A Seminar Paper
on

Skin Microbiome Alteration by Skin Care Products

Course Title: Seminar
Course Code: BGE 598
Term: Winter 2022

Submitted to:

Course Instructors

Dr .A.K.M Aminul Islam
Professor
Department of Genetics and Plant Breeding, BSMRAU

Dr. Satya Ranjan Shaha
Professor
Department of Agroforestry and Environment, BSMRAU

Dr. Shaikh Shamim Hasan
Professor
Department of Agricultural Extension and Rural Development, BSMRAU

Dr. Dinesh Chandra Shaha
Associate Professor
Department of Fisheries Management, BSMRAU

Major Professor

Dr. Shah Mohammad Naimul Islam
Associate Professor
Institute of Biotechnology and Genetic Engineering, BSMRAU

Submitted by:
Mahjabin Ferdaous Mim
Reg. No: 17-05-4250
MS Student
Institute of Biotechnology and Genetic Engineering

BANGABANDHU SHEIKH MUJIBUR RAHMAN AGRICULTURAL UNIVERSITY
SALNA, GAZIPUR-1706

Skin microbiome alteration by skin care products[1]

By

Mahjabin Ferdaous Mim[2]

ABSTRACT

Healthy skin reflects healthy microbiome and vice versa. The modernized civilization with a perpendicular upraise in skin irritation has bound researchers, dermatologists, and cosmetic industries to find a relationship between skin microbiomes and skin care product use. Different cosmetics are able to bring changes in common skin dweller species confirming both increase and decrease in microbe alteration solely or while these products are used in a combination. Though the usage category of products is same, they show different level of changes. Not all the changes and usages of cosmetics are meant to be a threat as some are altering microbes for skin restoring (Actibiome), some are able to have skin resilience (Mymicrobiome). But as alteration is directly linked with diseases, it is us to be more cautious while choosing skin care regimes. Different study techniques alike artificial skin models, metagenomic analysis, culture-based approaches have strengthened the basis for thinking of skin care products to be one of the important and effective factors of microbial alteration. Collectively, this article reviewed the current knowledge about microbial community shifts caused by the use of various cosmetics and a framework of skin microbe identification and screening skin care products upon them. It offers to think about how lifestyle related product choices remake the skin microbial makeup and alter our skin dwellers microbes. Further studies are obliged to understand the extra products' effects on different ages, genders, and body sites with a multi-study approach, along with the possible altered microbial consequences.

Keywords: skin microbiome, skin care products, microbial diversity, microbial alteration.

---

[1]A seminar paper presented at seminar course on April 15, 2023

[2]MS student, Institute of Biotechnology and Genetic Engineering, BSMRAU, Gazipur-1706

LIST OF TABLES

LIST OF FIGURES

CHAPTER 1

INTRODUCTION

Beauty is something that we all cherish. Development of the awareness of a person's inner intelligence as well as outer beauty is a huge motivational drive nowadays. For glorifying us in a neat and exquisite manner, the easiest, hassle less approach is using cosmetics or any skin care products in daily, weekly or monthly basis. This practice enforces global cosmetics market size skyrocketing with an anticipation to reach $463.5 billion in 2027 with a growth in CAGR (Compound annual growth rate) of 5.3% (Shankar, 2021). Due to media, research, advertising claims, rather than consuming pills or supplements, application of cosmetics in skin is more appreciated to confer beauty ubiquitously (Jillian, 2020). So skin, the most versatile interface organ of the body, comprising an average 30 m^2 surface area in adults is the center of interest here (Gallo, 2017). Along with diversified chemicals and structural regime, one thing that boosts skins' anisotropic heterogeneous nature is the composition of skin dwelling microbiota. This is an absolute habitat for diverse group of microorganisms including bacteria, fungi, micro-eukaryotes (mites), archaea, viruses and phage (Verbanic *et al.,* 2019). A newborn baby gets colonized hugely after birth (Byrd *et al.,* 2018). Gradually due to topographical diversity, site-specific diversity the skin microbiota turns into a highly variable composition of extremely versatile community depending on the areas of the body, between individuals, and over time. Contrary to a popular myth, not all skin microorganisms are dangerous by origin; pathogenicity only happens when the ecosystem's equilibrium is interrupted and variety is diminished. This fear of alteration is grasping attention to the health conscious minds.

In the last 5 to 10 years, there has been a considerable increase in the rate of skin damage. Although there are many causes, the increased usage of synthetic chemical components in modern-day cosmetics, being the primary culprit has proved to be a threat (Wallen-Russell & Wallen-Russell, 2017). Skin care products are appreciated until they summon some uninvited guests. In the personal care business, the skin microbiota represents a typically untapped but quickly developing area, as evidenced by the rise in formulations including chemicals that could affect the balance of the skin microbiota. Here remains instances of the occurrence of numerous skin diseases caused by this dysbiosis or perturbation of the skin microbiome (Myles *et al.,* 2016). It is needed to find out in depth relationship of skin microbes, skin chemistry along with their shifts in divergence in terms of cosmetics application that is yet

fully to be discovered thoroughly. Importance of skin microbiome highlights that by focusing upon those we can state one's skin health, dwelling situation, and environment (Wallen-Russell & Wallen-Russell, 2017). Considering all the facts a better understanding of correlation of microorganisms with skin care routines may fuse and widen the knowledge of the relationship among the skin microbiome, skin diseases, skin health and open a way of more ensured sustainable, healthy human existence.

The current study is generalized with two objectives-

1. To elucidate the most recent findings of how differently skin care products alter the skin microbiome.
2. To overview the ways of human skin microbe determination with the screening approach towards skin care products application.

CHAPTER 2
MATERIALS AND METHODS

This is a review paper. So, the data gathered for writing this paper are secondary data collected from different papers, published reports, articles from various journals and websites, and other books available on the internet. I improved this paper with the valuable suggestions from my respected major professor and course instructors. It was assembled and sequentially presented in its current form after being provided with all relevant information.

CHAPTER 3

REVIEW OF FINDINGS

3.1 Skin microbiome

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 (Byrd *et al.,* 2018). 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) (Barbieri *et al.,* 2014). There are more than 1200 bacterial species on the skin where more than 90% of bacteria belong to 4 phyla: Actinobacteria (52%) comprising *Micrococcus*, *Propionibacteria* and *Corynebacteria* genera; Firmicutes (24%) comprising *Staphylococcus*, *Lactobacillus*, and *Streptococcus* genera; Proteobacteria (16%) comprising *Paracoccus*, *Haematobacter*, and *Sphingomonas* genera, and Bacteroidetes (6%) including the genera *Porphyromonas*, *Prevotella*, and *Flavobacterium* (Zhou *et al.,* 2013). Among all, according to estimates, the *Cutibacterium*, *Staphylococcus*, and *Corynebacterium* genera, isolated from nearly all sites of skin, may make approximately 45 to 80% of the skin microbiome (Samaras & Hoptroff, 2020). Up to 4.2% of the prokaryotic skin microbiome is made up of archaea (Probst *et al.,* 2013). Regarding fungus, *Malassezia* spp., *Aspergillus*, *Cladosporium*, *Epicoccum*, *Phoma*, *Saccharomyces*, *Candida* etc. are markedly found in different body skin regions (Li *et al.,* 2018). Molluscum contagiosum virus, Merkel cell polyomavirus, Simian virus, *Actinomyces* phage, *Propionibacterium* phage, Polyomavirus, *Streptococcus* phage, *Stenotrophomonas* phage etc. are found (Byrd *et al.,* 2018). The resident microflora is advantageous in modifying the immune system, subjugating a niche and negating dangerous and contagious transients via skin. Although skin microorganisms have been identified and categorized broader (Sfriso *et al.,* 2020), but quantitative measurements are still necessary to compare investigations carried out by various experimenters in various ways for bringing all of them in one point.

3.2 Cosmetics used in skin

A wide range of skin care products, including body washes, gels, lotions, exfoliants, moisturizers, toners, and sunscreens are available for practically any beauty condition one might have. These products target either the entire body or specify a body site depending on

the uniqueness of the skin (Draelos, 2005), focusing mostly on assisting skin from the inside out. Despite this affirmative fact, researchers cannot but accept that the skin's microbiota is impacted both positively and negatively by cosmetic components (Bouslimani *et al.*, 2015). Another thing is, under right physiochemical circumstances, cosmetic compounds can serve as nutrient sources to promote the growth of opportunistic pathogenic microorganisms that results in significant infection and diseases (Neza & Centini, 2016). Though skin wash lowers the concentrations of products dramatically by diluting 5–10 times, but their durability varies from site to site of application and their impact last for weeks with highly individual reactions, including changes in steroid and pheromone levels as well as in the structure and dynamics of microbes, conferring the altered scenario (Murphy *et al.*, 2021). As richness in microbial diversity has been proven to be linked with healthy skin (Finlay & Arrieta, 2016), any kind of effect upon them destines changes leading to threats. But due to the broader range studying on their variations over skin has always been a challenge. For launching cosmetics, in depth studies are needed in context of microbiome. It is a fact of optimism that such practices are being encouraged now-a-days in modern cosmetics. The first "Microbiome-friendly" cosmetic product was premiered in 2019 and was established by 'MyMicrobiome' ensuring microbiome diversity and skin's natural balance (Noleo, 2022).

3.3 Cosmetics' effects on the skin's microbiome

3.3.1 Effect of frequently used cosmetic preservatives on skin microbe dynamics

In cosmetics, ingredients like water, oils, peptides, and carbohydrates foster the growth of microorganisms. To inhibit them, preservatives are one of the most commonly added components. They remain active on skin upon application. Blind use of these supposed to work for preservation and act as antimicrobial entity but are not serving their foreknown purpose only (Cao *et al.*, 2017). A research conducted by Pinto *et al*. in 2021 showed that different tested preservatives were responsible for impacting on the dynamic of the targeted bacterial development of *Cutibacterium acnes* (previously known as *Propionibacterium acnes*), *Staphylococcus epidermidis*, and *Staphylococcus aureus*. Here for screening preservatives 3D skin models and culture-dependent methods were applied. The microbial modifications due to different formulations of some commonly used preservatives are noted below with their inhibition and antimicrobial activity expressed as Log_{10} CFU/cm^2:

Table 1. Activity of the different combination of preservatives tested on growth dynamic expressed as % of inhibition. I= Inhibition; +++= strongly inhibited [< 75%]; ++= moderately inhibited [90–80%]; += weakly inhibited [98–91%]; - = no inhibition

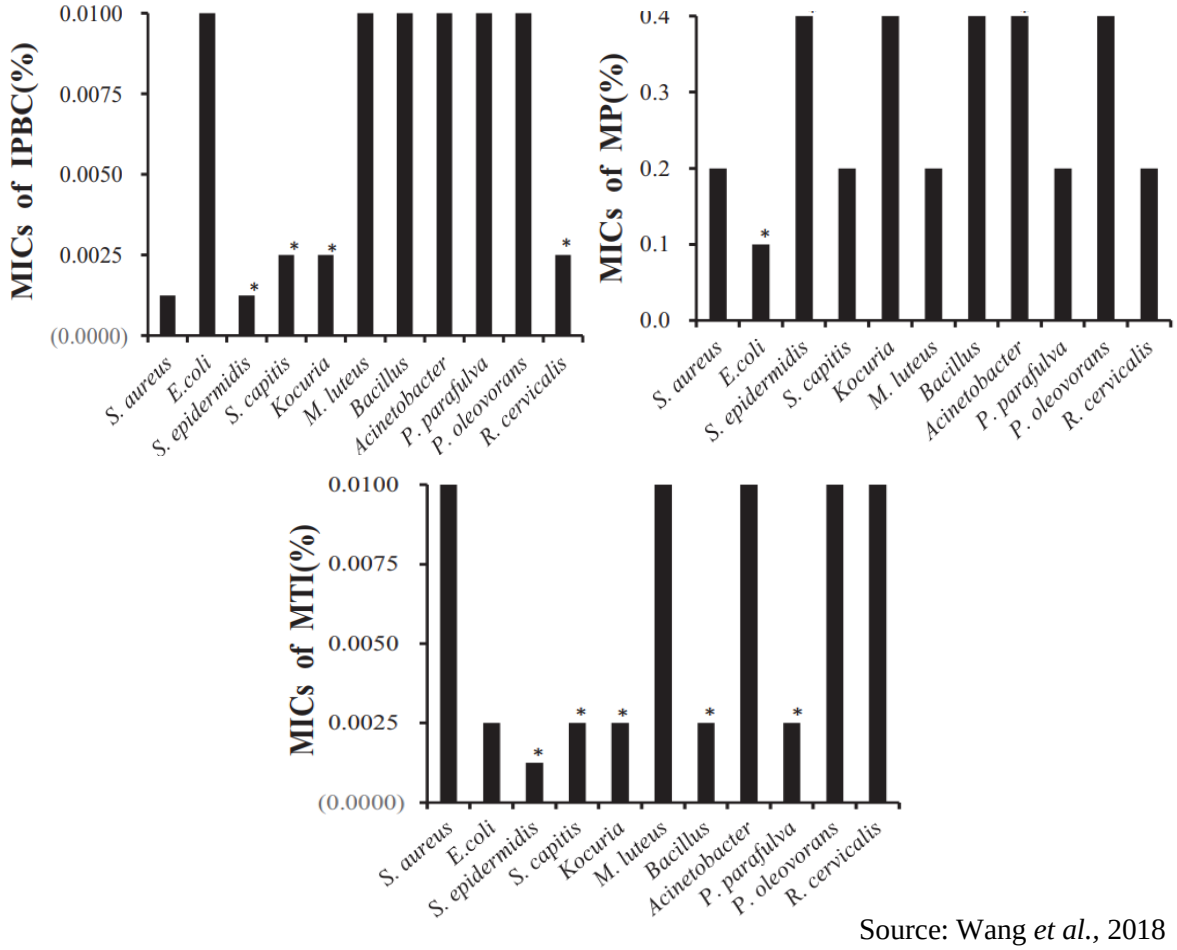
Composing denote	Preservative name	Effects on bacterial strain					
		Cutibacterium acnes		*Staphylococcus aureus*		*Staphylococcus epidermidis*	
		I	Log_{10} CFU/ cm^2	I	Log_{10} CFU/ cm^2	I	Log_{10} CFU/ cm^2
C1	Sodium benzoate, phenoxyethanol, ethylhexylglycerin	+	9.58	++	7.67	_	7.06
C2	Hydroxyacetophenone, tocopherol,phenylpropanol, caprylyl glycol	++	8.67	+++	6.21	_	6.85
C3	Hydroxyacetophenone, phenylpropanol, propanediol, caprylyl glycol, tocopherol	++	9.02	+++	5.83	_	6.92
C4	Sodium anisate, 1,2-hexanediol	+	9.63	+++	5.95	−	6.85
C5	Sodium benzoate, 1,2-hexanediol	−	10.12	++	5.97	−	6.26
C6	Hydroxyaceto-phenone, caprylyl glycol, tocopherol, disodium EDTA	+	9.74	++	6.80	+	7.20
C7	Benzyl alcohol, benzoic acid, dehydroacetic acid	+	9.75	+++	6.23	−	7.41
C8	1,2-hexanediol,benzyl ether myristate	−	10.16	+++	5.98	−	5.86
C9	1,2-hexanediol, caprylyl glycol, tropolone, sodium levulinate, glycerin	_	10.16	+++	5.77	++	5.62
C10	Phenylpropanol, propanediol, caprylyl glycol, tocopherol, disodium EDTA	_	10.65	+++	5.59	+	6.61
C11	Potassium sorbate, sodium benzoate,copolymer	−	10.01	++	5.06	−	7.07
Un-treated	No preservatives	No	10.02	No	6.24	No	6.92

Source: Pinto *et al.*, 2021(modified)

Combinations of preservatives C6, C9, C10 had a negative impact on *S. epidermidis'* development dynamics which is one of the most abundant and human friendly bacteria

dwelling on skin and was therefore not advised for use in topical therapies. Again, because combination C2, C3 function to moderately inhibit *C. acnes* and C2, C3, C4, C7, C8, C9,C10 to significantly inhibit *S. aureus* were shown to be the most effective for regaining a pre-existing dysbiosis. The finest combinations to use in topical solutions for the skin to maintain the eubiosis of the microbiota are C1, C4, C6, and C7.

Wang et al., (2018) showed minimal inhibitory concentrations (MICs) that is inversely proportional to its antibacterial activity of some preservatives against some skin-resident bacteria by using culture dependent broth dilution method was used.



Source: Wang *et al.*, 2018

Figure 1. Minimal inhibitory concentrations of 3 preservatives for skin-resident bacteria. IPBC- iodopropynyl butylcarbamate; EHG-ethylhexyl glycerin; MTI- methyliso thiazolinone. E.- *Escherichia*, M.- *Micrococcus*, P.- *Pseudomonas*, R.- *Roseomonas*, S.- *Staphylococcus.*

In Figure 1, IPBC and MTI were most effective against all tested bacteria, with MICs ranging from 0.00125% to 0.01%. MP was the next most effective preservatives, with MICs ranging from 0.1% to 0.4%. Toner, emulsion, cream and baby cream contains 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 *Staphylococcus epidermidis, Shigella flexneri*, *Enterobacter aerogenes* etc. that are not the target at all (Jeong & Kim, 2015).

3.3.2 Microbiome change caused by the active ingredients of cosmetics

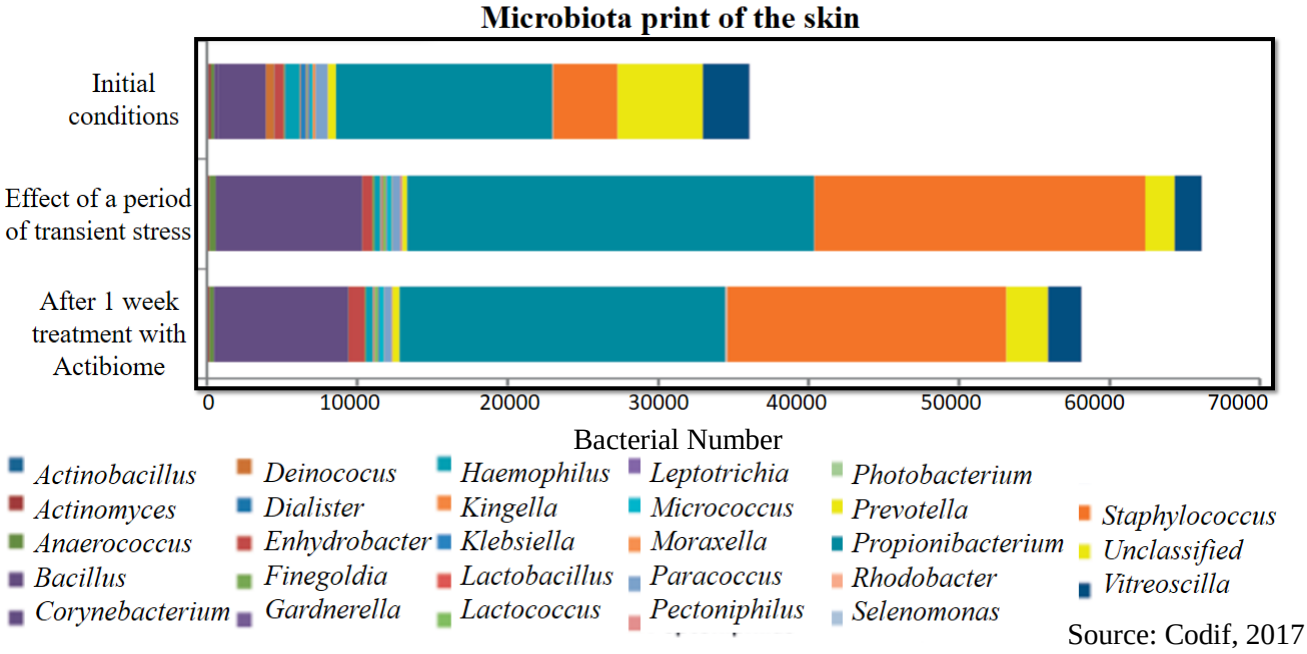
Active ingredients are addressed to skin care products in a purpose specified manner like for brightening, dryness, ageing, sun burn, acne treatment etc. Apart from different chemicals or extracts of plant, fruit, sea weed, pre-pro-postbiotics are included in this list. Plant extracts, fruit extract, sea weed extracts used in cosmetics modified *C. acnes* populations showing incredible feature of combating skin pathogenesis like acne vulgaris (Gervason *et al.,* 2020; Lee *et al.,* 2014). The table beneath (Table 2) highlights some research findings indicating the changes in skin microbes caused by the active ingredients of cosmetics:

Table 2. 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
1. Isotretinoin	Increased *Rothia, Flavobacterium, Enterobacter, Micrococcus.* Decreased *Cutibacterium acnes.*	(McCoy *et al.,* 2019)
2. Maltodextrin, Aqua, *Zymomonas* ferment extract, Honey extract	Increased *Corynebacterium jeikeium, Micrococcus luteus, Staphylococcus aureus.* Decreased *Micrococci, Staphylococcus epidermidis, Staphylococcus hominis, Micrococcus flavus, Cutibacterium avidum.*	(Rademacher *et al.,* 2022)
3. Aqua, Seawater, Glycerin, seaweed extract, Saccharide isomerate, Phenoxyethanol, Ethylhexylglycerin	Increased *Staphylococcus aureus, Staphylococcus hominis, Micrococcus luteus, Cutibacterium avidum.* Decreased *S.* epidermidis, *Micrococcus flavus.*	(Rademacher *et al.,* 2022)
4. ExpoZenfi by Greentech	Increased the bacterial diversity and *Staphylococcus epidermidis* level.	(Filaire *et al.,* 2019)

Kojic acid that is present in skin lightening creams, lotions can travel into blood (Fukase, 2005). Apart from this fact, 100% pure kojic acid along with UV had seen to have potential to induce gene mutation of *E. coli* strain (Wollny, 1998). As *E. coli* strains avail in skin at lower amount, their mutation might lead to destructive consequence (Petkovšek *et al.*, 2009).

Microbiome friendly Actibiome is an active that strengthens and rebalances the diversity of cutaneous flora to get rid of redness and blemishes. It has a varied and balanced composition with a mixture of a mixture of extracts from the brown seaweed *Laminaria digitata*, marine exopolysaccharides solutions, green microalgae *Chlorella vulgaris*, and earth marine water. The following figure (Figure 2) shows how quickly a skin alteration might occur by active ingredient application (Actibiome).



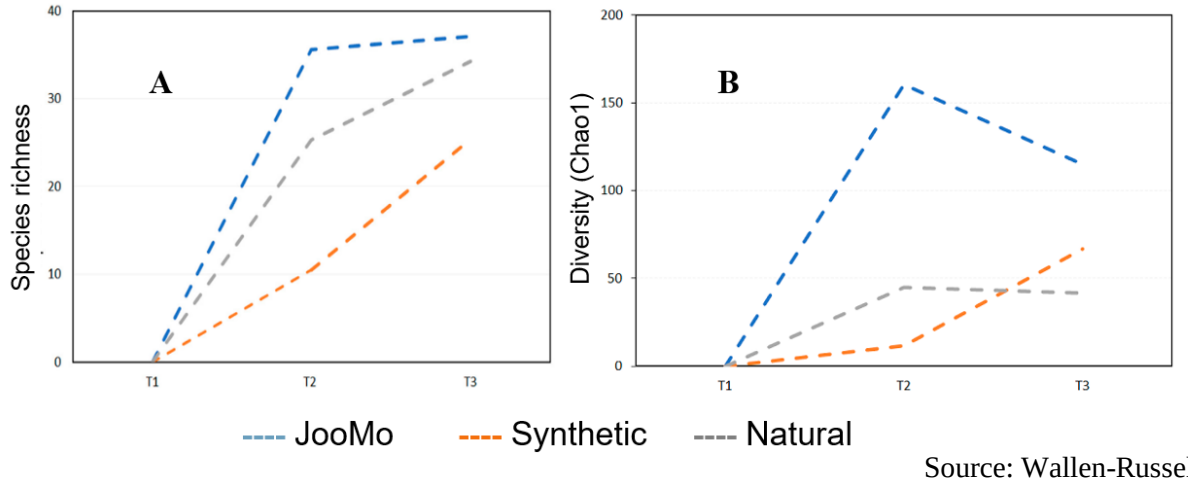
Source: Codif, 2017

Figure 2. Alteration of the number of representatives of bacterial genus by Actibiome application on skin.

From the figure 2 it is seen that this active ingredient mostly increased *Corynebacterium*, *Bacillus*, *Actinomyces*, *Enhydrobacter*, *Staphylococcus*, and decreased *Prevotella*, *Propinibacterium*, *Vetrioscilla*, and some unknown community. By altering microbes, Actibiome corrects the imbalance, restores the skin microbiota to its initial state after one week of twice-daily treatment. After one week, the skin is more consistent, more attractive, and healthier.

Contrary to synthetic substances, which humans have only come into contact with in the last 60 years of their 200,000-year history, natural components, in the quantities found in nature, are not perceived as "alien" to the skin's natural condition (Blaser & Falkow, 2009). Thus, branding by “natural or organic products” easily catches attentions. Sometimes by having a ted of concerns about our skin, consumers prefer using products tagged with “natural cosmetics”. Yet, natural products are not as pure as they sound to be in reality. Methyliso thiazolinone (MI), one of the synthetic compounds used in the 'natural' tagged product, had been associated with potential harm confirming to be a reason of possible neurotoxicity (Burnett *et al.*, 2010), allergic reactions (Scherrer *et al.*, 2015) and microorganisms alteration (Fournière *et al.*, 2020; Šikić *et al.*, 2018). Direct application at lower concentration upon skin was done by Scherrer *et al.*,(2015). An alarming thing is this MI preservative is being used in not only adult products but also in baby’s wipes and bath products.

A research conducted by Wallen-Russell in 2018 showed the microbial community shifts by using 3 of the foreknown cosmetics condition: one is 100% truly natural product (JooMo’s face wash- claiming to be the world’s first 100% truly natural face and body wash (Simon, 2016), second one is a natural product (labeled but actually is not as it contains 70% synthetic products), third one a synthetic product (containing 75% synthetic products). The microbiome culture swabs were used for sampling, later genome sequencing were performed. Sampling was performed three times; before product use (T1), after two weeks of product use (T2), and after 4 weeks of product use (T3). The following 2 figures show the structural changes in diversity and richness of these three products among skin microbiome.



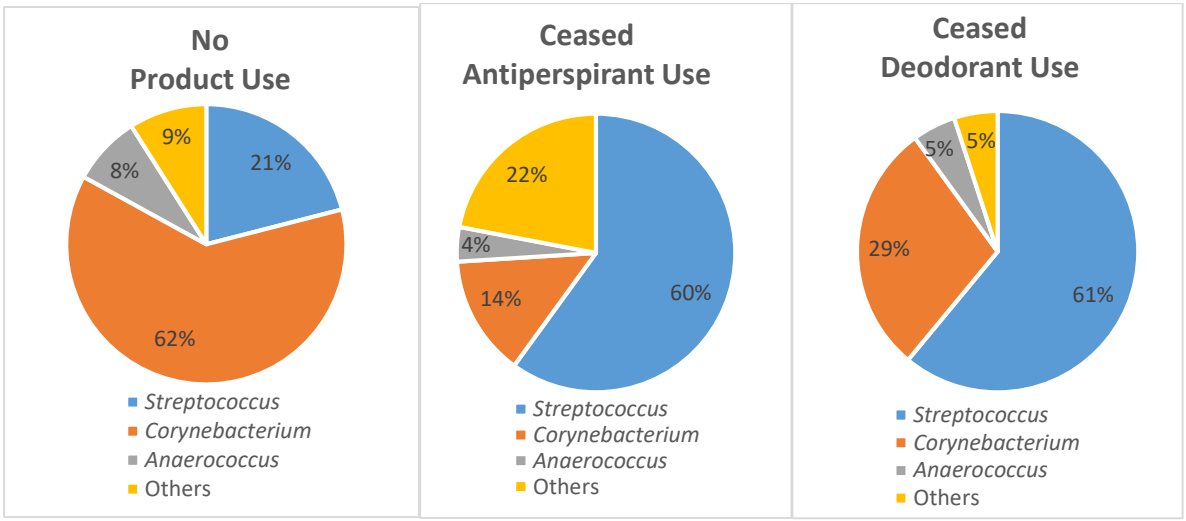
Source: Wallen-Russell, 2018

Figure 3. A. Average change in species richness at every time point of 3 different product use. B. Average change in biodiversity for all time periods of 3 different product use.

It can be said that JooMo (with no synthetic ingredients) demonstrated the fastest average microbial.

3.3.3 Microbiome changes due to the use of deodorants and antiperspirants on skin microbe dynamics

Deodorants, antiperspirants, and germicidal soaps are a few examples of cosmetics made to reduce the number of microbes that cause odors, etc. with no site specificity of storage (Holland & Bojar, 2002). A strong effect of these products' usages on the bacterial composition of armpits is profoundly noticed through some recent studies. Use of antiperspirant - deodorants led armpit communities dominated by Staphylococcaceae family (having both beneficial and pathogenic members), but individuals' armpit with no such products use was dominated by odor causing *Corynebacterium* (Urban *et al.*, 2016). Both culture and sequence based sampling, analysis were used in this study for getting precise results. The following chart shows how the product use status alters armpit dwellers. It also shows that antiperspirant causes higher bacterial diversity than deodorants.



Source: Urban *et al.*, 2016

Figure 4. Mean composition and richness of bacterial OUT (Operational taxonomic unit) for three product user types, combined OTU data from 2 and 5 days after stopping product use.

No product to antiperspirant and deodorant use are causing changes with the lowest value in antiperspirant for *Streptococcus* (60%), *Corynebacterium* (14%), *Anaerococcus* (5%). Other bacterial community is lowest for deodorant (5%). This study narrated that antiperspirant users had much richer armpits proving the microbial shift and also notified that antiperspirant caused higher bacterial diversity than deodorants.

According to the study conducted by Bouslimani *et al.*, in 2019 showed that in armpits of both male and female, deodorants use caused the increase of genera *Anaerococcus* and *Peptoniphilus,* decrease in genera *Corynebacterium, Staphylococcus*, while antiperspirant led to a noteworthy increase in gram-negative bacterial abundance including the phyla Proteobacteria and Bacteroidetes. Their action wasn't site specific. For instance, use of antiperspirant in armpit resulted in increase of *Cyanobacteria* in face; *Acinetobacter* and *Paracoccus* in face and arm for both genders. It is to be noted that antiperspirant and deodorant use's effects on one's overall health have not been thoroughly investigated yet.

3.3.4 Changes in hand and palm microbiome

The amount of exposure to environmental elements, how often hands are washed all likely play a role in hand skin microbiota variation by damaging the protective surface of 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 (Two *et al.,* 2016). Healthcare personnel who routinely washed their hands have more pathogenic bacteria on them than those who didn't (Larson, 1999) indicating less microbial diversity led to the potentiality to increase pathogenic species including *S. aureus* , *Enterococcus* spp., *Candida albicans* (Rosenthal *et al.,* 2013). The alcohol-based hand sanitizer and ethanol showed the reduction of the levels of viable aerobic- anaerobic bacteria (Zapka *et al.,* 2017). Many cleansers use surfactant that misbalances the pH of skin. 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 (Rippke *et al.,* 2018). Extreme amount of citric acid and lactic acid in cleanser or exfoliants lowered normal skin pH causing decreased *C. acnes*.

3.3.5 Variety in personal care products leads to variety in skin microbiome

The topical application of personal hygiene products is able to change lipid film that covers the skin, resulting the alteration of the microbial diversity, total bacterial species richness in skin. The active body wash offered potentially interesting benefits by eliminating *Brevibacterium casei* and *Rhodotorula mucilaginosa* that are linked to skin illnesses and increasing beneficial bacterium, *Cutibacterium acnes* (Sfriso & Claypool, 2020). The basic skin care routine comprising skin softener, lotion, essence, and cream containing moisturizing compounds all together was able to alter two of the most common skin phyla: Actinobacteria (decreased) and Proteobacteria (increased) (Lee *et al.,* 2017) in facial cheeks. Here may be the cosmetics are preventing the normal skin bacterial groups from growing, or the cosmetics

has forces skin environment to change. The following table (Table 3) shows some product basis variations upon skin microbes.

Table 3. Some common skin care products causing microbial alteration in skin

SL	Product category	Alteration in skin microbes	References
1.	Foot powder use	Significant increase in foot bacteria such as *Micrococcus, Anaerococcus, Streptococcus, Brevibacterium, Moraxellaceae* and *Acinetobacter*.	(Bouslimani *et al.,* 2019)
2.	Lotion in lower foot (against xerosis, extreme dryness)	Increase *in Staphylococcus epidermidis, Xanthomonas* and *X. campestris.*	(Murphy *et al.*, 2022)
3.	Short chain fructo-oligosaccharides (A prebiotic used in powder)	Significant increase in *Staphylococcus epidermidis* at lower concentration (0.5 to 5%) and decrease at higher concentration (10 to15%). Decrease in *Staphylococcus aureus* growth and complete halt of *Cutibacterium acnes*.	(Le *et al.*, 2022)
4.	Serum cosmetics containing galacto-oligosaccharides	Decrease in *Staphylococcus aureus* (significantly), *Staphylococcus*, *Cutibacterium, Pediococcus*, *Enhydrobacter*, Enterobacteriaceae. Increase in *Burkholderia*, *Bifidobacteria*, *Lactobacilli*, *Lactococcus*, *Sphingomonas*, *Thermoanaerobacterium*.	(Hong *et al.*, 2020)
5.	Spermidine used in lotion, cream etc.	Increase in *Staphylococcus pneumonia* and *Staphylococcus infantis.* Decrease in *Staphylococcus thermophiles.*	(Kim *et al.*, 2021)
6.	Lipids in moisturizers	Promotes *Staphylococcus and Propionibacterium*	(Bouslimani *et al.*,2015)
7.	Ceramides in moisturizers	Affects *Streptococcus* abundance	(Howard *et al.*, 2022)
8.	Selenium in lotion, sunscreen, creams	Reduction in both gram-negative and gram-positive (*Staphylococcus aureus*) bacteria	(Michelle *et al.*, 2016)

Comparing makeup user with non- makeup users, significantly higher microbial diversity was seen on forehead skin including the increase in the genera *Selenomonas, Aggregatibacter* and *Aquicella* (Staudinger *et al.,* 2011). Most frequently changed skin microbes are quite intertwining. Figure 5 and 6 underneath highlight which products frequently alter bacterial or fungal species and which have single product-based impacts found from different research articles.

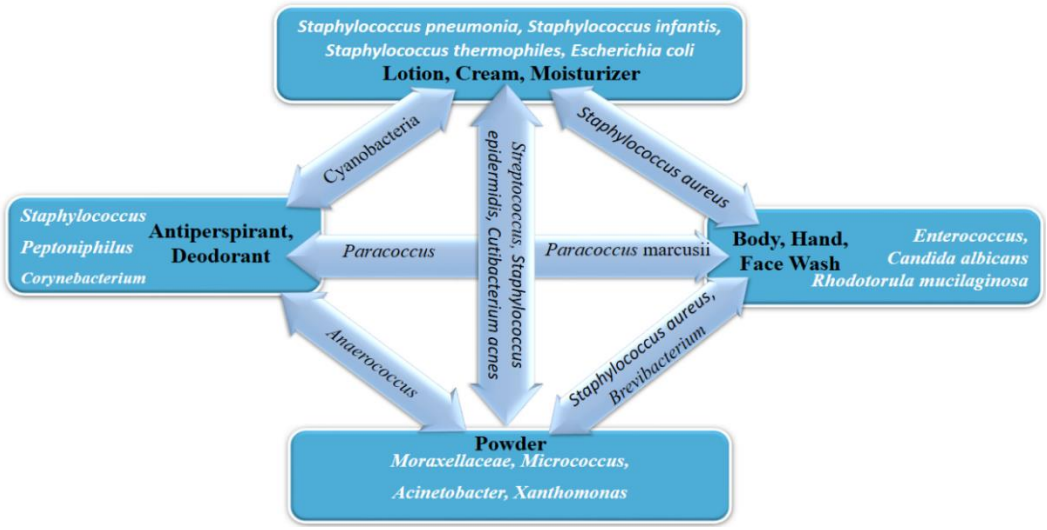


Figure 5. A diagram showing the specified and some common microbes changed directly by skin care products.

Figure 5 illustrates the type based microbial alteration. Lotion, Cream, Moisturizer changes *S. pneumonia*, *S.infantis*, *S.thermophiles*, *E.coli;* antiperspirant deodorant changes *Staphylococcus*, *Peptoniphilus*, *Corynebacterium;* powder changes Moraxellaceae, *Micrococcus*, *Acinetobacter*, *Xanthomonas;* body, hand, face wash changes *Enterococcus*, *Candida albicans*, *Rhodotorula mucilaginosa.* Their combined effects are shown as well.

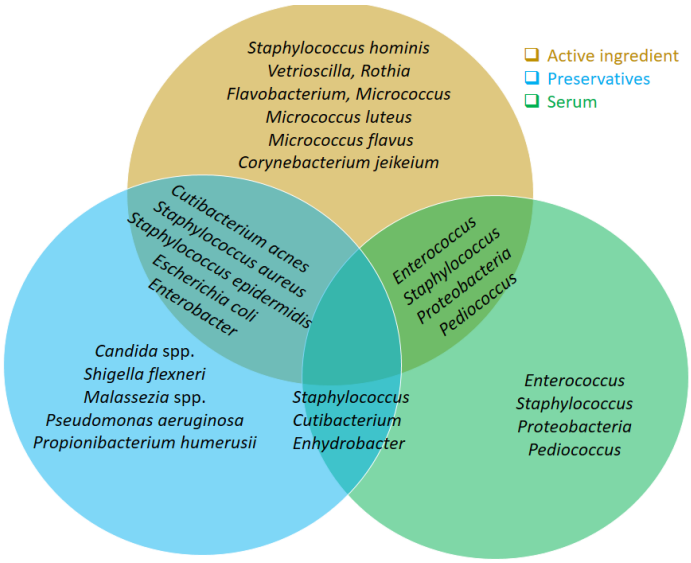


Figure 6. A Venn diagram showing the specified and some common microbes changed by basic ingredients used in skin care products. Different color code represents different groups (Bronze- Active ingredient; Blue- Preservative; Green- Serum).

The Venn diagram (Figure 6) shows microbial alteration by some common group of product types. Active ingredients and serum changes *Enterococcus*, *Staphylococcus*, *Proteobacteria*,

Pediococcus; active ingredients and serum changes *S. aureus, S. epidermidis, C. acnes, E. coli, Enterobacter;* preservatives and serum changes *Staphylococcus, Cutibacterium, Enhydrobacter.* They have effects individually as well.

3.4 Effective ways to determine skin microbiome and screening the cosmetics' response upon those

It is needed to fine some effective approaches to compare the skin microbiome after skin care products use for the determination of divergence from normal skin conditions. This would be a first step in determining a connection between a product's amount of synthetic ingredients and its impact on skin health. American dermatologist Albert Kligman initiated the first human microbiota research in dermatology in the 1950s with advanced cell culture methods (Dréno *et al.,* 2016; Pillsbury & Donald 1943). With the advancement in modern research techniques, the non-culturable newer forms of microbes homing in the surface and deeper layers of human skin can now be identified. Limitation of culture-dependent studies like detecting less than 1% bacterial species precisely (Staley and Konopka, 1985) can be overcome by molecular methods for instance by multi-omics approach integration (Bouslimani *et al.,* 2019). The 18S and 16S rRNA gene sequencing, DNA barcoding, PCR–denaturing gradient gel electrophoresis sequencing (Li *et al.,* 2014) etc. which allow for the detection of microbes found in low quantities. Even by studying the microbes generated chemicals through mass spectrometry visualization approach (Boya *et al.,* 2017), molecular networking can provide vast range of microbes studies (Bouslimani *et al.,* 2015).

Skin swabs, which represent the skin's surface, have been used as the basis for the majority of published research on the cutaneous microbiota. It is utilized as a sampling procedure because it is less invasive than punch biopsy, skin scraping, or tape removal, and it also lowers the potential of human DNA contaminating the sample. The skin should be stroked with the same number consistently and pressure throughout the entire sample procedure (Sfriso & Claypool, 2020). But the presence of microorganisms in the dermis and superficial adipose layer was shown by Nakatsuji *et al.* in 2013. Hence, surface based swabs might not be sufficient for analyzing the skin microbiota. Use of biopsy might overcome this problem. Along with the local anesthetic treatment, biopsy is done. This is mostly done in wounded skins.

After swabbing, biopsy or tape stripping (Kong *et al.,* 2017) which protocol is to follow will be determined by categories of microbe to be identified (Verbanic *et al.,* 2019). For checking

the ultimate outcomes due to different product application, use of artificial 3D skin model and leather skin model is being popular (Pinto *et al.*, 2021; Rademacher *et al.*, 2022). Other methods include screening via duel culture method, mass spectrophotometry (Coenye & Nelis, 2010; Gannesen *et al.*, 2019). The bioinformatics study can be included by having the effects of chemicals along with the bioactive products from microbes. The following figure (Figure 7) represents a work flow of identifying skin microbes with the probable approaches that can be taken for screening the cosmetics with skin microbial changes.

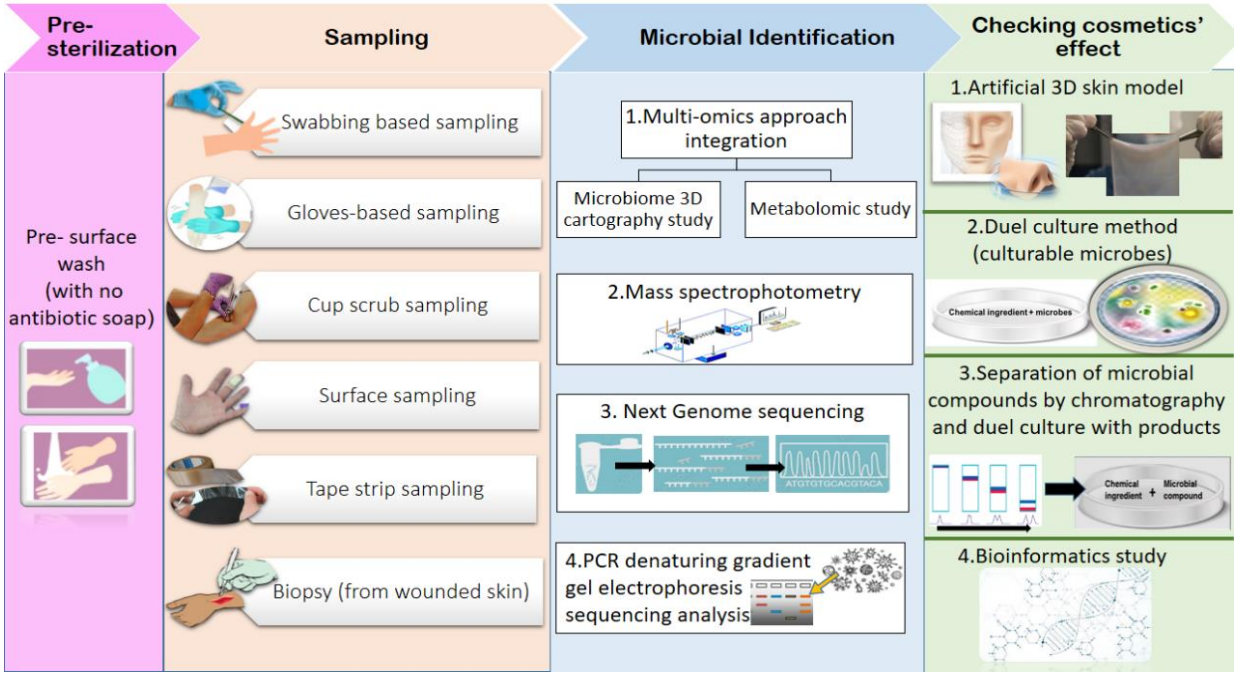


Figure 7. A work flow of skin microbe identification and screening of cosmetics' response upon the microbes.

Molecular approaches are appreciable but possess some counter-thoughts like they are not able to distinguish between the genes of living versus dead organisms, leading to a confusing result. So along with the whole genome sequencing, combination of skin models, cultural approaches are needed to get in depth scenario upon skin microbes.

3.5 Several consequences of altered microbiome

It is established that microbial alteration is intrigued by the use of different skin care products. 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 variety of favors in skin commensals. But we cannot ignore the other side of the coin. One of the consequences

that terrifies all is microbes misbalance causes their shifting from friend to foe for instance *C. acnes* (Dessinioti & Katsambas, 2010). Dysbiosis and altered microbial biodiversity of the skin microbiome has been linked with many diseases (McDonald *et al.,* 2016).

Table 4. Alteration of skin microbes causing skin diseases.

SL	Skin diseases	Skin microbes	References
1.	Acne	*Staphylococcus epidermidis*	(Brown & Horswill, 2020)
		Cutibacterium acnes	(Balato *et al.,* 2018)
2.	Atopic dermatitis	*Streptococcus*	(Coughlin *et al.,* 2017)
		Staphylococcus epidermidis	(Wang *et al.,* 2013)
		Malassezia species	(Grice, 2014)
		Staphylococcus aureus, *Staphylococcus epidermidis, Staphylococcus haemolyticus*	(Henley *et al.,* 2014)
3.	Psoriatic lesion	*Propiniumbacterium, Corynebctarium Streptococcus*	(Gonzalez *et al.,* 2016)
		Streptococcus, *Staphylococcus, Corynebacterium, Propionibacterium*	(Yerushalmi *et al.,* 2019)
4.	Rosacea	*Staphylococcus epidermidis Gordonia, Geobacillus*	(Zaidi *et al.,* 2018)
		Malassezia species	(Schommer & Gallo,2013)
5.	Folliculitis	*Malassezia* species	(Velegraki *et al.,* 2015)
6.	Skin allergies	*Staphylococcus aureus*	(Tsilochristou *et al.,* 2019)
		Acinetobacter lwoffii	(Fyhrquist *et al.,* 2014)

Regarding bodies defense mechanism, some ardently serious issues are involved. Shifting of normal microbiome of *Staphylococcus*, and in particular results in the disruption of skin immune system causing the natural antimicrobial bacteriocins production hampered (Christensen & Brüggemann, 2014). *Porphyromonas*, *Streptococcus, Peptostreptococcus, Sphingomonas, Stenotrophomonas, Anaerococcus*, *Staphylococcus, Corynebacterium* changes were related to wound healing process (Gardner *et al.,* 2013). Even skin cancer had proved to have connections with skin microbes (*S. epidermis*) (Nakatsuji *et al.,* 2018), viruses (Spurgeon & Lambert, 2013) notifying minor shifts resulting into catastrophe. These findings are important from an immunological point of view, as they suggest direct communication between microbial cells in skin and host health.

CHAPTER 4

CONCLUSION

Extra skin care products applied on skin disturb microbial diversity resulting noteworthy differences both positively and negatively. Preservatives, combination of them include sodium benzoate, hydroxyacetophenone, phenoxyethanol, phenylpropanol, copolymer, parabens, 1, 2-hexanediol, iodopropynyl butylcarbamate, ethylhexyl glycerin, methyliso thiazolinone and so on with a range of concentration (0.00125% to 0.4%) causing common skin dwellers' shifts. Different chemicals, extracts as active ingredients do so while some acts as a skin restorer (Actibiome). Apart from the conjugating effects products are seen to have individual effects changing *Staphylococcus pneumonia, Staphylococcus infantis, Staphylococcus thermophiles, Escherichia coli, Peptoniphilus, Corynebacterium, Xanthomonas, Micrococcus, Acinetobacter, Enterococcus, Candida albicans* etc. As *Staphylococcus aureus, Staphylococcus epidermis, Corenybacterium, Cutibacterium acnes, Malazzizia* species are mostly common on skin, they are seen to be altered by almost all types of skin care products.

Researches linked cosmetics with the microbial alteration by proper sampling to analyses. Arrays of sampling techniques such as swabbing (most popular), tape stripping, cup scrub, biopsy (for wounded skin) are applied prior to microbial identification. Instead of a sole method like culture-based strategy only (identifying around 1% of skin dwellers), modernized study tools alike artificial skin models, spectrophotometry, bioinformatics and metagenomic analysis are needed to be applied together for precise study.

No complete scenario has been found to declare a kind of product to be ubiquitously either positive or negative. Here comes the question that whether the negative scenario over crosses the positive ones or not. Nevertheless, further investigations regarding ages, locations, and body sites must be performed to gain a complete picture of the skin's microbiome, their complex interactions on applying diversified cosmetics, guaranteeing a healthy human.

REFERENCES

Balato, A., Cacciapuoti, S., Di Caprio, R., Marasca, C., Masarà, A., Raimondo, A., & Fabbrocini, G. (2018). Human microbiome: composition and role in inflammatory skin diseases. *Archivum Immunologiae et Therapiae Experimentalis*, *67*, 1-18.

Barbieri, J. S., Wanat, K., & Seykora, J. (2014).Skin: basic structure and function. *Elsevier*, 1134-1144.

Blaser, M. J., & Falkow, S. (2009). What are the consequences of the disappearing human microbiota? *Nature Reviews Microbiology*, *7*, 887-894.

Bouslimani, A., da Silva, R., Kosciolek, T., Janssen, S., Callewaert, C., Amir, A., Dorrestein, K., Melnik, A. V., Zaramela, L. S., & Kim, J.-N. (2019). The impact of skin care products on skin chemistry and microbiome dynamics. *BMC Biology*, *17*, 1-20.

Bouslimani, A., Porto, C., Rath, C. M., Wang, M., Guo, Y., Gonzalez, A., Berg-Lyon, D., Ackermann, G., Moeller Christensen, G. J., & Nakatsuji, T. (2015). Molecular cartography of the human skin surface in 3D. *Proceedings of the National Academy of Sciences*, *112*, 7, E2120-E2129.

Boya P, C. A., Fernández-Marín, H., Mejía, L. C., Spadafora, C., Dorrestein, P. C., & Gutiérrez, M. (2017). Imaging mass spectrometry and MS/MS molecular networking reveals chemical interactions among cuticular bacteria and pathogenic fungi associated with fungus-growing ants. *Scientific Reports*, *7*, 1, 5604.

Brown, M. M., & Horswill, A. R. (2020). *Staphylococcus epidermidis*—Skin friend or foe?. *PLoS Pathogens*, *16*, 11, e1009026.

Burnett, C. L., Bergfeld, W., Belsito, D. V., Klaassen, C. D., Marks, J. G., Shank, R. C., Slaga, T. J., Snyder, P. W., & Andersen, F. A. (2010). Final report of the safety assessment of methylisothiazolinone. *International Journal of Toxicology*, *29*, 187S - 213S.

Byrd, A. L., Belkaid, Y., & Segre, J. A. (2018). The human skin microbiome. *Nature Reviews Microbiology*, *16*, 3, 143-155.

Cao, M., Feng, T., & Zhang, X. (2017). Investigation on preservatives use in commercial cosmetics. *J Environ Hyg*, *7*, 4, 296-300.

Christensen, G. J. M., & Brüggemann, H. (2014). Bacterial skin commensals and their role as host guardians. *Beneficial Microbes*, *5*, *2*, 201-215.

Codif (2017). Actibiome: For a completely healthy and uniform complexion. Retrieved from https://www.codif-tn.com/wp-content/uploads/2017/09/ACTIBIOME-GB.pdf.

Coughlin, C. C., Swink, S. M., Horwinski, J., Sfyroera, G., Bugayev, J., Grice, E. A., & Yan, A. C. (2017). The preadolescent acne microbiome: A prospective, randomized, pilot study investigating characterization and effects of acne therapy. *Pediatric Dermatology*, *34*, 661 - 664.

Dessinioti, C., & Katsambas, A. D. (2010). The role of *Propionibacterium acnes* in acne pathogenesis: facts and controversies. *Clinics in Dermatology, 28 1*, 2-7.

Draelos, Z. D. (2005). Cosmetic formulation of skin care products. *In Cosmetic Formulation of Skin Care Products*, 25-26, CRC Press.

Filaire, E., Vialleix, C., Cadoret, J. P., Dreux, A., & Berthon, J. Y. (2019). ExpoZen®: an active ingredient modulating reactive and sensitive skin microbiota.

Finlay, B. B., & Arrieta, M. C. (2016). *Let Them Eat Dirt: Saving Your Child from an Oversanitized World*. Greystone Books. https://books.google.com.bd/books?id=hOslDQAAQBAJ.

Fournière, M., Latire, T., Souak, D., Feuilloley, M. G., & Bedoux, G. (2020). Staphylococcus epidermidis and Cutibacterium acnes: two major sentinels of skin microbiota and the influence of cosmetics. *Microorganisms, 8*, 11, 1752.

Fukase, H. (2005). Percutaneous absorption study of Kojic Acid in humans. *CPC Clinic,* Medical facility, Kagoshima, Japan.

Fyhrquist, N., Ruokolainen, L., Suomalainen, A., Lehtimäki, S., Veckman, V., ….. & Alenius, H. (2014). Acinetobacter species in the skin microbiota protect against allergic sensitization and inflammation. *The Journal of Allergy and Clinical Immunology*, *134 6*, 1301-1309.e1311.

Gallo, R. L. (2017). Human skin is the largest epithelial surface for interaction with microbes. *Journal of Investigative Dermatology*, *137*, 6, 1213-1214.

Gardner, S. E., Hillis, S. L., Heilmann, K. P., Segre, J. A., & Grice, E. A. (2013). The Neuropathic Diabetic Foot Ulcer Microbiome Is Associated With Clinical Factors. *Diabetes*, *62*, 923 - 930.

Gonzalez, M. E., Schaffer, J. V., Orlow, S. J., Gao, Z., Li, H., Alekseyenko, A. V., & Blaser, M. J. (2016). Cutaneous microbiome effects of fluticasone propionate cream and adjunctive bleach baths in childhood atopic dermatitis. *Journal of the American Academy of Dermatology*, *75 3*, 481-493.e488.

Grice, E. A. (2014). The skin microbiome: potential for novel diagnostic and therapeutic approaches to cutaneous disease. *Seminars In Cutaneous Medicine And Surgery*, *33 2*, 98-103.

Henley, J. B., Ing, R. M. M., & Hana Zelenkova, M. D. (2014). Microbiome of affected and unaffected skin of patients with atopic dermatitis before and after emollient treatment. *Journal of Drugs in Dermatology, 13*, 11,1365-1372.

Holland, K. T., & Bojar, R. A. (2002). Cosmetics: what is their influence on the skin microflora? *American Journal Of Clinical Dermatology*, *3*, 7, 445-449.

Hong, K. B., Hong, Y. H., Jung, E. Y., Jo, K., & Suh, H. J. (2020). Changes in the diversity of human skin microbiota to cosmetic serum containing prebiotics: Results from a randomized controlled trial. *Journal of Personalized Medicine, 10,* 3, 91.

Howard, B., Bascom, C. C., Hu, P., Binder, R. L.,….& Isfort, R. J. (2022). Aging-associated changes in the adult human skin microbiome and the host factors that affect skin microbiome composition. *Journal of Investigative Dermatology*, *142*, 7, 1934-1946.

Jeong, J. J., & Kim, D. H. (2015). Effects of cosmetics and their preservatives on the growth and composition of human skin microbiota. *Journal of the Society of Cosmetic Scientists of Korea*, *41*, 2, 127-134.

Jillian Kubala (2020, April 6). Do You need supplements for better skin? here's what the science says. Healthline. https://www.healthline.com/health/beauty-skin-care/supplements-for-better-skin.

Kim, G., Kim, M., Kim, M., Park, C., Yoon, Y., Lim, D. H., ... & Lee, D. G. (2021). Spermidine-induced recovery of human dermal structure and barrier function by skin microbiome. *Communications Biology*, *4*, 1, 231.

Kong, H. H., Andersson, B., Clavel, T., Common, J. E., Jackson, S. A., Olson, N. D., Segre, J. A., & Traidl-Hoffmann, C. (2017). Performing skin microbiome research: a method to the madness. *Journal of Investigative Dermatology*, *137*, 3, 561-568.

Larson, E. (1999). Skin hygiene and infection prevention: more of the same or different approaches?. *Clinical Infectious Diseases*, *29*, 5, 1287-1294.

Le Bourgot, C., Meunier, C., Gaio, E., Murat, V., Micheletto, M., Tedesco, E., & Benetti, F. (2022). Effects of short chain fructo-oligosaccharides on selected skin bacteria. *Scientific Reports*, *12*, 1, 9702.

Lee, H. J., Jeong, S. E., Lee, S., Kim, S., Han, H., & Jeon, C. O. (2018). Effects of cosmetics on the skin microbiome of facial cheeks with different hydration levels. *Microbiologyopen*, *7*, 2, e00557.

Li, H., Goh, B. N., Teh, W. K., Jiang, Z., Goh, J. P. Z., Goh, A., Wu, G., Hoon, S. S., Raida, M., & Camattari, A. (2018). Skin commensal Malassezia globosa secreted protease attenuates Staphylococcus aureus biofilm formation. *Journal of Investigative Dermatology*, *138*, 5, 1137-1145.

Li, W., Han, L., Yu, P., Ma, C., Wu, X., & Xu, J. (2014). Nested PCR-denaturing gradient gel electrophoresis analysis of human skin microbial diversity with age. *Microbiological Research*, *169*, 9-10, 686-692.

McCoy, W. H., Otchere, E., Rosa, B. A., Martin, J., Mann, C. M., & Mitreva, M. D. (2019). Skin Ecology during Sebaceous Drought-How Skin Microbes Respond to Isotretinoin. *The Journal of Investigative Dermatology*, *139* , 3, 732-735.

McDonald, D., Ackermann, G., Khailova, L., Baird, C., Heyland, D., Kozar, R., ... & Wischmeyer, P. E. (2016). Extreme dysbiosis of the microbiome in critical illness. *Msphere*, *1*, 4, e00199-16.

Michelle, S., Steve, W. L., & Thomas, W.(2016). Efficacy and mechanism of selenium nanoparticles as antibacterial agents. *Frontiers in Bioengineering and Biotechnology*, *4*.

Murphy, B., Grimshaw, S., Hoptroff, M., Paterson, S., Arnold, D., Cawley, A., Adams, S. E., Falciani, F., Dadd, T., Eccles, R., Mitchell, A., Lathrop, W. F., Marrero, D., Yarova, G., Villa, A., Bajor, J. S., Feng, L., Mihalov, D., & Mayes, A. E. (2022). Alteration of barrier properties, stratum corneum ceramides and microbiome composition in response to lotion application on cosmetic dry skin. *Scientific Reports*, *12*, 1, 5223.

Murphy, B., Hoptroff, M., Arnold, D., Eccles, R., & Campbell-Lee, S. (2021). In-vivo impact of common cosmetic preservative systems in full formulation on the skin microbiome. *PLoS One*, *16*, 7, e0254172.

Myles, I. A., Williams, K. W., Reckhow, J. D., Jammeh, M. L., Pincus, N. B., Sastalla, I., Saleem, D., Stone, K. D., & Datta, S. K. (2016). Transplantation of human skin microbiota in models of atopic dermatitis. *JCI Insight*, *1*, 10.

Nakatsuji, T., Chen, T. H., Butcher, A. M., Trzoss, L. L., Nam, S. J., Shirakawa, K. T., ... & Gallo, R. L. (2018). A commensal strain of *Staphylococcus epidermidis* protects against skin neoplasia. *Science Advances*, *4*, 2, 4502.

Nakatsuji, T., Chiang, H. I., Jiang, S. B., Nagarajan, H., Zengler, K., & Gallo, R. L. (2013). The microbiome extends to subepidermal compartments of normal skin. *Nature Communications*, *4*, 1, 1431.

Neza, E., & Centini, M. (2016). Microbiologically contaminated and over-preserved cosmetic products according Rapex 2008–2014. *Cosmetics*, *3*, 1, 3.

Noleo (2022, 17 October). How does a product become certified microbiome-friendly? Noleocare. Retrieved from: https://www.noleocare.com/blogs/news/how-does-a-product-become-certified-microbiome-friendly.

Petkovšek, Z., Eleršič, K., Gubina, M., Zgur-Bertok, D., & Starčič Erjavec, M. (2009). Virulence potential of Escherichia coli isolates from skin and soft tissue infections. *Journal Of Clinical Microbiology*, *47*, 6, 1811-1817.

Pillsbury, Donald M. M. D. (1943). Manual of dermatology. *American Journal of Nursing*, 43, 8, 91.

Pinto, D., Ciardiello, T., Franzoni, M., Pasini, F., Giuliani, G., & Rinaldi, F. (2021). Effect of commonly used cosmetic preservatives on skin resident microflora dynamics. *Scientific Reports*, *11*, 1, 1-7.

Probst, A. J., Auerbach, A. K., & Moissl-Eichinger, C. (2013). Archaea on human skin. *PLoS One*, *8*, 6, e65388.

Rademacher, M., Zinn, M.-K., Beinio, R., & Bockmühl, D. P. (2022). A new model to investigate the effects of cosmetics on skin microorganisms in vitro.*Cosmetics*, *9*, 4, 88.

Rippke, F., Berardesca, E., & Weber, T. (2018). ph and microbial infections. *Current Problems in Dermatology*, 54, 87-94.

Rosenthal, M., Aiello, A. E., Larson, E. L., Chenoweth, C. E., & Foxman, B. (2013). Healthcare workers' hand microbiome may mediate carriage of hospital pathogens. *Pathogens, 3*, 1 - 13.

Samaras, S., & Hoptroff, M. (2020). The Microbiome of Healthy Skin. *Skin Microbiome Handbook: From Basic Research to Product Development*, 1-32.

Scherrer, M. A. R., Rocha, V. B., & Andrade, A. R. C. (2015). Contact dermatitis to methylisothiazolinone. *Anais Brasileiros De Dermatologia, 90*, 912-914.

Schommer, N. N., & Gallo, R. L. (2013). Structure and function of the human skin microbiome. *Trends in Microbiology, 21, 12*, 660-668.

Sfriso, R., & Claypool, J. (2020). Microbial reference frames reveal distinct shifts in the skin microbiota after cleansing. *Microorganisms, 8*, 11, 1634.

Sfriso, R., Egert, M., Gempeler, M., Voegeli, R., & Campiche, R. (2020). Revealing the secret life of skin-with the microbiome you never walk alone. *International journal of Cosmetic Science, 42*, 2, 116-126.

Shankar (2021, February).Cosmetics market by category, gender and distribution channel: opportunity analysis and industry forecast, 2021–2027. Allied market research. Retrieved from: https://www.alliedmarketresearch.com/press-release/cosmetics-market.html.

Šikić, P. M., Maver, U., Marčun Varda, N., & Mičetić-Turk, D. (2018). Diagnosis and management of diaper dermatitis in infants with emphasis on skin microbiota in the diaper area. *International Journal of Dermatology, 57*.

Simon Pitman (2016, June 23). Joomo makes claim to world's first 100% natural face wash. Retrieved from: https://www.cosmeticsdesign-europe.com/Article/2016/06/24/Joomo-makes-claim-to-world-s-first-100-natural-face-wash.

Spurgeon, M. E., & Lambert, P. F. (2013). Merkel cell polyomavirus: a newly discovered human virus with oncogenic potential. *Virology, 435*, 1, 118–130.

Staudinger, T., Pipal, A., & Redl, B. (2011). Molecular analysis of the prevalent microbiota of human male and female forehead skin compared to forearm skin and the influence of make-up. *Journal of Applied Microbiology, 110*, 6,1381-1389.

Tsilochristou, O., du Toit, G., Sayre, P. H., Roberts, G. C., Lawson, K., Sever, M. L., Bahnson, H. T., Radulovic, S., Basting, M., Plaut, M., & Lack, G. (2019). Association of *Staphylococcus aureus* colonization with food allergy occurs independently of eczema severity. *Journal of Allergy and Clinical Immunology, 144*, 2, 494-503.

Two, A. M., Nakatsuji, T., Kotol, P., Arvanitidou, E., Du-Thumm, L., Hata, T. R., & Gallo, R. L. (2016). The Cutaneous Microbiome and Aspects of Skin Antimicrobial Defense System Resist Acute Treatment with Topical Skin Cleansers. *The Journal of Investigative Dermatology, 136,* 10, 1950-1954.

Urban, J., Fergus, D. J., Savage, A. M., Ehlers, M., Menninger, H. L., Dunn, R. R., & Horvath, J. E. (2016). The effect of habitual and experimental antiperspirant and deodorant product use on the armpit microbiome. *PeerJ, 4*, e1605.

Velegraki, A., Cafarchia, C., Gaitanis, G., Iatta, R., & Boekhout, T. (2015). Malassezia infections in humans and animals: pathophysiology, detection, and treatment. *PLoS Pathogens*, *11*, 1, e1004523.

Verbanic, S., Kim, C. Y., Deacon, J. M., & Chen, I. A. (2019). Improved single-swab sample preparation for recovering bacterial and phage DNA from human skin and wound microbiomes. *BMC Microbiology, 19*, 1, 1-13.

Wallen-Russell, C. (2018). The role of every-day cosmetics in altering the skin microbiome: a study using biodiversity. *Cosmetics*, *6*, 1, 2.

Wallen-Russell, C., & Wallen-Russell, S. (2017). Meta analysis of skin microbiome: new link between skin microbiota diversity and skin health with proposal to use this as a future mechanism to determine whether cosmetic products damage the skin. *Cosmetics*, *4*, 2, 14.

Wang, Q., Cui, S., Zhou, L., He, K., Song, L., Liang, H., & He, C. (2018). Effect of cosmetic chemical preservatives on resident flora isolated from healthy facial skin. *Journal of Cosmetic Dermatology*, *18*, 652 - 658.

Wang, Y., Kuo, S., Shu, M., Yu, J., Huang, S., Dai, A., Two, A. M., Gallo, R. L., & Huang, C.M. (2013). *Staphylococcus epidermidis* in the human skin microbiome mediates fermentation to inhibit the growth of *Propionibacterium acnes*: implications of probiotics in acne vulgaris. *Applied Microbiology and Biotechnology*, *98*, 411-424.

Wollny, H. E. (1998). *Salmonella typhimurium* and *Escherichia coli* reverse muation assay with kojic acid. *RCC-CCR Project Number*, *612701*.

Yerushalmi, M., Elalouf, O., Anderson, M., & Chandran, V. (2019). The skin microbiome in psoriatic disease: a systematic review and critical appraisal. *Journal of Translational Autoimmunity, 2*, 100009.

Zaidi, A. K., Spaunhurst, K., Sprockett, D., Thomason, Y., Mann, M. W., Fu, P., ... & Popkin, D. L. (2018). Characterization of the facial microbiome in twins discordant for rosacea. *Experimental Dermatology*, *27*, 3, 295-298.

Zapka, C., Leff, J., Henley, J., Tittl, J., De Nardo, E., Butler, M., ... & Edmonds-Wilson, S. (2017). Comparison of standard culture-based method to culture-independent method for evaluation of hygiene effects on the hand microbiome. *MBio*, *8*, 2, e00093-17.

Zhou, Y., Gao, H., Mihindukulasuriya, K. A., La Rosa, P. S., Wylie, K. M., Vishnivetskaya, T., ... & Weinstock, G. M. (2013). Biogeography of the ecosystems of the healthy human body. *Genome Biology, 14*, 1-18.