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Review Article

# External Factors and the Cutaneous Microbiome

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The human skin microbiome consists of over 500 bacterial species that play a vital role in protecting the skin from external stressors, inhibiting the colonization of pathogenic microbes, and regulating skin immunity. While the healthy cutaneous microbiome remains relatively stable and maintains microbial diversity, many external factors can affect this system and disrupt the integrity of the natural skin microbiome, leading to "skin dysbiosis" common in skin conditions such as psoriasis and atopic dermatitis. Despite increasing research on the cutaneous microbiome in skin disorders, the stability and response of the microbiome under various external factors are incompletely understood. In this systematic review, we examine 32 published articles that evaluate 4 major types of external factors that can potentially influence the cutaneous microbiota. While the results of these studies are promising, there are several limitations and variations in the methods and sampling between studies. While further validation studies are warranted, this systematic review shows some clear trends in responses to external factors and suggests the importance of individually tailored treatments in regulating the cutaneous microbiome.

## INTRODUCTION

The skin is the body's first line of defense against environmental stressors and the external world. It serves as a major physical and immunological protective barrier, and harbors diverse microbial communities. The phyla Actinobacteria (genera *Cutibacterium*, *Corynebacterium*), Firmicutes (genera *Staphylococcus*, *Streptococcus*), Proteobacteria (genera *Pseudomonas*, *Acinetobacter,* and *Janthinobacterium*), and Bacteroides (*Sphingobacterium* and *Chryseobacterium*) are dominant skin bacteria generally found on the skin surface of healthy people.[1] In the absence of external factors, the healthy skin microbiome remains relatively stable, suggesting that mutualistic and/or commensal interactions exist between the microbes and host.[2] For example, *Staphylococcus epidermidis* upregulates tight junction expression in keratinocytes to enhance skin barrier integrity and indirectly regulates the growth of *Cutibacterium acnes*, which is linked to acne.[3] And, counterintuitively, in a non-acne state, *C. acnes* metabolizes sebum into free fatty acids that helps prevent pathogenic microbes from colonizing.[4] Overall, the skin microbiota inhibits the spread and colonization of pathogenic bacteria and plays a vital role in regulating skin immunity.[5] Therefore, a diverse skin microbiota with many beneficial microbes plays a crucial role in protecting the skin from environmental factors that can disrupt the integrity of the natural skin microbiome.

Despite the increasing understanding of interactions between the skin microbiome and host, the stability and response of the skin microbiota under various external factors–such as temperature, ultraviolet (UV) radiation, personal products, and even other humans–are incompletely understood. Any disruptions to this carefully balanced system may shift the bacterial interactions, causing what is is called "skin dysbiosis," which enables the overgrowth of pathogenic species common in skin conditions such as acne, psoriasis, atopic dermatitis, and rosacea.[6] This review aims to summarize and discuss the external factors that can potentially influence the cutaneous microbiota directly or indirectly by altering the skin microenvironment.

## MATERIALS AND METHODS

A PubMed, Embase, and RFUMS Boxer Library database search for articles with the following keywords was performed: ("skin" OR "cutaneous") AND ("microbiome" OR "microbiota") AND ("external" OR "environment" OR "lifestyle" OR "weather" OR "outside" OR "occupation"). Results were filtered to only include clinical trials with human subjects, published within the last 5 years, and in English. 120 PubMed, 157 Embase, and 175 RFUMS Boxer Library articles resulted. Article titles and abstracts were reviewed; those with relevant subject matter were retrieved for full-text review. In addition, their associated references were scanned for relevant reports and 13 additional studies that did not appear in our literature search were discovered. Figure 1 lists the 32 clinical studies that were included in the efficacy analysis.

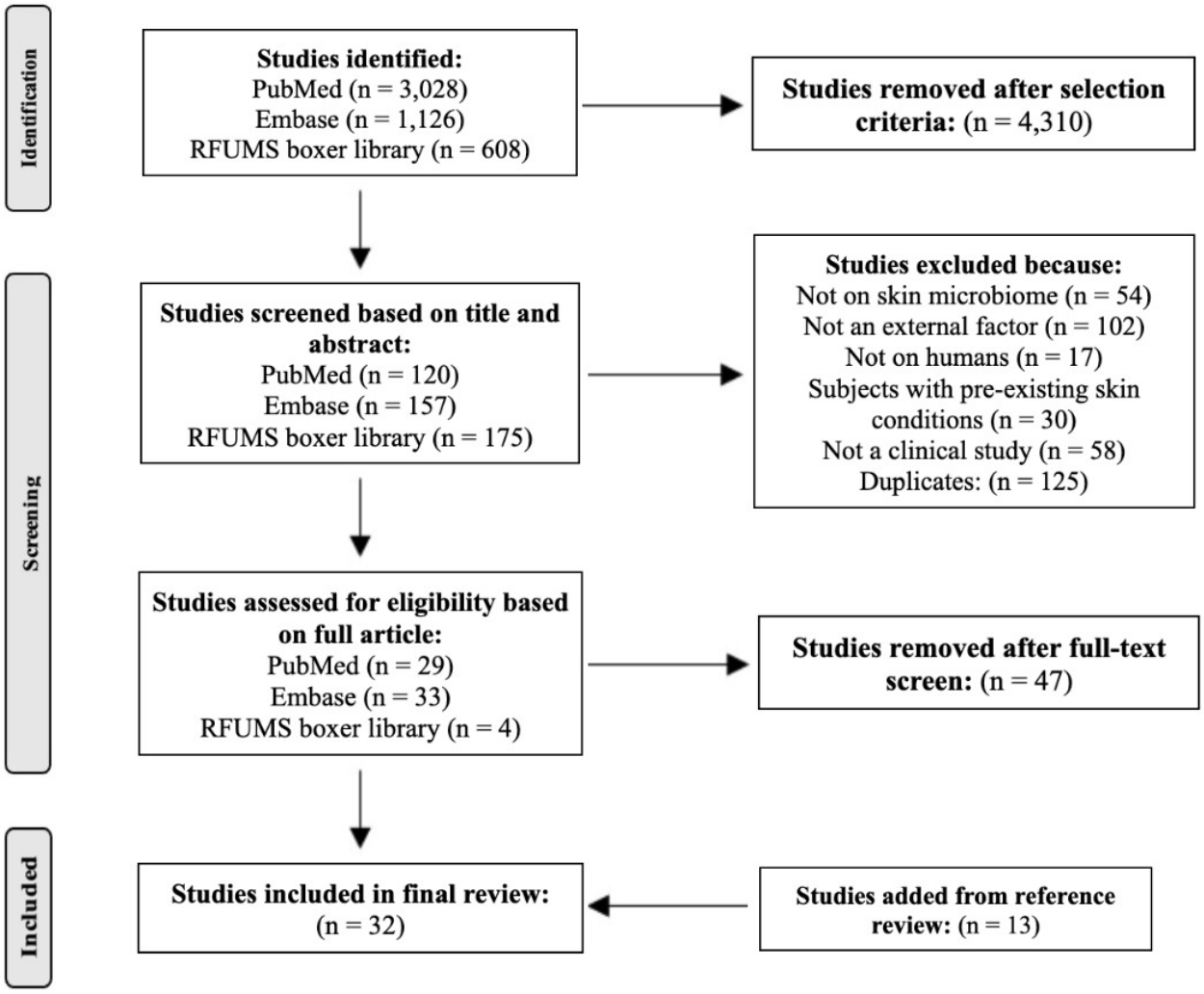


**Figure 1. Article selection flowchart detailing external factors on the human cutaneous microbiome in literature**

## RESULTS

### 1) OUTDOOR ENVIRONMENTAL FACTORS

High altitude is unique in that extreme environmental conditions like high UV radiation (UVR), low temperature, low humidity, and hypoxia all coexist in these regions. To see how differing levels of these stressors affect the cutaneous microbiome, Wang et al performed a meta-analysis of 233 human skin samples from eight elevation sites in western China, ranging from 501 meters (m) above sea level to 3,431 m above sea level.[1] The skin microbiome alpha diversity, which measures the average microbial richness of a single individual, as well as beta diversity, which quantifies the skin microbiome variability between individuals, were calculated.[7] *Lactobacillus* and *Cyanobacteria* showed positive growth with rising altitude.[1] Interestingly, both can tolerate hypoxia and overcome oxidative stress through unique mechanisms including producing UV-absorbing compounds and vitamin B6 metabolism.[8,9] Further elucidating the mechanisms used by microorganisms that can tolerate extreme outdoor conditions could point out useful strategies and compounds to incorporate into skin protection for various outdoor environments.

Furthermore, while the alpha diversity generally decreased with increasing altitude, the beta diversity increased based on the Jaccard or Bray-Curtis dissimilarity matrix, indicating greater differences in microbial communities between individuals.[9] This may be because high-altitude environmental pressures may elicit unique responses for each individual, increasing the difference of interpersonal skin microbiota. The bacterial networks of high-altitude skin had fewer links than those of low-altitude skin, suggesting a more fragile and less interconnected network.[9] Interestingly, a study on the Dead Sea region, which also harbors extreme climatic conditions like low humidity and high UVR, as well as a study on the skin microbiome before and after summer in lifeguards living on the Mediterranean coast with daily exposure to high UVR during a 5-month period, also showed significantly lower mean alpha diversity in the skin microbiome as well as significant increases in beta diversity.[10,11] This decrease in commensal skin microbiome diversity, change in the normal microbial composition, and weakening of the skin bacterial network might

possibly contribute to the higher incidence of dysbiotic skin diseases in more extreme outdoor environments.[12]

However, living in non-extreme climatic conditions does not necessarily keep one safe from outdoor environmental stressors. In the modern world, air pollutants exist all around us. Specifically, polycyclic aromatic hydrocarbons (PAHs) are associated with premature skin aging, pigmentary disorders, and skin cancer.[13] Leung et al looked at the skin microbiota of 204 Chinese individuals from Boading (a heavily polluted area) and Dalian (a less polluted area) with varying exposure levels of PAHs.[13] While degradation of PAHs to benign byproducts by skin microbiota can potentially eliminate the detrimental effects of PAHs on the skin, too much exposure to PAHs can lead to their partial metabolism and yield a wide variety of intermediate metabolites that may exacerbate skin disorders.[13] Greater exposure to PAHs led to weaker skin bacterial connections, similar to the bacterial networks of high-altitude skin.[13] This suggests that outdoor environmental forces that disrupt microbial diversity–and therefore the natural connections found between commensal bacterial communities–decrease the resilience of the skin microbiome to recover from these disruptions. This may lead to associated skin conditions like acne, dandruff, and atopy.[12,14] All outdoor environmental factor studies are summarized in Table 1.

## 2) INDOOR ENVIRONMENTAL FACTORS

Due to an increased hygiene level in the developed world, there has been a decrease in microbial diversity in the urban environment, far less contact with nature, and extensive use of antibiotics. This has led to a reduction in exposure to environmental microbes, which may be one of the major reasons for the rise in skin dysbiosis and immune-mediated diseases. Natural vegetation tends to be more microbially rich than artificial landscapes, and populations who are often around or in greater proximity to natural environments may benefit through re-diversification of their human cutaneous microbiome.

Roslund et al studied the effect of 3 different daycare environments on 75 urban children for 28 days: (i) standard yards, (ii) intervention yards with biodiversity elements, and (iii) nature-oriented daycare centers where children visited nearby forests on a daily basis.[16] The intervention yards not only showed greater skin bacterial diversity than standard yards, but also the increase in the intervention group's skin bacterial diversity appeared to have a compound effect after each day, indicating the importance of longer-term, consistent exposures.[16] Furthermore, the diversities in the intervention group became more similar to those in nature-oriented daycares, showing no significant differences in skin Proteobacterial alpha diversity between the two groups after the study.[16] Specifically, there was a positive shift in skin Gammaproteobacteria–previously associated with a decreased risk of atopy and allergies[17]–in the intervention group, and this was associated with increased IL-10 levels ($p = 0.001$) and IL-10 to IL-17A ratio ($p = 0.02$) in plasma.[16] IL-10 is an anti-inflammatory cytokine involved in the prevention of autoimmune diseases by limiting the secretion of pro-inflammatory cytokines, and by regulating key immune cells.[17] These results suggest biodiversity interventions can restore microbial diversity comparable to those in nature-oriented daycares and can potentially regulate communication between the immune system and skin. Furthermore, 1-year skin swabs showed consistently higher Alpha-, Beta-, and Gammaproteobacteria in the intervention group ($p < 0.001$),[18] suggesting that the beneficial effects of letting children play in microbially rich spaces could last on the skin long-term, especially if there is consistent exposure. This brings up the question of whether greater scale interventions such as urban green spaces in cities can also promote healthy skin for communities.

Selway et al surveyed human skin microbiota of 3 subjects that were exposed to urban green space in 3 different cities (Adelaide, Australia (1 hr exposure); Bournemouth, United Kingdom (~15 min exposure); New Delhi, India (~15 min exposure)).[19] In Adelaide, there was a significant increase in skin microbiota diversity after urban green space exposure, and the microbiome became more similar to the natural vegetation in the urban green space after this exposure.[19] For Bournemouth and New Delhi, which are vastly different in terms of outdoor environments, both skin microbial richness and diversity significantly increased after exposure as well despite the shorter exposure time of ~15 minutes.[19] This suggests that increases in microbial diversity and richness can occur even after brief green space exposure. Providing people with a chance for daily contact with biodiverse vegetation may re-diversify the cutaneous microbiome and increase microbes that can regulate immune pathways as seen in the mentioned studies. This prompts us to ask whether biodiverse vegetation can be brought indoors, and whether that will have the same beneficial effects.

To see the effects of vegetation in indoor spaces, Soininen et al looked at the effect of vegetated walls brought into work offices for 2 weeks in 28 adults.[20] Soininen et al showed that the abundance of *Lactobacillus* increased with indoor green wall compared to control on Day 14 ($p = 0.0058$).[20] The bacteria from the *Lactobacillaceae* family are known to act against pathogens and inflammation on skin.[20] Therefore, spending time in green wall spaces may also increase the abundance of healthy skin microbiota within a relatively short time period. Biodiverse vegetation may release live bacteria on the skin, remove air pollutants that affect skin microbiome, or both. However, the exact mechanism must be further studied. Summarized findings on indoor environmental factors are in Table 2. Implementing biodiverse vegetation in the management and planning of urban environments and indoor spaces can possibly enhance healthy commensal microbiota on a community level and reduce dysbiosis.

## 3) SOCIAL DYNAMICS & LIFESTYLE

An ecological perspective is important to consider due to the constant contact we have with other people. People regularly in our close proximity will most likely influence our skin microbiome. Sharma et al conducted a 5-month longitudinal study of the bacterial community of 34 United

**Table 1. Published studies on outdoor environmental factors on the human cutaneous microbiome**

| Citation | Study Type | Duration | Participants | Independent variable | Outcome | Notes or Limitations |
|---|---|---|---|---|---|---|
| Wang et al (2021)[1] | - Comparative study and meta-analysis | - January and April of 2019 | - 24 volunteers; 5 body parts. 128 effective samples total | - Elevation gradient | - *Proteobacteria* decreased with increased altitude, whereas strict anaerobic bacteria such as *Lactobacillus* showed positive growth with altitude (R2 = 0.130, p = 0.001) | - Did not measure skin biophysical parameters which can be associated with skin microbial diversity<br>- Future research can explore temporal monitoring of human skin microbiomes over the long term to better understand the relationship between the skin microbiome and public health |
| Li et al (2019)[9] | - Comparative Study | - 2 weeks | - 35 healthy human subjects across 3 body areas (forehead, opisthenar and palm) | - Seven elevation gradients from 501 to 3431 m | - Alpha diversity values decreased with increasing elevation regardless of the body site, while beta diversity showed an increasing trend with elevation. (Jaccard R2 = 0.059, p < 0.001; Bray–Curtis R2 = 0.149, and p < 0.001)<br>- Skin microbiotas at high elevation with more than 3000 m had a significant structural or functional separation from those at low elevation with less than 3000 m (Jaccard R2 = 0.079, p < 0.001; Bray–Curtis R2 = 0.179, p < 0.001) | - Other unmeasured environmental factors (eg air temperature, UV) associated with elevation may influence the skin microbiota structure |
| Harel et al (2023)[10] | - Comparative study | - 5 months | - The Mediterranean coast group[15]: volunteers with a total of 120 samples. The Dead Sea area group: 17 residents, a total of 102 samples | - Dead Sea area environment | - Significantly mean lower diversity of microorganism in the skin microbiome, measured by the Shannon index, of the Dead Sea area inhabitants, as compared to the Mediterranean coast residents (p < 0.05, Kruskale Wallis test)<br>- The bacteria in the skin microbiome of the Dead Sea area residents were composed of significantly different species than those in the skin microbiome of Mediterranean coast residents. (Anosim, p = 0.001, R = 0.23 for Jaccard; Anosim, p = 0.001, R = 0.39 for Braye Curtis) | - Did not determine which of the factors are important in the build-up of the skin microbiome<br>- Future studies should look at the skin microbiome of individuals with unhealthy skin conditions<br>- A need for follow up research to determine whether potential environmental factors or other factors contribute to the differences between the skin microbiomes of the two regions and affect the presence of non-skin bacteria |
| Harel et al (2022)[11] | - Comparative study | - 3 months | - 122 samples: 66 samples of male lifeguards and 56 samples of ultra orthodox males | - Exposure level to sun radiation | -In the group exposed to the sun during the summer months, there were significant differences in low-abundance species in sun-exposed areas of the skin (the inner and outer arm) | - Future studies should explore the secreted metabolome of skin microorganisms across different seasons, and its effects on the human host |
| Burns et al (2019)[8] | - Pilot study | - 24 hour swab collection | - Men (n = 6) between the ages of 19 and 35 years, with no skin disease | - UVA1 (340-400 nm) and narrowband UVB (308 nm) sources | - General increase in *Cyanobacteria* following UVR exposure. Two other phylum trends noted were the increases of both *Fusobacteria* and *Verrucomicrobia* following UVR | - Future studies should increase the number of participants, as well as include females and a wider range of Fitzpatrick skin types would be |

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| | | | | | - *Lactobacillaceae* and *Pseudomonadaceae* decreased following all UVR exposure | beneficial to acquiring more generalizable findings |
| Leung et al (2020)[13] | - Comparative study | - Two weeks | - Cheek and scalp microbiota of 204 individuals residing in two cities in China | - PAH exposure: with different levels of exposures to PAHs and related pollutants, one heavily polluted (Baoding) and the other less so (Dalian) | - Shannon diversity increase was correlated to exposure levels of PAHs in a dose-dependent manner<br>- A diversification of the microbiota was observed along with a reduction in *Propionibacterium* (Spearman's rho = −0.162, p = 0.022)<br>- The diversification also included the enrichment of taxa belonging to genera with biodegradation potentials in the more polluted city of Baoding | - Future studies focusing on the roles of PAHs in potentially altering microbial network characteristics may provide solutions for alleviating any adverse effects of PAHs on skin physiology |

**Table 2. Published studies on indoor environmental factors on the human cutaneous microbiome**

| Citations | Study Type | Duration | Participants | Independent Variable | Outcome | Notes or Limitations |
|---|---|---|---|---|---|---|
| Soininen et al (2022)[20] | - Randomized control trial (RCT) | - 2 weeks | - 28 healthy adults | - Vegetated walls (green walls) (size 2 m × 1 m × 0.3 m) | - The relative abundance of *Lactobacillus* spp. was higher in the skin samples of the experimental group than the control group during the treatments, on Day 14 (Wilcoxon p = 0.0058) | - Cannot separate the role of the green wall removal of volatile organic compounds (VOC) by the green walls |
| Roslund et al (2020)[16] | - Clinical trial | - 28 days | - 75 children age 3-5 years | - 3 types of centers: (i) standard yards, (ii) intervention yards with biodiversity elements, and (iii) nature-oriented daycare centers where children visit nearby forests on a daily basis | - Children in intervention daycares had more diverse skin *Proteobacterial* and *Gammaproteobacteria* communities than children in standard daycares. (p = 0.03 and Padj = 0.05)<br>- The commensal microbiota of children in intervention daycare centers became more similar to that observed in children attending nature-oriented daycares | - No controlling home environment |
| Roslund et al (2022)[21] | - Placebo-controlled double-blinded test | - 14 days | - 26 children age 3-5 years | - Playground sand enriched with microbially diverse soil | - Bacterial richness ($p < 0.001$) and diversity ($p < 0.05$) were higher in the intervention than placebo sand. Skin bacterial communities shifted only in the intervention treatment to resemble the bacterial community in the enriched sand<br>- The richness of *Firmicutes*, particularly classes *Bacilli* and *Clostridia*, increased in the intervention treatment compared to baseline ($p < 0.001$) | - Lack of longitudinal follow up<br>- The study being conducted in late spring and early summer can be a potential reason for proinflammatory changes and poor environmental microbiota in the built environment |
| Grönroos et al (2018)[22] | - Experimental study | - 3 hrs of exposure | - 2 volunteers | - 8 composted, soil, and plant based materials. Altogether 16 materials were tested. | - Intervention exposures increased the total diversity of skin microbiota and the diversity of *Acidobacteria*, *Actinobacteria*, *Bacteroidetes*, *Proteobacteria* and *Alpha-*, *Beta-* and *Gammaproteobacteria* (p = .001, V = 9) | - Future studies should examine (1) how long the change in skin microbiota is preserved, (2) does the exposure translate into changes in gut microbiota, and (3) if the exposure induces beneficial changes in the immune system markers |
| Roslund et al (2021)[18] | - Longitudinal study | - 2 years | - 89 urban day-care children | - Two different day-care environments: (1) intervention yards amended with biodiversity elements and (2) standard urban control yards with no amendments | - Within the first 28 days, the intervention shifted the relative abundances of 60 soil bacterial genera compared with the baseline<br>- 1 year samples, the intervention was associated with an increase in *Acidobacteria* and *Proteobacteria* Gp1 Shannon diversity and richness, whereas these indices decreased at the standard yards | - Future studies should investigate how biodiversity interventions shape airborne microbiomes, and how these are connected to the human commensal microbiome<br>- Future intervention trials should pay attention to seasonal variation in the context of human commensal microbiota |

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| Selway et al (2020)[19] | - Environmental interventional study | - 1 month | - 3 subjects | - Urban green space | - Microbial richness and phylogenetic diversity increased after urban green space exposure in skin and nasal samples collected in two of the three locations. The microbial composition of skin samples also became more similar to soil microbiota after exposure<br>- Increases in diversity and shifts in microbial abundances are linked to an increase in rare taxa and a decrease in common, human-associated taxa after green space exposure at this city | - Longitudinal investigations into microbial changes associated with different environmental contexts (eg indoor, non-green space, and different urban environments) are needed to understand the role of environmental exposure in shaping the human microbiome |
| Mills et al (2023)[23] | - Interventional study | - 45 min exposures over 3 consecutive days | - 57 healthy 10-to-11-year-old students | - School environment—either a 'classroom' (n = 20), 'sports field' (n = 14), or biodiverse 'forest' (n = 23)—for 45 min | - The disturbance immediately followed by outdoor exposure, especially the 'forest,' had an enriching and diversifying effect on skin microbiota ($R2 = 0.07$, $p < 0.05$), while 'classroom' exposure homogenized interpersonal variability<br>- Each effect compounded over consecutive days after each 45-min exposure from days one to three. This was not so for the 'classroom' nor 'sports field' groups | |
| Mhuireach et al (2022)[24] | - Experimental study | - Three 24 hr periods | - Sixteen adult subjects between the ages of 18–35 | - Collected microbial samples from substrates and leaves of five different indoor plant types | - Alpha diversity of skin receiving soil microbes increased immediately after the transfer event and remained elevated for at least 24 h (paired t-test: $t\ 15 = -8.1$, $p < 0.005$) | |

States Air Force cadets to determine how co-occupancy influenced the skin microbiota of individuals with similar diet, lifestyle, and age,[25] which diminished the potential influence of confounding variables. While roommates did not display a significant increase in the similarity of the skin microbiota, they were significantly more similar (ANOSIM R = 0.231, panosim < 0.05) compared to non-roommates (ANOSIM R = 0.474, panosim < 0.01).[25] There were two breaks during the semester when the cadets were required to vacate their rooms. The absence and its duration were both associated with significant decreases in the similarity between the skin microbiome immediately after each break.[25] This is likely due to the acquisition of new bacteria during the break, a reduction in bacterial sharing between roommates and perhaps reduction in lifestyle similarity during the break.

To address more socio-cultural complexities that shape skin microbiomes, a cross-sectional study recruited 119 skin bacterial samples from 47 infants in Evanston, IL, US [high socioeconomic status (SES)] and in three different populations in Veracruz, Mexico (MEX) [Xalapa (urban middle SES), Coatepec (peri-urban low SES), and Ocotepec (rural low SES)] to capture lifestyle variation between populations.[26] Samples from infants in the rural MEX population displayed higher bacterial diversity compared to others, which could be due to increased exposure to microbes from the natural environment. In settings like the rural MEX population, frequent exposure to nature like farms and rivers resulted in "environmental" soil-derived microbes being more regular skin residents compared to urban settings. Furthermore, infants in the MEX population had regular access to an outdoor play area and were observed to be playing in grass and soil prior to sample collection.[26] This brings up the question of whether greater exposure of infants from MEX populations to more nature-derived microbes create a healthier, more biodiverse skin microbiota compared to infants from the US. Furthermore, the rural MEX group reported the largest household sizes and the greatest number of caregivers, suggesting that infants in this population are further exposed to more diverse microbes through bacterial sharing with more people at home.[26] Taken together, these results suggest that skin bacterial communities can reflect diverse geographic and household characteristics that vary with SES, occupation, and culture.

To elucidate the effect of various lifestyle factors on skin microbiome, a cross-sectional survey of skin microbiota from a population of adult Germans from Kiel was done, with a total of 647 participants (1,794 skin samples).[15] Various lifestyle factors, including diet, smoking, physical activity, alcohol consumption, etc were asked in the survey. Dietary intake of macronutrients was associated with 12 amplicon sequence variants (ASVs) from *Corynebacterium* and *Staphylococcus.*[15] ASVs refer to identifying and quantifying genetic variations in a sample differing from each other by even a single nucleotide to represent the diversity of microbial composition. Dietary factors can hypothetically influence skin bacteria from the inside out by changing skin biochemical composition through gut microbiota metabolites that reach skin tissue.[27] For instance, a high fat diet in mice was reported to lead to a change in skin lipid composition and associated with an increase in *Corynebacterium.*[15] Remaining lifestyle factors were associated with up to five ASVs from these two genera, including smoking, alcohol consumption, antibiotic use, skincare use, and sports.[15] Table 3 summarizes studies on social dynamics and lifestyle factors. Thus, we see a complex interplay between microbiome composition and metabolites in the skin from lifestyle factors. Future research should expand on these lifestyle behaviors that shape the host physiology and the skin microenvironment so that we have a better understanding of what controllable factors can significantly affect our skin microbiota and adopt healthier, more "microbiome-friendly" habits.

## 4) PERSONAL CARE PRODUCTS

Multi-step skincare routines have become an integral part of our daily lives. While modern cleansers are much gentler than traditional soaps, even mild detergents are known to interact with skin proteins and cause keratinocyte damage.[30] These products can come with a variety of ingredients that may interact with the host's microbiome, and may last on the skin for long periods of time, changing the skin's biochemical environment. To evaluate these variations, Bouslimani et al integrated metabolomics and microbiome data from skin samples of 11 healthy individuals.[31] The 4 selected commercial beauty products were applied once a day at specific body sites for 3 weeks (specific product information in Table 4). Although alterations to the individual skin microbiome and metabolome upon skin product use are site-, product-, and person-specific, the data generally showed that using skin products led to higher chemical and bacterial diversity.[31] Another study on the effect of a gentle emollient lotion with a mild cleanser found a greater increase in the relative abundance of commensal bacteria, including *Bacillales, Cutibacterium* and *Staphylococcus,* compared to cleanser alone.[32,33] Key ingredients that make the lotion gentle and moisturizing include cotton, dimethicone, glycerin, and isopropyl palmitate.[33] Specific information of the gentle emollient and cleanser is stated in **Table 4**. At the genus level, specifically, *Cutibacterium acnes* and *Staphylococcus epidermidis* are known to prevent pathogenic bacterial colonization and stimulate human keratinocytes and sebocytes to produce antimicrobial peptides to maintain a balanced skin microbiome.[32,33] As a result, gentle moisturizing skincare products appear to regulate and maintain the natural skin microbiome composition and suggest that the routine use of an appropriately formulated product can increase skin microbiome richness as well as optimize the growth of certain bacterial strains over others that might exert specific functions in providing benefits to the skin ecosystem like skin hydration, texture and pH.[32] The shift in bacterial composition caused by the use of skincare products has not been investigated extensively, and future studies should be performed to clarify the function of different microbes and, specifically, how they affect the human skin. Notably, skin products had a half-life of 0.5 to 1.9 weeks even though the volunteers reg-

**Table 3. Published studies on social dynamics and lifestyle factors on the human cutaneous microbiome**

| Citations | Study type | Duration | Participants | Independent variable | Outcome | Notes or limitations |
|---|---|---|---|---|---|---|
| Sharma et al (2019)[25] | - Longitudinal study | - 5 months | - United States Air Force Academy cadets (n = 34) | - Cohabitation in school dormitory | - Cohabitation was significantly associated with increased skin microbiota similarity. The skin microbiota from cohabitating roommates was significantly more similar (ANOSIM R = 0.231, panosim < 0.05) compared to non-roommates<br>- Following a departure from the occupied space of several weeks, the skin microbiota showed a significant reduction in similarity relative to the building | - Future longitudinal studies could register the time individuals spend together and the proximity between the occupants<br>- Limited by sampling one skin site |
| Manus et al (2020)[26] | - Cross-sectional study | - From February to September 2019 | - 119 skin bacterial samples from 47 infants aged 0.5 to 33 months | - Four populations (Evanston and Mexico) representing four SES and living situations | - Samples from infants in the rural MEX population displayed elevated bacterial diversity. (estimate = 21.061, p = 0.001). Samples from these infants harbored environmentally derived taxa<br>- Mothers in the rural MEX population reported the largest household sizes and the greatest number of caregivers | - Questionnaire did not quantify time spent playing between siblings, which may serve as another route for bacterial sharing between siblings<br>- Future work on the social transmission of microbes would benefit from documenting the frequency of contact with caregivers and other members of the social environment, including siblings<br>- Future work in this area would benefit from longitudinal sampling as well as direct participant observation |
| Wang et al (2023)[28] | - Longitudinal survey | - 9 months | - 9 trainee students, men with an average age of 24 years | - Occupational exposure during 3-month internships in two swine farms | - The exposure in farm A reduced the microbial diversity of skin and nasal microbiota (p = 0.048), whereas the microbiota of skin and nose increased after exposure in farm B (p < 0.01) | - Decline in diversity was possibly related to specific non-microbial factors in farm A, such as strict hygiene practices and sanitation procedures. The increase in diversity in farm B in contrast due to less strict hygiene practices and stronger microbial factors considering that livestock farms are rich habitats for microorganisms |
| Steglińska et al (2019)[29] | - Questionnaire study | | - 40 volunteers divided into four age groups (0–10, 11–17, 18–50 and >60 years) | - Feet-washing frequency (once/twice a day, every other day, once a week) and physical activity frequency (three or more times a week, 1–2 times per week, no activity) | - The number of bacteria, in most cases, decreased with age and with increased frequency of physical activity. Bacteria number significantly increased with decreasing feet washing frequency<br>- The highest biodiversity of cultured bacteria was noted in the group who washed feet once daily (16 species) followed by people washing feet twice daily (9 species) and finally lowest in feet washing every other | - Broadening of analysis by including more pathogenic bacterial and fungal strains occurring as natural foot microorganisms should be considered<br>- Combining culturing and high-throughput sequencing methods would reflect bacterial community composition more precisely than either of them can do alone |

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| | | | | | day (8 species) | |
| Moitinho-Silva et al (2021)[15] | - Cross-sectional study | - 1 year | - 647 participants from two population-based German cohorts, 1794 skin samples total | - Various lifestyle and host factors | - The amount of total energy and macronutrient intake was significantly associated with ASV abundances<br>- Dietary intake of macronutrients was associated with 12 ASVs from *Corynebacterium* and *Staphylococcus* genera | - Further work is required to establish the causal nature of the diet–skin microbiome relationship |

ularly showered or swam.[31] This indicates that a single application of some products has the potential to alter the microbiome and skin chemistry for extensive periods of time. This raises the question of how extra additives in skin care products marked as "microbiome enriching" could alter the skin further.

Probiotics are supplements of live bacterial strains that confer a health benefit on the host, parabiotics are non-viable cells (intact or broken), and postbiotics are non-viable bacterial products or metabolic byproducts of probiotics.[38] A study analyzed the impact of a parabiotic-containing (*Bifidobacterium lactis* and *Lactobacillus plantarum*) moisturizer vs control on the skin microbiome of 50 healthy subjects for 4 weeks.[38] The sequencing study showed significant changes in common commensals including *Cutibacterium* ($p = 0.0431$), *Corynebacterium* ($p = 0.0431$), and *Acinetobacter* ($p = 0.0431$) in the treatment group.[38] Other studies looking at products containing parabiotic technology overall showed a significant increase in alpha diversity of commensal bacteria, greater abundance of beneficial species, and no significant increases in pathogenic species, compared to control.[39] Other natural compounds and extracts are often added to skincare products as well, including emollients like saccharide isomerate and antimicrobial plant extracts such as lavender.[30,34] The desired effects sought from these added natural compounds are increased moisture, anti-inflammatory properties, reduction of pathogenic bacteria, and an increase in overall commensal and beneficial microbial diversity.

Synthetic additives in cosmetics have also become relatively common in the last few decades and underexplored in their effects on skin microbiota. A study compared the skin microbiome of 32 female participants after application of three different face washes: one synthetic product ("A"), one "natural" product with synthetics ("B"), and one 100% natural face wash ("C").[6] The brand behind "C" claims their definition of the word 'natural' is taken from food industry standards rather than the cosmetics industry where there are no legal definitions, and that every ingredient in "C" is sourced directly from nature, with no chemical or physical changes.[6] "B" was chosen because it is one of many products which is advertised as "natural" but actually contains multiple synthetic additives, including methylisothiazolinone, which is linked to allergic reactions and possible neurotoxicity, and methylchloroisothiazolinone.[6] When looking at the results using the Chao1 index, "C" with no synthetic ingredients displayed the fastest average increase in diversity and richness.[6] The moisture on the skin decreased quickly for the other two groups most likely because they contain harsh ingredients like alcohol, sulfates, and artificial fragrances, which can dry out the skin and strip it of its natural oils.[6] "C" was able to maintain the natural skin physiology compared to the other two products.[6] Therefore, natural additives seem to be more "microbiome-friendly" and better preserve the natural skin microenvironment than synthetic additives.

However, even natural skin products contain water and organic compounds that are prone to bacterial or fungal overgrowth. Therefore, chemical preservatives are often used in cosmetics to prevent microbial growth, provide product stability, and ensure a long shelf life.[5] To further investigate the effect of preservatives, Santamaria et al enrolled 14 volunteers in a double-blind randomized and controlled split-face design in which the participants applied a different set of products to each half of the face for 3 weeks.[5] One set was conventional skincare products with preservatives (set 1), and the other set was microbiome-supporting products without conventional preservatives (set 2). The specific preservatives in set 1 are listed in Table 4. The total number of reads mapped to unique bacterial species increased significantly ($p < 0.05$) after 3 weeks on set 2, while no significant difference could be observed on set 1.[5] Although the trend was that set 2 promoted greater Shannon microbial diversity, further research on the unique species that increased after set 2 is warranted to assure none are pathogenic strains and detrimental to product integrity. The Shannon diversity index characterizes species diversity in a community by analyzing both richness and evenness of the species present. Furthermore, different preservatives have varying antibacterial strengths (Table 4), and the sensitivities of the skin-resident bacteria are found to be distinct from those of pathogenic strains.[35] Therefore, finding cosmetic preservatives that exert strong inhibitory effects on opportunistic pathogens while preserving as much skin-resident bacteria as possible would be ideal. Findings on personal care products are summarized in Table 4.

## DISCUSSION

With the rising occurrence of inflammatory skin disease, better understanding of the regulatory relationship between the skin immune function and microbiome for maintaining homeostasis is essential. Although cutaneous microbiome research is recognized as one of the fastest-growing fields in dermatology, there are still limitations for human microbiome research. Limitations include the difficulty of gene sequencing because of the low efficiency of microbial DNA extraction, the various skin types of participants in each study, and unstandardized sampling methods used. In particular, different skin sites harbor different microbial communities, so accurate data organization of each topical site (eg forehead or elbow) is required. Sampling the microbiome of other skin sites might have resulted in different findings in several of the reviewed studies. Furthermore, intrinsic factors such as age and sex are also known to have an impact on the skin microbiota composition and chemical diversity. For example, the skin microbiota during puberty is vastly different from an infant or a post-menopausal individual, and hormonal levels on the skin differ between men and women.[40] Therefore, future studies should look at the same factors stratified by age group and sex to elucidate the complex interplay of external and host internal factors on cutaneous microbiome. Lastly, all future work would benefit from longitudinal sampling as well as larger pools of samples in order to capture how temporal, geographic, and behavioral variation impact the shifts in skin microbiome. Many of

**Table 4. Published studies on personal care products on the human cutaneous microbiome**

| Citations | Study Type | Duration | Participants | Independent variable | Outcome | Notes or limitations |
|---|---|---|---|---|---|---|
| Santamaria et al (2023)[5] | - Double-blind, RCT with a split-face design | - 3 weeks | - 14 healthy volunteers | - Skincare with or without conventional preservativesConventional preservatives included: SC , PG, PE, SB, EHG, PS | - The use of non-preservative products for 3 weeks significantly increased the total number of reads mapped to unique bacterial species ($p < 0.05$) and the number of different unique species ($p < 0.05$). Additionally, it showed a significantly improved diversity ($p < 0.05$) compared with the conventional side | - A larger sample would draw more definite conclusions about the differences between the treatments<br>- Future studies should look at men and women separately |
| Capone et al (2023)[33] | - Randomized, evaluator blind study | - 5 weeks | - 38 healthy infants (3-6 months old) | - Baby skin care products on the microbiome in infants Cleanser: JOHNSON's CottonTouch Newborn wash & shampoo; Emollient lotion: JOHNSON's CottonTouch Newborn face & body lotion | - Microbiome richness was statistically higher for the wash + lotion group compared with the wash-only group on Day 28 | - Smaller r than planned number of subjects enrolled, and the recruitment of subjects from one geographical area |
| Bialon et al (2019)[34] | - Comparative study | - 24 hr incubation of skin samples | - Microbiota of oily facial skin without signs of lesions | - ETJA lavender oil vs Crimean lavender oil | - The most effective inhibitory effect was lavender oil at the concentration of 70 µL/cm3, although no complete inhibition of the growth of the mixed microbiota from the skin was observed<br>- ETJA lavender oil inhibited the growth of most bacteria tested, but neither oil inhibited the growth of *E. faecium*<br>- The most sensitive to ETJA lavender oil were Gram-positive bacilli, and Gram-negative bacilli were the most sensitive to Crimean lavender oil. On the other hand, neither of the tested oils inhibited the growth of Gram-positive cocci | |
| Bouslimani et al (2019)[31] | - Experimental Study | - 9 weeks | - Skin of 12 healthy individuals | - Selected commercial skin care products: Nivea soft moisturizer cream on the arm, Aveeno Positively Radiant Daily Moisturizer SPF 15 sunscreen on the face, Dove Original Clean Antiperspirant Deodorant on the armpits, and CVS pharmacy Smoothing Powder on the foot | - Compounds from beauty products last on the skin for weeks after their first use despite daily showering<br>- Beauty products alter molecular and bacterial diversity as well as the dynamic and structure of molecules and bacteria on the skin<br>- Many of the molecules associated with the personal skin and hygiene products had a half-life of 0.5 to 1.9 weeks even though the volunteers regularly showered, swam, or spent time in the ocean | |
| Wang et al (2019)[35] | - Comparative Study | | - Facial skin of 14 Chinese adults aged 20-25 years | - The five common chemical preservatives that had been widely used in the cosmetic | - MTI and IPBC were the most effective, whereas PE exerted the least inhibitory effect on the tested bacteria. PE and MP had the least impact on skin- | |

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|---|---|---|---|---|---|---|
| | | | | products, including PE, EHG, MTI, MP, and IPBC | resident bacteria at concentrations that could inhibit *S. aureus* and *E. coli* - Specifically, IPBC and MTI were most effective against all tested bacteria, with MICs ranging from 0.00125% to 0.01%. PE had the mildest effect on all tested bacteria, with MICs ranging from 0.5% to 1% | |
| Hwang et a. (2021)[32] | - Pilot study | - 4 weeks | - 25 healthy Korean women between 30 and 58 years of age | - Skincare product on their face twice a day | - Shannon diversity increased after the use of the skincare product<br>- *Cutibacterium* and Staphylococcus displayed significant negative correlations in the T0 bacterial network | - Future studies should investigate direct interactions among microorganisms via co-culture experiments |
| Sfriso et al (2022)[4] | - Single-center, RCT | - 4 weeks | - 23 Caucasian females aged between 18 and 40. Five sampling areas of 4 $cm^2$ each were defined on the face of each study participant: (1) forehead, (2) nose, (3) front cheek, (4) lateral cheek, and (5) chin | - Topical application of a plant extract (*Epilobium fleischeri*) | - Observed shifts in microbial composition after 4 weeks of twice-daily product application. *Staphylococcus hominis*, *Staphylococcus epidermidis*, and *Micrococcus yunnanensis* appeared to be significantly enriched in the final microbiota composition of the active treatment group<br>- A significant decrease in porphyrins on the skin of volunteers who were applying the product containing the *Epilobium fleischeri* extract<br>- *Epilobium fleischeri* extract rich in oenothein B did not impact the natural skin microbial diversity, but increased microbial richness | |
| Callejon et al (2023)[36] | - Comparative study | - 4 days | - 20 Caucasian females between 24 to 46 years of age | - 3 skincare product types: hydrophilic solution, the micellar solution, and the emulsion | - The bacterial diversity and abundance were not affected by the products, and no dissimilarities versus the control nor between each product were noted at both times | - Preliminary results should be confirmed by assessment of daily application over a longer timeframe and by increasing the sample size |
| Wang et al (2023)[37] | - RCT, triple-blind | - 8 weeks | - 110 participants, Chinese females between 18 and 40 years of age with self-assessed dry, but healthy, facial skin | - 3 topical cosmetic moisturizers (water gel moisturizers with/without yeast extract (Moisturizers K and C) and a thick-emulsion cream moisturizer (Moisturizer L)) | - All moisturizers are well-tolerated and improve skin barrier function and surface moisture content from the baseline, and the improvement is maintained at the last analysis point (3 days after trial completion)<br>- Moisturizer K prevented decreases in the variety of bacterial species, whereas Moisturizer C showed no obvious effects on bacterial richness, and Moisturizer L had no significant impact on bacterial richness<br>- Moisturizer K increased certain bacterial strains like Staphylococcus and Ralstonia after week 4, showing postbiotic technology can alter the skin bacterial composition | - Used control for the same exposure, and skin explants of only three Caucasian women were chosen to investigate the protective effects of the studied moisturizers |

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|---|---|---|---|---|---|---|
| Wallen-Russell (2019)[6] | - Comparative study | - 4 weeks | - 32 female participants ages 20 to 45 | - 3 different face washes : One leading 'natural' brand full of synthetic ingredients, a leading synthetic brand and a 100% natural face wash were used | - All three groups display average increases in diversity over time. The slowest increase over two and four weeks is the synthetic and 'natural' product groups respectively<br>- 100% natural with no synthetic ingredients, displayed the fastest average increase in both (OTU p = 0.0219 anova) | - A larger sample size should be used along with a section detailing the exact skincare regime of the participants prior to the study. An increase in duration should see how long it takes the microbiome to stabilize after using different products on the skin |
| Sfriso and Claypool (2020)[30] | - Single-blind, RCT | - 14 days | - 30 healthy Caucasian female volunteers aged between 25 to 45 | - A base body wash formulation (placebo) and an active body wash formulation (treatment) consisting of the base formulation plus 0.5% saccharide isomerate | - The skin microbiota proved to be resilient and able to re-establish itself and to adapt its composition. The active body wash provided potential interesting benefits by reducing so called "coryneforms" such as *B. casei* and *R. mucilaginosa*, bacteria which are increasingly implicated in skin infections | - Limited to the volar forearm<br>- A wider age range should be implemented in the future |
| Chaiyasut et al (2022)[38] | - Pilot study | - 4 weeks | - Fifty healthy subjects randomly divided into treatment (n = 25) and control (n = 25) groups | - Paraprobiotics-containing moisturizer and its influences on the skin microbiome of healthy subjects | - Paraprobiotic treatment significantly reduced the transepidermal water loss (TEWL) and increased the stratum corneum moisture (SCM) values compared to the respective baseline values and controls. The sequencing study showed significant changes in *Cutibacterium* (p = 0.0431), *Corynebacterium* (p = 0.0431), and *Acinetobacter* (p = 0.0431) in the treatment group | - Small sample size and treatment period are limitations |
| Iglesia et al (2022)[39] | - A single center, open-label clinical study | - 4 weeks | - 25 female subjects between 35 and 65 years old | - The Gentle Cleansing Lotion | - The increase in diversity found at day 28 correlates with the appearance of bacterial species marginally represented at baseline (**p < 0.001) such as *Turicella otitidis* | - The short duration of the study and the lack of a placebo arm |

SC, sodium chloride; PG, pentyleneglycol; PE, phenoxyethanol; SB, sodium benzoate; EHG, ethylhexylglycerin; PS, potassium sorbate; MTI, methylisothiazolinone; IPBC, iodopropynyl butylcarbamate.

the reviewed studies took place for several weeks within participants from similar demographics. With longer tracking across more individuals and various settings, future research can investigate the chronic effects of these external factors, how these microbes colonize the human skin, how long it takes the microbiome to stabilize after exposure to these factors, and whether colonization has health benefits or risks in individuals. Although there are clear trends and patterns in the way the microbiota shifts and responds to certain environmental factors, individual traits and physiology make understanding the exact dynamics of skin microbiome difficult. These findings suggest that individually tailored treatment is needed to regulate skin microbiome in order to prevent or treat skin diseases.

## DISCLOSURES

Dr. Lio is on the speaker's bureau for AbbVie, Arcutis, Eli Lilly, Galderma, Hyphens Pharma, Incyte, La Roche-Posay/L'Oréal, MyOR Diagnostics, ParentMD, Pfizer, Pierre-Fabre Dermatologie, Regeneron/Sanofi Genzyme, Verrica; reports consulting/advisory boards for Alphyn, AbbVie, Almirall, Amyris, Arcutis, ASLAN, Bristol-Myers Squibb, Castle Biosciences, Codex Labs, Concerto Biosci, Dermavant, Eli Lilly, Galderma, Janssen, Johnson & Johnson, Kimberly-Clark, LEO Pharma, Lipidor, L'Oréal, Merck, Micreos, MyOR Diagnostics, Regeneron/Sanofi Genzyme, Skinfix, Theraplex, UCB, Unilever, Verrica Yobee Care; stock options with Codex, Concerto Biosciences and Yobee Care. In addition, Dr. Lio has a patent pending for a Theraplex product with royalties paid and is a Board member and Scientific Advisory Committee Member of the National Eczema Association.

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# REFERENCES


1. Wang Y, Yu Q, Zhou R, Feng T, Hilal MG, Li H. Nationality and body location alter human skin microbiome. *Appl Microbiol Biotechnol*. 2021;105(12):5241-5256. doi:10.1007/s00253-021-11387-8

2. Roux PF, Oddos T, Stamatas G. Deciphering the Role of Skin Surface Microbiome in Skin Health: An Integrative Multiomics Approach Reveals Three Distinct Metabolite-Microbe Clusters. *J Invest Dermatol*. 2022;142(2):469-479.e5. doi:10.1016/j.jid.2021.07.159

3. Saville CR, Metris A, Humphreys GJ, et al. Transitory Shifts in Skin Microbiota Composition and Reductions in Bacterial Load and Psoriasin following Ethanol Perturbation. *mSphere*. 2022;7(4):e0017122. doi:10.1128/msphere.00171-22

4. Sfriso R, Claypool J, Roche M, Imfeld D. 5-α reductase inhibition by Epilobioum fleischeri extract modulates facial microbiota structure. *Int J Cosmet Sci*. 2022;44(4):440-452. doi:10.1111/ics.12777

5. Santamaria E, Åkerström U, Berger-Picard N, Lataste S, Gillbro JM. Randomized comparative double-blind study assessing the difference between topically applied microbiome supporting skincare versus conventional skincare on the facial microbiome in correlation to biophysical skin parameters. *Int J Cosmet Sci*. 2023;45(1):83-94. doi:10.1111/ics.12826

6. Wallen-Russell C. The Role of Every-Day Cosmetics in Altering the Skin Microbiome: A Study Using Biodiversity. *Cosmetics*. 2019;6(1):2. doi:10.3390/cosmetics6010002

7. Walters KE, Martiny JBH. Alpha-, beta-, and gamma-diversity of bacteria varies across habitats. *PLoS One*. 2020;15(9):e0233872. doi:10.1371/journal.pone.0233872

8. Burns EM, Ahmed H, Isedeh PN, et al. Ultraviolet radiation, both UVA and UVB, influences the composition of the skin microbiome. *Exp Dermatol*. 2019;28(2):136-141. doi:10.1111/exd.13854

9. Li H, Wang Y, Yu Q, et al. Elevation is Associated with Human Skin Microbiomes. *Microorganisms*. 2019;7(12):611. doi:10.3390/microorganisms7120611

10. Harel N, Reshef L, Biran D, Ron EZ, Gophna U. Skin microbiome of people living at the Dead Sea area - The lowest place on earth. *Res Microbiol*. 2023;174(5):104059. doi:10.1016/j.resmic.2023.104059

11. Harel N, Reshef L, Biran D, Brenner S, Ron EZ, Gophna U. Effect of Solar Radiation on Skin Microbiome: Study of Two Populations. *Microorganisms*. 2022;10(8):1523. doi:10.3390/microorganisms10081523

12. Kim HJ, Kim H, Kim JJ, et al. Fragile skin microbiomes in megacities are assembled by a predominantly niche-based process. *Sci Adv*. 2018;4(3):e1701581. doi:10.1126/sciadv.1701581

13. Leung MHY, Tong X, Bastien P, et al. Changes of the human skin microbiota upon chronic exposure to polycyclic aromatic hydrocarbon pollutants. *Microbiome*. 2020;8(1):100. doi:10.1186/s40168-020-00874-1

14. Hew KM, Walker AI, Kohli A, et al. Childhood exposure to ambient polycyclic aromatic hydrocarbons is linked to epigenetic modifications and impaired systemic immunity in T cells. *Clin Exp Allergy*. 2015;45(1):238-248. doi:10.1111/cea.12377

15. Moitinho-Silva L, Boraczynski N, Emmert H, et al. Host traits, lifestyle and environment are associated with human skin bacteria. *Br J Dermatol*. 2021;185(3):573-584. doi:10.1111/bjd.20072

16. Roslund MI, Puhakka R, Grönroos M, et al. Biodiversity intervention enhances immune regulation and health-associated commensal microbiota among daycare children. *Sci Adv*. 2020;6(42):eaba2578. doi:10.1126/sciadv.aba2578

17. Lunjani N, Ahearn-Ford S, Dube FS, Hlela C, O'Mahony L. Mechanisms of microbe-immune system dialogue within the skin. *Genes Immun*. 2021;22(5-6):276-288. doi:10.1038/s41435-021-00133-9

18. Roslund MI, Puhakka R, Nurminen N, et al. Long-term biodiversity intervention shapes health-associated commensal microbiota among urban day-care children. *Environ Int*. 2021;157:106811. doi:10.1016/j.envint.2021.106811

19. Selway CA, Mills JG, Weinstein P, et al. Transfer of environmental microbes to the skin and respiratory tract of humans after urban green space exposure. *Environ Int*. 2020;145:106084. doi:10.1016/j.envint.2020.106084

20. Soininen L, Roslund MI, Nurminen N, et al. Indoor green wall affects health-associated commensal skin microbiota and enhances immune regulation: a randomized trial among urban office workers. *Sci Rep*. 2022;12(1):6518. doi:10.1038/s41598-022-10432-4

21. Roslund MI, Parajuli A, Hui N, et al. A Placebo-controlled double-blinded test of the biodiversity hypothesis of immune-mediated diseases: Environmental microbial diversity elicits changes in cytokines and increase in T regulatory cells in young children. *Ecotoxicol Environ Saf*. 2022;242:113900. doi:10.1016/j.ecoenv.2022.113900

22. Grönroos M, Parajuli A, Laitinen OH, et al. Short-term direct contact with soil and plant materials leads to an immediate increase in diversity of skin microbiota. *Microbiologyopen*. 2019;8(3):e00645. doi:10.1002/mbo3.645

23. Mills JG, Selway CA, Thomas T, et al. Schoolyard Biodiversity Determines Short-Term Recovery of Disturbed Skin Microbiota in Children. *Microb Ecol*. 2023;86(36):658-669. doi:10.1007/s00248-022-02052-2

24. Mhuireach GÁ, Fahimipour AK, Vandegrift R, et al. Temporary establishment of bacteria from indoor plant leaves and soil on human skin. *Environ Microbiome*. 2022;17(1):61. doi:10.1186/s40793-022-00457-7

25. Sharma A, Richardson M, Cralle L, et al. Longitudinal homogenization of the microbiome between both occupants and the built environment in a cohort of United States Air Force Cadets. *Microbiome*. 2019;7(1):70. doi:10.1186/s40168-019-0686-6

26. Manus MB, Kuthyar S, Perroni-Marañón AG, Núñez-de la Mora A, Amato KR. Infant Skin Bacterial Communities Vary by Skin Site and Infant Age across Populations in Mexico and the United States. *mSystems*. 2020;5(6):e00834-20. doi:10.1128/mSystems.00834-20

27. Mahmud MR, Akter S, Tamanna SK, et al. Impact of gut microbiome on skin health: gut-skin axis observed through the lenses of therapeutics and skin diseases. *Gut Microbes*. 2022;14(1):2096995. doi:10.1080/19490976.2022.2096995

28. Wang X, Chen D, Du J, et al. Occupational exposure in swine farm defines human skin and nasal microbiota. *Front Microbiol*. 2023;14:1117866. doi:10.3389/fmicb.2023.1117866

29. Steglińska A, Jachowicz A, Szulc J, et al. Factors Influencing Microbiological Biodiversity of Human Foot Skin. *Int J Environ Res Public Health*. 2019;16(18):3503. doi:10.3390/ijerph16183503

30. Sfriso R, Claypool J. Microbial Reference Frames Reveal Distinct Shifts in the Skin Microbiota after Cleansing. *Microorganisms*. 2020;8(11):1634. doi:10.3390/microorganisms8111634

31. Bouslimani A, da Silva R, Kosciolek T, et al. The impact of skin care products on skin chemistry and microbiome dynamics. *BMC Biol*. 2019;17(1):47. doi:10.1186/s12915-019-0660-6

32. Hwang BK, Lee S, Myoung J, et al. Effect of the skincare product on facial skin microbial structure and biophysical parameters: A pilot study. *Microbiologyopen*. 2021;10(5):e1236. doi:10.1002/mbo3.1236

33. Capone KA, Friscia DL, Nikolovski J, Telofski LS, Stamatas GN. A randomized clinical study on the effects of emollient use on the developing infant skin microbiome and metabolome. *Exp Dermatol*. 2023;32(1):75-77. doi:10.1111/exd.14684

34. Białoń M, Krzyśko-Łupicka T, Nowakowska-Bogdan E, Wieczorek PP. Chemical Composition of Two Different Lavender Essential Oils and Their Effect on Facial Skin Microbiota. *Molecules*. 2019;24(18):3270. doi:10.3390/molecules24183270

35. Wang Q, Cui S, Zhou L, et al. Effect of cosmetic chemical preservatives on resident flora isolated from healthy facial skin. *J Cosmet Dermatol*. 2019;18(2):652-658. doi:10.1111/jocd.12822

36. Callejon S, Giraud F, Larue F, et al. Impact of Leave-on Skin Care Products on the Preservation of Skin Microbiome: An Exploration of Ecobiological Approach. *Clin Cosmet Investig Dermatol*. 2023;16:2727-2735. doi:10.2147/CCID.S409583

37. Wang DQ, Li X, Zhang RY, et al. Effects of Investigational Moisturizers on the Skin Barrier and Microbiome following Exposure to Environmental Aggressors: A Randomized Clinical Trial and Ex Vivo Analysis. *J Clin Med*. 2023;12(18):6078. doi:10.3390/jcm12186078

38. Chaiyasut C, Sivamaruthi BS, Tansrisook C, Peerajan S, Chaiyasut K, Bharathi M. Influence of Paraprobiotics-Containing Moisturizer on Skin Hydration and Microbiome: A Preliminary Study. *Applied Sciences*. 2022;12(23):12483. doi:10.3390/app122312483

39. Iglesia S, Kononov T, Zahr AS. A multi-functional anti-aging moisturizer maintains a diverse and balanced facial skin microbiome. *J Appl Microbiol*. 2022;133(3):1791-1799. doi:10.1111/jam.15663

40. Townsend EC, Kalan LR. The dynamic balance of the skin microbiome across the lifespan. *Biochem Soc Trans*. 2023;51(1):71-86. doi:10.1042/BST20220216