on the skin's microbiome. Plant extracts, fruit extracts, and seaweed extracts used in cosmetics have shown incredible potential in modifying *C. acnes* populations, effectively combating skin pathogenesis like acne vulgaris [47,48]. However, certain ingredients, like kojic acid found in skin lightning creams and lotions, have been found to be capable of traveling into the bloodstream [49]. Moreover, pure kojic acid, when exposed to UV light, has the potential to induce gene mutations in *E. coli* strains [50]. As *E. coli* strains naturally occur on the skin in small amounts, such mutations might lead to harmful consequences [51]. Table 1 provides an overview of research findings highlighting the changes in skin microbes caused by the active ingredients of cosmetics and Fig. 2 shows microbial changes caused by active ingredients along with preservatives and serum. In contrast to synthetic substances, which humans have only encountered in the last 60 years of their 200 000-year history, natural components, in the quantities found in nature, are not perceived as "foreign" to the skin's natural condition [52]. This is why branding products as "natural or organic" easily captures attention. Consumers often prefer using products labelled as "natural cosmetics" due to concerns about their skin. However, it's essential to recognize that natural products may not be as pure as they seem in reality. For instance, Methylisothiazolinone (MI), a synthetic compound used in some 'natural' labelled products, has been associated with potential harm, including neurotoxicity [53], allergic reactions [54], and changes in microorganisms [55]. Alarmingly, this MI preservative is not limited to adult products like makeup, eyeliners, makeup removers, blush, face powder, hair care products, nail and waxing products, moisturizing creams, and sunscreen; it is also used in baby wipes and bath products. Even in toddlers, their diapers, skin pH, and dermatitis are linked with *Candida albicans* and *S. aureus* [56]. The research conducted by Wallen-Russell [57] investigated the microbial community shifts caused by using three different cosmetic conditions: a 100 % truly natural product (JooMo's face wash), a product labelled as natural but containing 70 % synthetic ingredients, and a synthetic product with 75 % synthetic components. Microbiome sampling was done before product use (T1), after two weeks (T2), and after four weeks (T3) of product use. During the transition from T1 to T2 and T1 to T3, JooMo showed the fastest rise in Chao1 diversity and species richness. This suggests that cosmetics companies should conduct studies on skin microbiota when launching new active ingredients to ensure their products maintain, improve, or restore a healthy skin-microbiome balance, especially in cases of a disrupted microbiome.

6.4. Alternation of skin microbiome by different types of cosmetics

The topical application of personal hygiene products can alter the skin's lipid film, affecting microbial diversity and the overall richness of bacterial species on the skin. For instance, active body wash products have demonstrated potential advantages, as they can eliminate harmful bacteria such as *Brevibacterium casei* and *Rhodotorula mucilaginosa*, while promoting the growth of beneficial bacteria like *C. acnes* [62].

Furthermore, a basic skin care routine consisting of skin softener, lotion, essence, and cream with moisturizing compounds was found to impact the abundance of two common skin phyla: Actinobacteria (decreased) and Proteobacteria (increased) on facial cheeks [63]. The cause of these changes could be attributed to other skin bacteria growing and utilizing ingredients from the basic cosmetics,

Table 2
Some common skin care products causing microbial alteration in skin.

Product category	Alteration in skin microbes	References
Lotion application in lower foot (against xerosis, extreme dryness)	*Staphylococcus epidermidis* ⬆ *Xanthomonas campestris* ⬆ *Xanthomonas* spp. ⬆	[64]
Short chain fructo-oligosaccharides (A prebiotic used in powder etc.)	*Staphylococcus epidermidis* at ⬆ lower concentration (0.5–5 %) *Staphylococcus aureu* ⬇*s* *Staphylococcus epidermidis* at ⬇ higher concentration (10–15 %) *C. acnes* (complete halt) ⬇	[65]
Spermidine used in lotion, cream	*Staphylococcus pneumonia* ⬆ *Staphylococcus infantis* ⬆ *Staphylococcus thermophiles* ⬇	[66]
Ceramides in moisturizers	*Streptococcus* spp. ⬇	[67]
Serum cosmetics containing galacto-oligosaccharides	*Burkholderia* ⬆ *Bifidobacteria* ⬆ *Lactobacilli* ⬆ *Lactococcus* ⬆ *Sphingomonas* ⬆ *Thermoanaerobacterium* ⬆ *Staphylococcus aureus* ⬇ *Staphylococcus* ⬇ *Proteobacteria* ⬇ *Cutibacterium* ⬇	[68]

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Table 2 (*continued*)

Product category	Alteration in skin microbes	References
	Pediococcus ⬇	
	Enhydrobacter ⬇	
	Enterobacteriaceae family ⬇	
Foot powder use	*Micrococcus* ⬆	[20]
	Anaerococcus ⬆	
	Streptococcus ⬆	
	Brevibacterium Acinetobacter ⬆	
	Moraxellaceae family ⬆	
Selenium in lotion, sunscreen, creams	*Staphylococcus aureus* ⬇	[69,70]
Moisturizers containing lipids	*Staphylococcus* ⬆	[16,71,72]
	Propionibacterium ⬆	

⬆ indicates increase, ⬇indicates decrease.

or the cosmetics may be hindering the growth of normal skin bacterial groups, or even altering the skin environment itself. The following Table 2 provides an overview of product-based variations that influence skin microbes.

Sebocytes create sebum, a natural moisturizer that is essential for maintaining healthy skin. Excessive sebum production can lead to issues like acne, greasy skin, and clogged pores. To prevent such problems, many individuals use different skin care products, such as lotions [73], which have proven to be effective in reducing sebum production. However, decreased sebum can also result in a reduced food source for microbes, leading to a decline in the number of *Staphylococcus* bacteria and causing an imbalance in the skin microbiome. A comparison between makeup users and non-users revealed significantly higher microbial diversity on the forehead skin of makeup users, including an increase in the genera *Selenomonas*, *Aggregatibacter*, and *Aquicella* [74].

The changes in skin microbes are intricate and interconnected. Fig. 3A–F depicts the range of products (lotion, cream and moisture; powder, antiperspirant and deodorant; body, hand and face wash) that commonly influence bacterial or fungal populations, detailing those that have individual and combined effects on these species as evidenced by multiple research studies.

6.5. Microplastic

Microplastics and nanoplastics are ubiquitous constituents of human daily consumption, serving as pervasive pollutants that appear in many forms such as microbeads and fibers. The impact of microplastic load is terrifying for flora-fauna, terrestrial, ocean organisms [75,76] and soil microbiota [77], covering all sort of environmental microbiomes [78]. They can adsorb organic and inorganic contaminants on their surface [79]. In addition, biofilms can form on their surface and act as carriers of pathogenic vectors and antimicrobial resistance [80], career for pollutants [81], microorganisms and resistance genes [82]. Their effects on different animals' microbiome had been notified.

Polystyrene reduced of the relative abundance of phyla Firmicutes, Bacteroidetes and Verrucomicrobia, increased Actinobacteria with 0.5 μm particles size in the gastrointestinal tract of mice [83]. Polystyrene microplastics fibres and fragments reduced Actinobacteria; fibers affected specific bacteria genera while fragments caused a decrease in *Pseudomonas* and *Aeromonas* genus and all three shapes increased the relative abundance of *Gordonia* [84]. It's 5 μm increased *Staphylococcus* and 200 μm boosted the genera *Vibrio*, *Acinetobacter*, *Porphyromonas*, *Haemophilus*, *Neisseria* and *Lactococcus* in zebra fish [85]. Phyla Cyanobacteria, Chloroflexi, Fusobacteria and Proteobacteria were increased, while Nitrospirae, Bacteroidetes, and Firmicutes were reduced in freshwater crabs [86] via

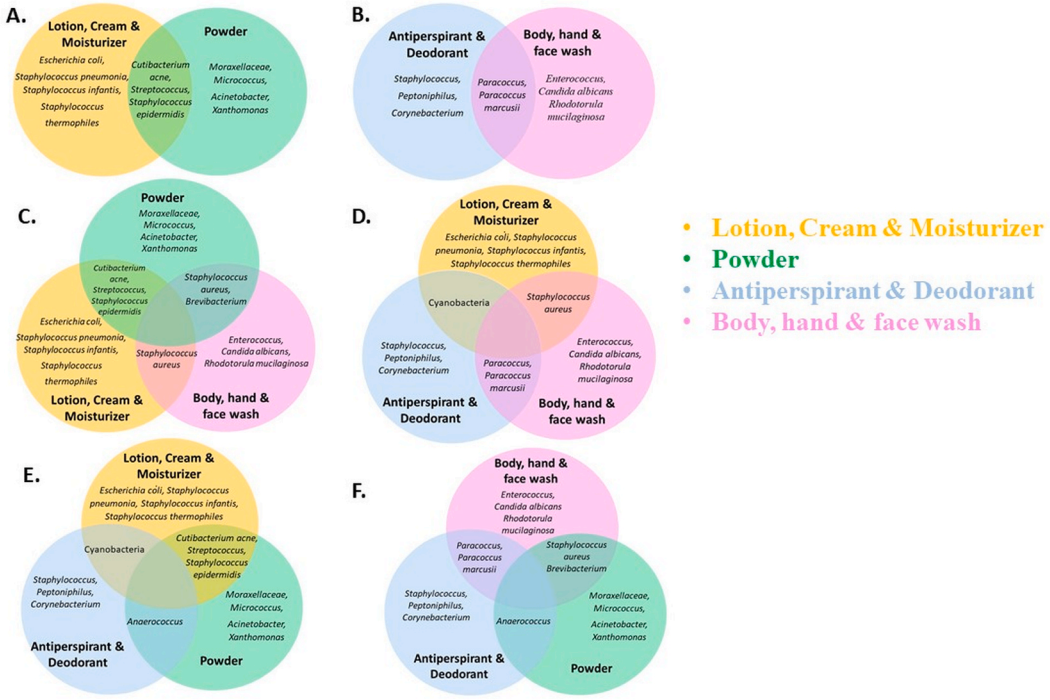

Fig. 3. Venn diagrams illustrating the specific and common microbial changes influenced by skincare products. A: Alteration of microbes by Lotion, Cream & Moisturizer + Powder. B: Alteration of microbes by Antiperspirant & Deodorant + Body, hand & face wash. C: Alteration of microbes by Powder + Lotion, Cream & Moisturizer + Body, hand & face wash. D: Alteration of microbes by Lotion, Cream & Moisturizer + Antiperspirant & Deodorant + Body, hand & face wash. E: Alteration of microbes by Lotion, Cream & Moisturizer + Antiperspirant & Deodorant + Powder. F: Alteration of microbes by Body, hand & face wash + Antiperspirant & Deodorant + Powder.

microplastic intervention. In Human, exposure to Polystyrene MPs induced gut microbial shifts increasing α-diversity and abundance of potentially harmful pathobionts, such as Dethiosulfovibrionaceae and Enterobacteriaceae family [87]. Polyethylene alters Firmicutes, Bacteroidetes, Proteobacteria, and Verrucomicrobia phyla [88]. Reductions in *Bifidobacterium* spp., *Clostridium* spp., *Staphylococcus* spp., total aerobic and anaerobic bacteria, and increase in *Escherichia* or *Shigella*, *Cloacibacillus*, *Bilophila*, *Eisenbergiella*, *Megasphaera* and *Oscillibacter* genus including rise in Firmicutes phylum [89] had been shown in different chambers of gut. Polypropylene microplastics caused significant changes in fish gut microbiome, reducing beneficial lactic acid bacteria and increasing potential pathogenic microorganism Proteobacteria and Vibrionales [90].

Regarding human microbiomes, mammal microbiomes are more similar to that of humans than non-mammal microbiomes. Microbead is the primary source of Microplastics used as cleansing or exfoliating agents in a diversity of personal care and cosmetic products such as shower gels, toothpaste, nail polishes, or eye shadows, amongst many others. From the above-mentioned studies, we can predict there is highest possible chance of those microplastic altering our normal skin microbiome. In a research conducted in Macao showed 100 skin care products (facial skin, body skin, cosmetics) out of 144 are with microplastic [91]. A significant quantity of personal care and cosmetics products are found to include microplastics such as polyethylene, polyethylene terephthalate, polypropylene, and other similar substances. The aforementioned alterations in the environment and gut microbiota may lead us to speculate that they could potentially impact the composition of the skin microbiome. Unfortunately, there is a lack of relevant data regarding this particular matter. A comprehensive investigation is necessary to ascertain the impact of microplastic exposure, either alone or in conjunction with skin-care products, on the host microbiome.

7. Consequences of altered microbiome

In contrast to individual variances, it is a well-known fact that most adult human microbiomes remain stable without intervention [9,92,93]. However, shifts can occur due to both intrinsic and extrinsic factors, leading to the opposite phenomenon. Thus far, it has been established that the use of various skincare products can trigger microbial alterations. Whether this shifting will be named after positive or negative, is dependent upon the species of microbes being changed. Depending upon the types of products use, the consequences might vary. For sure, many of the skin care products offer us a variety of favors in skin commensals. One of the consequences that terrifies all is microbes misbalance causes their shifting from friend to foe for instance *C. acnes* [94]. The same statement is justified as commensals *S. epidermidis* would be turned into pathogen if its number is increased creating serious skin irritation by boosting atopic dermatitis [95]. But in normal skin, *S. epidermidis* aids in skin homeostasis and lowers the pathogenic inflammation triggered by

C. acnes as it drops off the TLR2 protein (Toll like receptor 2 protein) production, which reasons skin inflammation [96]. Dysbiosis and altered microbial biodiversity of the skin microbiome has been linked with many diseases [97]. Acne was modulated by Proteobacteria, Firmicutes and Actinobacteria [98] and also by many species like *C. acnes* [99], *Streptococcus* [100], *S. epidermidis* [101], *Malassezia* species [102,103] etc. Atopic dermatitis, a chronic skin inflammatory disease impacts roughly 15 %–20 % of children and 1 %–3 % of adults worldwide and has skyrocketed 2- to 3-fold [104]. It had seen to have relation with significant skin microbial changes such as *S. aureus*, *S. epidermidis* and *Staphylococcus haemolyticus* [105,106], *Propiniumbacterium*, *Corynebctarium* and *Streptococcus* [105, 107]. Some common skin dwellers *Staphylococcus, Corynebacterium, Streptococcus* and *Propionibacterium* were related to skin diseases like psoriatic lesion [108]. Malassezia fungal species linking with folliculitis [109], *Staphylococcus* with diabetic skin [110], *S. aureus with* allergies [111], *Streptococcus*, *Staphylococcus*, *Fusobacterium* with leishmaniasis [112], *Acinetobacter lwoffii* with allergic sensitization and inflammation [113] had been reported. Apart from the common one (*Malassezia* fungi) [114] some low abundant genera like *Gordonia* and *Geobacillus* also had seen linking with skin disease-rosacea [115]. Regarding bodies defense mechanism, some ardently serious issues are involved. Shifting of normal microbiome of *Staphylococcus*, and in particular *S. epidermidis* results in the disruption of skin immune system causing the natural antimicrobial bacteriocins production hampered [116]. Changes in *Porphyromonas*, *Streptococcus, Peptostreptococcus*, *Sphingomonas*, *Stenotrophomonas, Anaerococcus*, *Staphylococcus, Corynebacterium etc.* were related to wound healing process [117]. So even minor shift may result some catastrophe. These findings hold significance from an immunological perspective, as they imply a direct communication link between host health and microbial cells in the skin.

While individual microorganisms alone may or may not directly cause cancer, the overall composition and diversity of the skin microbiome can have an impact. Cosmetics can alter the skin microbiome by reducing its diversity and balance, resulting in microbial imbalance (dysbiosis). This, in turn, can lead to inflammation, immune suppression, oxidative stress, and infections, all of which can contribute to the promotion of skin cancer [118]. The studies mentioned above indicate varying levels of microbial increase and decrease in the skin microbial community. Some of these common microbes have been shown to be linked to cancer. For instance, *S. aureus* is associated with the carcinogenic progression from actinic keratosis to squamous cell carcinoma (SCC), a type of skin cancer that develops in the flat squamous cells located in the outer layer of the skin." [119,120]. Moreover, it can influence the expression of Human beta-defensin-2, thereby causing SCC proliferation [121]**. Cutaneous T cell lymphoma, another type of skin cancer had been linked with** *S. aureus* [122]. Some research showed that *Corynebacterium* species may influence the development of malignant melanoma, the deadliest form of skin cancer, accounting for 75 % of all skin cancer-related deaths [123,124]. Skin cancers might be boosted as a result of skin microbiome alteration demonstrating skin barrier disruption [125] for Staphylococcus epidermidis [126].

Coffee aqueous extract is being used in many skins care formula that had demonstrated links with Colorectal cancer [127]. Tryptophan, a microbial metabolite detected on skin, also used in cosmetics [128] has effect on aryl hydrocarbon receptor. Imbalanced regulation of aryl hydrocarbon receptor expression or activity promotes cancer development alike breast cancer [129], lung cancer [130], oesophageal cancer [131] etc. Malassezia sp. affects skin cancer [132]. It increased aryl hydrocarbon receptor activity conferring increased tumorigenesis [133]. *Candida* is related with an increased risk of numerous malignancies, including hematologic, head and neck, pancreatic, skin, and thyroid cancer [134]. Viruses are also included in this list [135]. More study is needed to better understand how various cosmetics products promoter different forms of cancer and how they can be managed to prevent or treat cancer.

8. Conclusion

A diverse and thriving skin microbiome is essential for human health, making it a novel objective for skin care products to focus on maintaining or restoring the skin's microbiota. The application of additional skin care products can significantly impact the microbial diversity on the skin, resulting in both positive and negative differences. Each type of product used on the skin has its own individual and combined effects. Common skin microbes like *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Corynebacterium*, *Cutibacterium acnes*, and *Malassezia* spp. are frequently altered by diversified arrays of such products application. As microbial alteration is linked with lots of diseases ranging from skin irritation to cancers not only in skin but also of other organs, precise studies are needed. A combination of sampling methods, culture-based strategies, and modernized research tools, such as artificial skin models, spectrophotometry, bioinformatics, and metagenomic analysis, is necessary. To gain a comprehensive understanding of the skin's microbiome and its complex interactions when using various cosmetics, further investigations considering factors like age, location, and specific body sites are essential. Ultimately, these studies aim to ensure a healthy human skin microbiome. No definitive conclusion has been reached to universally categorize any product as entirely positive or negative. The question arises whether the negative impacts outweigh the positive ones.

Data availability statement

No data was used for the research described in the article.

CRediT authorship contribution statement

Mahjabin Ferdaous Mim: Writing – original draft, Visualization, Data curation, Conceptualization. **Mahmudul Hasan Sikder:** Writing – review & editing. **Md. Zahid Hasan Chowdhury:** Visualization, Data curation. **Ashkar-Ul-Alam Bhuiyan:** Visualization. **Nayeematul Zinan:** Data curation. **Shah Mohammad Naimul Islam:** Writing – review & editing, Conceptualization.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:Shah Mohammad Naimul Islam reports administrative support was provided by Bangabandhu Sheikh Mujibur Rahman Agricultural University.

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