

ORIGINAL ARTICLE

Skin aging-related microbial types separated by *Cutibacterium* and α -diversity

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Abstract

Background: Studies on the skin microbiome have been conducted to uncover the relationship between skin microbes and the host. However, most of these studies have primarily focused on analyzing individual microbial compositions, which has resulted in a limited understanding of the overall relationship.

Methods: We analyzed the facial skin characteristics and microbial profiles of 100 healthy Korean female volunteers using the V1-V2 region of the 16S ribosomal RNA gene.

Results: The two most prominent features of the facial skin microbiome, the proportion of *Cutibacterium* and α -diversity, were associated with most of the skin characteristics. Based on clustering results, we proposed four types of facial skin microbiome: type C for *Cutibacterium*, type B for balanced, type CB for those between types C and B, and type O for others. Type C, which has a high proportion of *Cutibacterium*, showed high levels of pigmentation, wrinkles, pores, and sagging pores, indicating a tendency for severe skin aging. Type B, which has no dominant species and high microbial diversity, had lower values for pigmentation and wrinkles indicating less severe skin aging. Type CB was an intermediate type between type C and type B in terms of microbial composition and the level of skin aging. Type O dominated by microorganisms other than *Cutibacterium*, had high levels of sebum and pores but low levels of wrinkles.

Conclusion: We proposed a criterion for classifying facial skin microbial types, each of which showed distinct facial skin aging features. Our simplified microbial types will contribute to a better understanding of facial skin microbial studies.

KEYWORDS

facial skin characteristics, facial skin microbiome, microbial type of facial skin, skin aging

Sangseob Leem, Hye Lim Keum and Hae Jung Song are contributed equally.

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1 | INTRODUCTION

The relationship between skin aging and microorganisms has been well established, with numerous studies indicating that microorganisms play a role in the aging process of the skin.^{1,2} The facial skin microbiome is composed of many abundant genera, including *Cutibacterium* (formerly *Propionibacterium*), *Enhydrobacter*, *Staphylococcus*, *Bacteroides*, *Acinetobacter*, *Corynebacterium*, and *Streptococcus*.^{3–7} Among these dominant genera, *Cutibacterium*, which includes *Cutibacterium acnes*, is the most abundant in many individuals and is known to have age-related characteristics, as it tends to be found in higher concentrations in younger populations.⁵ Additionally, α -diversity, measured by the Shannon index, has also been shown to be related to age, with low diversity in young individuals and high diversity in the elderly.⁵ Aside from the relationship with age, these two factors have significant relationships with the skin characteristics, so they are widely used in research on the relationship between skin and microorganisms.

In recent times, advanced analyses including microbial typing have been conducted, which have the potential to yield more comprehensive results and enhanced utility. For example, in a study of the gut microbiome, enterotypes were defined and their association with long-term diet was discovered.⁸ Also, in the case of skin microbiome, two studies identified the microbial subtypes of the female skin using principal coordinate analysis and functional analysis.^{6,7} These studies highlighted the importance of functional studies and provided clues about microbial types on our body. However, the type classifiers in these studies were counter-intuitive and complex to use for actual type classifications.

In this study, we focused on the two most representative indicators, *Cutibacterium* and the Shannon index, to classify facial skin microbiome types. Rather than comparing the skin microbiome simply by age, we sought to find a meaningful way to classify microbial types using skin aging features. To prevent misunderstandings due to chronological age, age-adjusted analyses were performed. Our results showed that, when compared in the same age group, healthy skin has higher microbial diversity, consistent with the general trend. The samples were then divided into four skin types based on the Shannon index and the proportion of *Cutibacterium*. Finally, we found significant differences in skin aging characteristics between each type. The type classification system developed in this study improves our ability to interpret and explain the results in the field of microbial research, as well as facilitating the explanation of skin conditions to consumers.

2 | MATERIALS AND METHODS

2.1 | Study participants and sampling method

A total of 101 healthy Korean women aged 18–70 years old, without any skin diseases such as acne vulgaris and psoriasis, were recruited in Seoul, and their skin microbiomes were sampled from November 18 to November 22, 2019. Basic characteristics of the

participants are summarized in Table 1. They were fully informed of the study and provided written consent after reading the research protocol, which was approved by the institutional review board. All research was conducted in accordance with relevant guidelines and regulations.

On the day before sampling, participants were instructed to clean their facial skin before 10:00 p.m. On the following day, their facial skin microbiome was collected from the right cheek using the MySkin® kit (sampling tape) according to the manufacturer's protocol. The sampling was performed at the Research Center of LG H&H without any makeup or cleansing on the skin. Participants were then instructed to cleanse their face and wait in a room with a constant temperature (20–24°C) and humidity (40%–60%) for 30 min. After skin stabilization, the facial skin characteristics were measured using the Janus-III measurement system.

2.2 | Measurement of skin characteristics by Janus-III

Using the Janus-III measurement system, three images of the participants' faces were captured using different light sources (normal, polarized, and ultraviolet). The images were then segmented into the forehead, beside left/right eyes, under left/right eyes, nose, and left/right cheeks. In cases of poor segmentation, manual adjustments were made. Pores, wrinkles, and pigmented spots were calculated as the weighted sum of areas separated by color differences with adjacent pixels, with values ranging from 0 to 100. Facial skin color was extracted from the left and right cheeks using the CIE-LAB space. Sebum and porphyrin were evaluated by counting the fluorescent dots above a certain size and dividing them into sebum or porphyrin based on color criteria. The values of sebum and porphyrin were then log-transformed before analysis.

2.3 | Bacterial community analysis

The library construction and sequencing were conducted by TAK Inc. (Japan) using the V1–V2 region of the 16S ribosomal RNA (rRNA) gene. During the extraction process, one sample was excluded due to low quality control as determined by the MySkin® protocol. The V1–V2 region of the 16S rRNA gene was amplified using the primers 28F (5'-GRGTTTGATYMTGGCTCAG-3') and 338R (5'-TGCTGCCTCCGTTAGGAGT-3').

On average, 46,987 reads were obtained from 100 samples, and community analysis was performed with an average of 42,763 reads after quality control using DADA2⁹ and the QIIME2¹⁰ pipeline. The analysis was performed at the genus level as assigned by the Greengenes¹¹ reference database. For evaluating microbial diversity, the Shannon index was used to quantify the number of discovered taxa and their evenness. The Jensen–Shannon divergence was used as a distance metric to measure the β -diversity of the microbiome, considering both the presence/absence of taxonomy and differences

TABLE 1 Characteristics of study participants.

Characteristics	Distribution			
	Mean		Standard deviation	
Age	40.5 years		15.5 years	
Height	160.2 cm		6.2 cm	
Weight	55.6 kg		7.9 kg	
Sun exposure per day	Long-term (≥ 3 h)	Daily exposure	Short-time (< 1 h)	
	11 (11%)	22 (22%)	67 (67%)	
Sun block usage	Never	Seldom	Always	
	12 (12%)	25 (25%)	63 (63%)	
Outdoor activities	Frequent (≥ 3 times)	Mainly on weekends	Rare	
	43 (43%)	42 (42%)	15 (15%)	
Smoking	Regular (every day)	Occasionally	Non-smoking	
	0 (0%)	2 (2%)	98 (98%)	
Meat diet	Frequent (≥ 4 times)	2–3 times per week	One times per week	Vegetarian
	19 (19%)	51 (51%)	27 (27%)	3 (3%)

in relative abundances, particularly in taxa that are present in multiple samples with drastic differences in abundance. PICRUST2¹² was used to infer the gene contents of the microbial community and map them to KEGG pathways.¹³

2.4 | Statistical analysis

All statistical analyses and visualization were carried out using R (version 3.6.1). Linear regressions were used for association tests and residuals calculation with age adjustments because age was strongly associated with both skin characteristics and microbial features such as *Cutibacterium* and Shannon index. The Kruskal–Wallis test was used to compare skin characteristics (after adjusting for age) between microbial types, while the Jonckheere–Terpstra test was used for ordered trend tests. False-discovery rates were calculated using the Benjamini–Hochberg procedure to adjust for multiple testing. Hierarchical clustering, partitioning around method, and density-based clustering were used to identify distinct microbial clusters and defined types. The functions of skin microbes that were most likely to explain differences among the facial skin microbial types were predicted using linear discriminant analysis (LDA) effect size analysis,¹⁴ with a minimum LDA score of 2.0 and a “one-against-one” testing option.

3 | RESULTS

3.1 | Association between skin microbiome and skin characteristics

Linear regression tests were performed to assess the relationship between skin characteristics and representative microbial factors, the Shannon index and *Cutibacterium* (Table 2). The results showed

that facial pigmented spots-polarized light (FPS-PL), sagging pores, pores, LAB-a*, sebum, and porphyrin had negative associations with the Shannon index and positive associations with the proportion of *Cutibacterium*. LAB-L* showed a negative association only with *Cutibacterium*. The beta coefficient signs of the linear regression results for the Shannon index and *Cutibacterium* proportion were opposite directions, but the association significance (*p*-value) was similar for each skin trait.

In summary, more age-related skin features were observed when the abundance of *Cutibacterium* was relatively higher and the Shannon index was relatively lower in the subjects. The skin features such as pigment spots, pores, skin redness, and skin darkening were more prominent in *Cutibacterium*-rich subjects (Table 3).

3.2 | Microbial types of facial skin

We applied clustering methods to determine the microbial types of facial skin and compared the results. Through hierarchical clustering of 100 samples based on the relative abundance of skin bacteria, three distinct clusters were identified, as shown by the thick black squares in Figure 1. The Shannon index decreased from left to right, and this decrease in diversity generally coincided with the increase in *Cutibacterium*, except for the rightmost group, where Neisseriaceae (classified only at the family level) were dominant.

As results of applying clustering methods, groups were distinguished based on the proportion of *Cutibacterium* and the Shannon index, and the isolated group dominated by other genera was clearly separated from other groups (Figure 2A–H). Accordingly, we defined the microbial types using the two most prominent factors in the facial skin microbiome, the Shannon index and the abundance of *Cutibacterium*, as classification criteria (Figure 2I). A regression line of $4C + S = 4$ was found between the Shannon index and the proportion

TABLE 2 Relationship between the skin microbiome and skin characteristics.

Skin characteristics	Shannon index		Cutibacterium		Age	
	Beta coefficient	p-value (FDR)	Beta coefficient	p-value (FDR)	Beta coefficient	p-value (FDR)
FPS-PL	-1.534	2.5E-02 (4.2E-02)	6.637	1.7E-03 (5.7E-03)	0.574	1.9E-30 (1.9E-29)
FPS-UV	0.345	7.4E-01 (7.4E-01)	5.139	1.1E-01 (1.2E-01)	0.732	2.0E-25 (1.0E-24)
Wrinkles	-0.780	4.6E-01 (5.1E-01)	5.996	6.6E-02 (8.2E-02)	0.498	1.1E-15 (3.7E-15)
Sagging pores	-4.866	2.4E-04 (6.0E-04)	11.969	4.2E-03 (7.0E-03)	0.372	3.0E-07 (4.3E-07)
Pores	-3.880	3.3E-05 (1.1E-04)	8.635	3.7E-03 (7.0E-03)	0.397	8.0E-13 (1.6E-12)
LAB-L*	0.706	5.1E-02 (7.3E-02)	-2.829	1.2E-02 (1.7E-02)	-0.088	3.9E-06 (4.9E-06)
LAB-a*	-0.701	4.5E-03 (9.0E-03)	2.278	3.0E-03 (7.0E-03)	0.072	9.1E-08 (1.5E-07)
LAB-b*	-0.415	1.8E-01 (2.3E-01)	1.221	2.0E-01 (2.0E-01)	0.126	8.0E-13 (1.6E-12)
Sebum	-1.475	2.3E-11 (2.3E-10)	4.131	4.6E-09 (4.6E-08)	-0.043	7.0E-04 (7.0E-04)
Porphyryn	-1.357	1.8E-09 (9.0E-09)	3.755	1.7E-07 (8.5E-07)	-0.044	4.9E-04 (5.4E-04)

Note: *p*-values and beta coefficients were calculated using linear regression with an age covariate. Significant *p*-values (<0.05) and the corresponding beta coefficient values are shown in bold.

Abbreviations: FPS-PL, facial pigmented spots-polarized light; FPS-UV, facial pigmented spots-ultraviolet light.

TABLE 3 Summary of the attributes of each classified group.

Type	(a) Microbial characteristics		(b) Skin characteristics		(c) Microbial functional characteristics
	Cutibacterium	Shannon index	FPS-PL, wrinkles, and darkening of skin color	Pore, sagging pores, sebum, and porphyryn	
C	High	Low	High	High	Carbohydrate and lipid metabolism-related pathways
CB	Moderate	Moderate	Moderate	Moderate	–
B	Low	High	Low	Low	Xenobiotic biodegradation and DNA repair-related pathways
O	Low	Low	Low	High	Bacterial cell growth and death

Note: Darkening of skin color represents decrease of L* value.

of *Cutibacterium*, where C and S represent the relative abundance of *Cutibacterium* and the Shannon index, respectively.

The classification process consisted of the following steps. First, samples with $4C+S<3.2$ were classified as type O, which was far from the regression line. Among the remaining samples, those with $4C-S>1$ were classified as type C, those with $-1.6\leq 4C-S\leq 1$ were classified as type CB, and those with $4C-S<-1.6$ were classified as type B. Comparison of sample distances showed that the average between-group distance (0.283) was 1.5 times greater than the average within-group distance (0.189).

The proposed model divided the samples into four microbial types: C ($n=22$, 22%), CB ($n=41$, 41%), B ($n=22$, 22%), and O ($n=15$, 15%) (Figure 2b, Table 3(a)). Type C was abundant in *Cutibacterium* and had low values of the Shannon index, while type B was a balanced microbial composition with relatively low *Cutibacterium* and high Shannon index values. Type CB had properties intermediate between types C and B, and type O was independent of the pattern, with both low values of *Cutibacterium* and Shannon index. Type O was dominated by several major genera other than *Cutibacterium*, including *Neisseriaceae* (F), *Staphylococcus*, and *Enhydrobacter*.

3.3 | Differences in skin characteristics among microbial types

To verify the relevance of type classification in skin aging research, we compared and analyzed differences in skin characteristics based on microbial type (Figure 3) and briefly summarized them in Table 3. With the exception of facial pigmented spots-ultraviolet light (FPS-UV) and LAB-b*, all other skin characteristics showed a clear difference between type C and type B. Type C had more severe skin aging-related features such as pigmentation, wrinkles, pores, and sagging pores. Additionally, type C had darker, redder skin, and higher levels of sebum and porphyryn. On the contrary, type B did not have high values for these skin characteristics and had a lower overall degree of skin aging. Type O had high levels of sagging pores, pores, sebum, porphyryn, and LAB-L*, but low levels of FPS-PL, and wrinkles. Type O was similar to type C in its high levels of sebum and pores, but different from type C in that it had low levels of FPS-PL and wrinkles.

Furthermore, we examined the trend of skin characteristics among the four microbial types by aligning their values (Table 4). The *p*-value of the Kruskal-Wallis test indicates the statistical

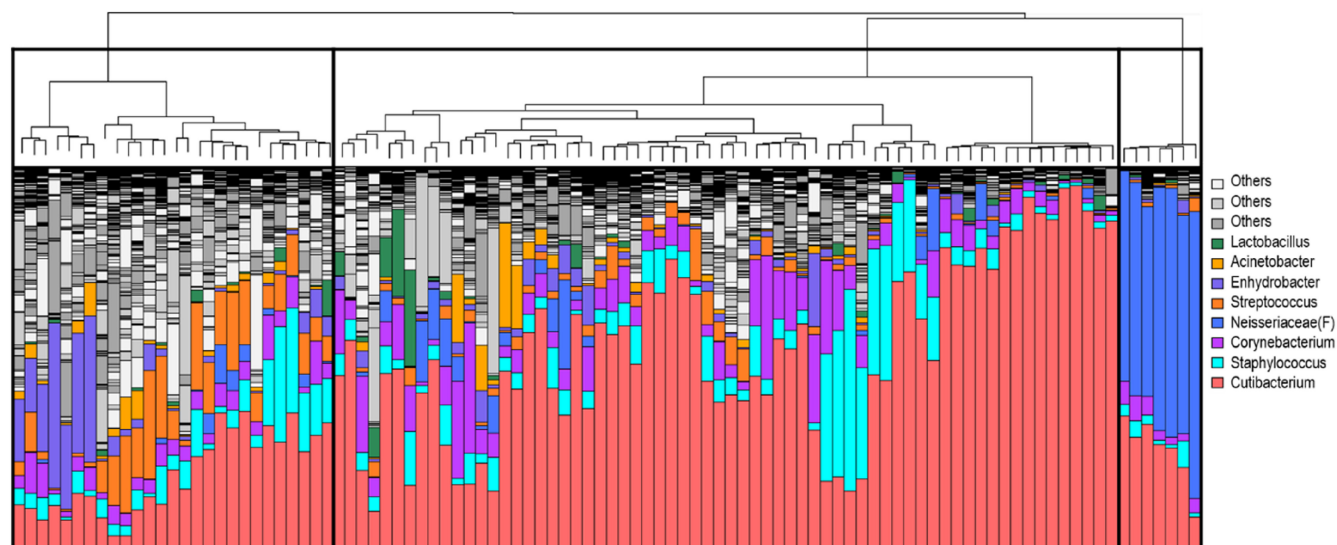


FIGURE 1 Hierarchical clustering of skin microbiome composition across all subjects. Hierarchical clustering was performed using Ward's method in which the distance between two groups was determined as the error sum of the squares. Black rectangles represent the groups of dividing into three clusters.

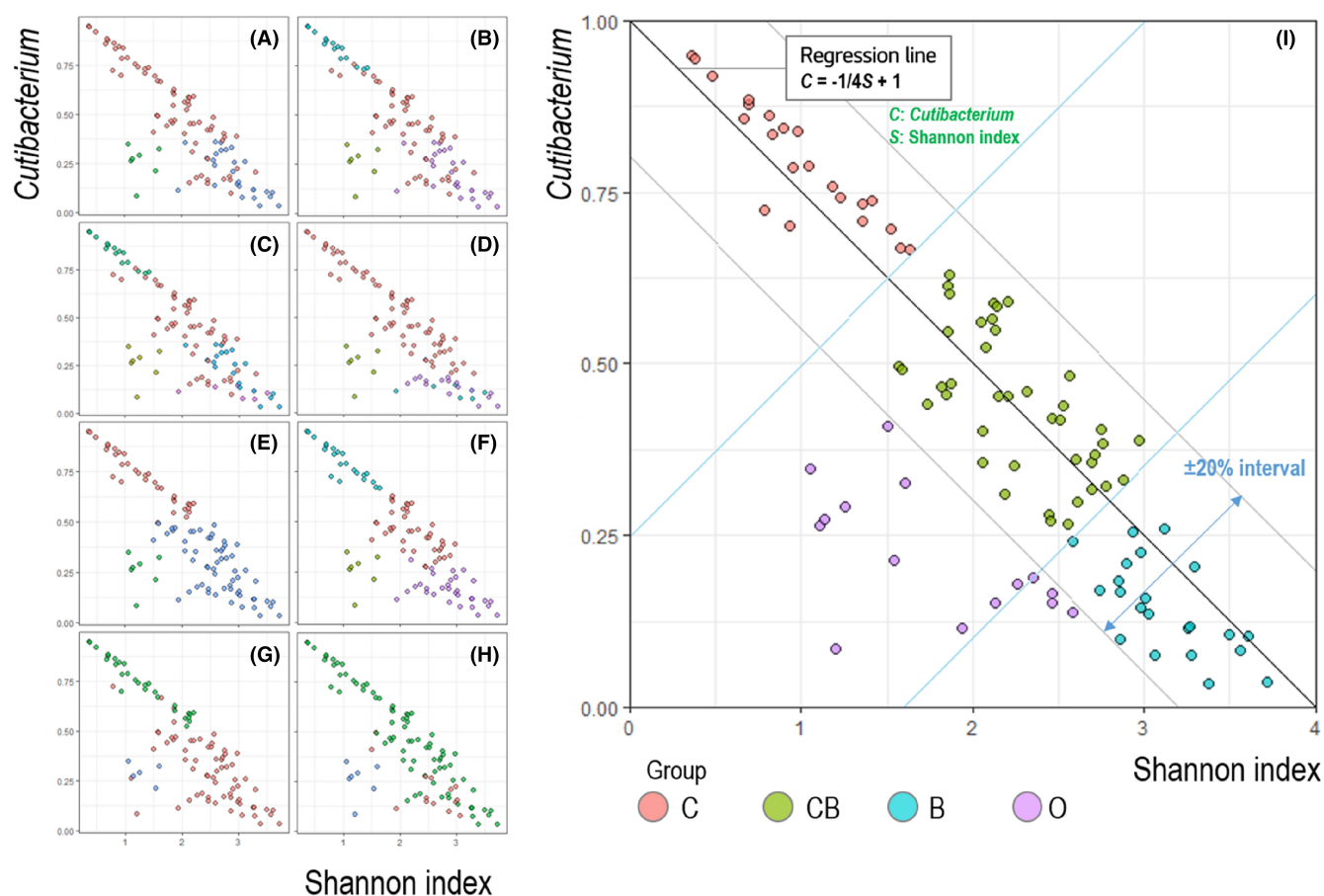


FIGURE 2 Clustering results and proposal of microbial type classification criteria for the comparison with the clustering results: (A) hierarchical clustering ($k=3$), (B) hierarchical clustering ($k=4$), (C) hierarchical clustering ($k=5$), (D) clustering based on the most dominant genus, (E) partitioning around method ($k=3$), (F) partitioning around method ($k=4$), (G) density-based clustering (eclipse=1.96 times standard deviance of distances), (H) density-based clustering (eclipse=standard deviance of distances) and (I) classification criteria of microbial type.

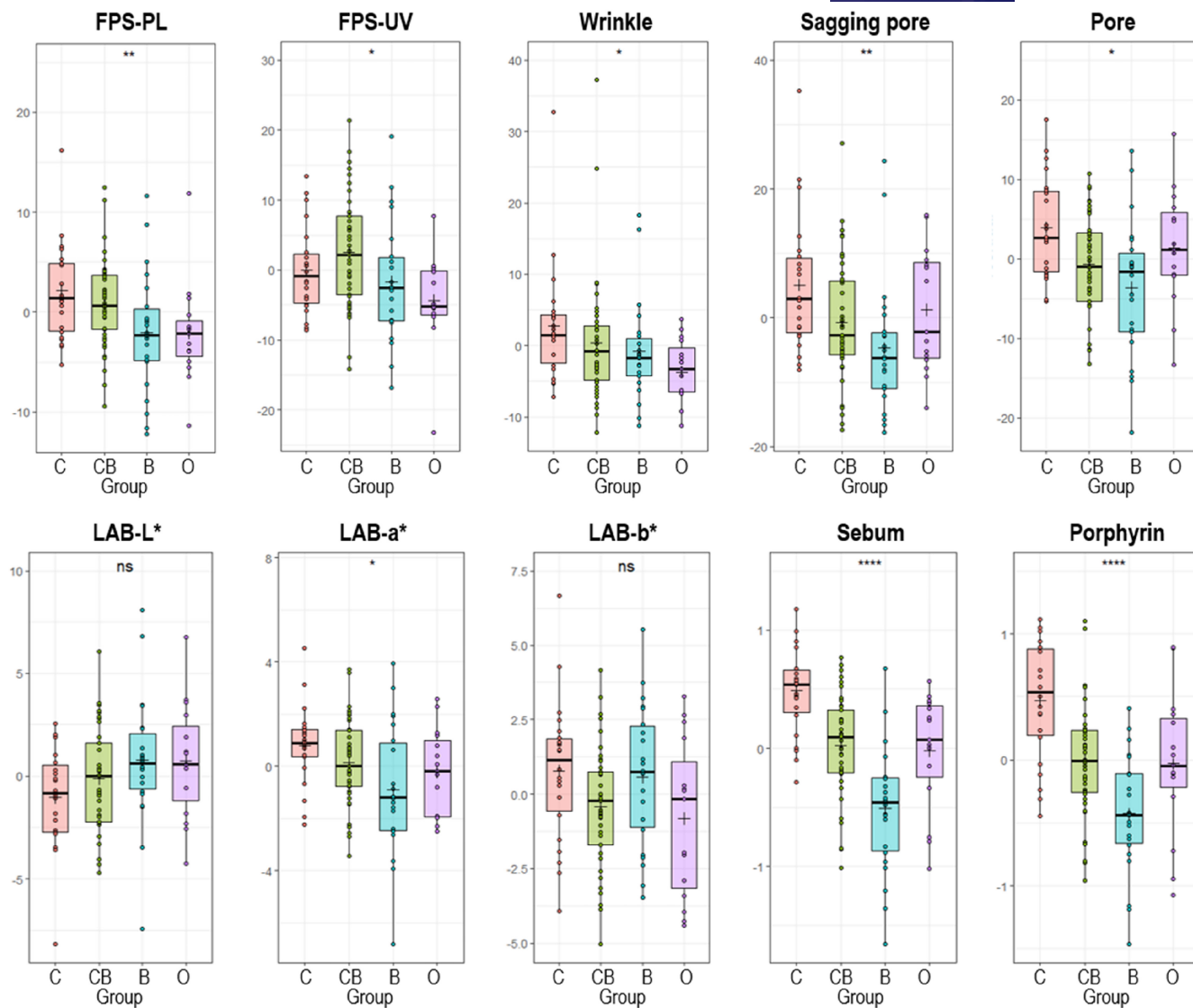


FIGURE 3 Skin characteristics of microbial types. ^{ns} $p > 0.05$; $*p \leq 0.05$; $**p \leq 0.01$; $****p \leq 0.0001$.

TABLE 4 Relationships between skin characteristics and microbial types.

Skin characteristics	p -value of Kruskal-Wallis test (FDR)	p -value of Jonckheere-Terpstra test	
		Increasing (FDR)	Decreasing (FDR)
FPS-PL	7.2E-03 (1.9E-02)	9.9E-01 (1.0E+00)	5.5E-03 (9.2E-03)
FPS-UV	1.9E-02 (3.2E-02)	7.3E-01 (1.0E+00)	2.7E-01 (3.4E-01)
Wrinkles	3.8E-02 (4.8E-02)	9.5E-01 (1.0E+00)	4.6E-02 (6.6E-02)
Sagging pores	7.6E-03 (1.9E-02)	1.0E+00 (1.0E+00)	6.7E-04 (2.2E-03)
Pores	1.7E-02 (3.2E-02)	1.0E+00 (1.0E+00)	1.9E-03 (4.8E-03)
LAB-L*	1.1E-01 (1.1E-01)	2.4E-02 (2.4E-01)	9.8E-01 (9.8E-01)
LAB-a*	3.4E-02 (4.8E-02)	1.0E+00 (1.0E+00)	3.5E-03 (7.0E-03)
LAB-b*	9.8E-02 (1.1E-01)	6.4E-01 (1.0E+00)	3.6E-01 (4.0E-01)
Sebum	1.5E-07 (1.5E-06)	1.0E+00 (1.0E+00)	1.3E-08 (1.3E-07)
Porphyrin	5.9E-06 (3.0E-05)	1.0E+00 (1.0E+00)	3.8E-07 (1.9E-06)

Note: Significant p -values (< 0.05) values are shown in bold.

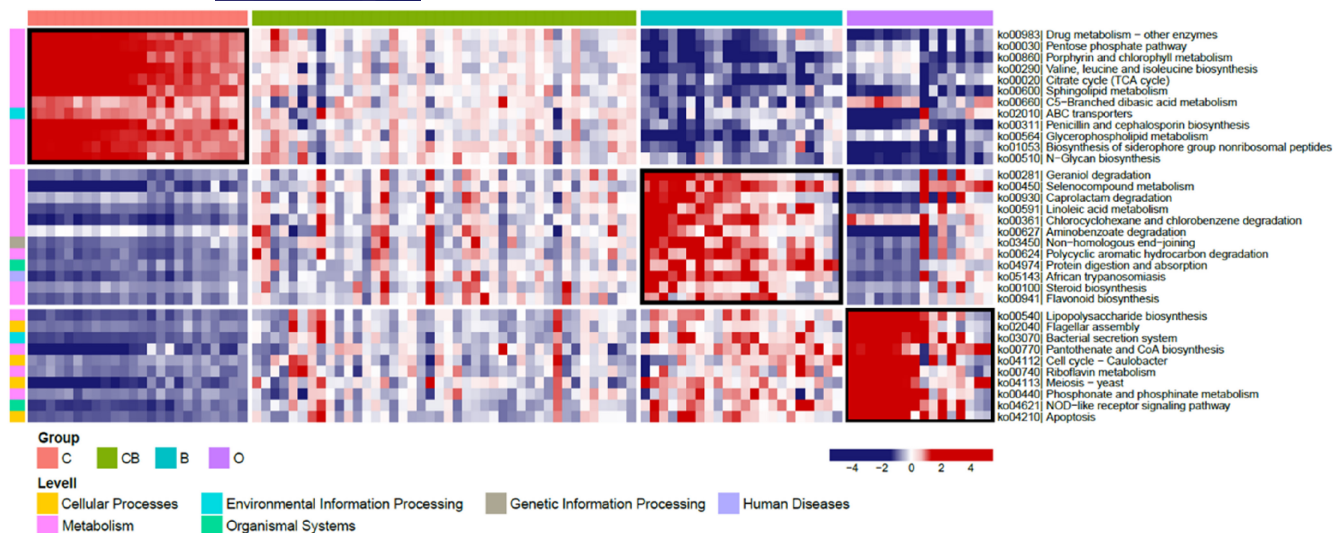


FIGURE 4 Predictive functions significantly present in each microbial type.

significance of differences in skin properties between microbial types C, CB, B, and O (the significance p -value is shown in Figure 3), and the Jonckheere–Terpstra test p -value indicates the statistical significance of the ordered trend of skin features between microbial types C, CB, and B (the increasing trend for $C \leq CB \leq B$ or decreasing trend for $C \geq CB \geq B$). The results of the Kruskal–Wallis and Jonckheere–Terpstra tests were similar in terms of p -values. The Kruskal–Wallis test showed that the microbial types were most strongly associated with sebum, followed by porphyrin, FPS-PL, and sagging pores. The Jonckheere–Terpstra test showed that the microbial types were most closely related to sebum, followed by porphyrins, sagging pores, pores, and LAB-a*.

3.4 | Functional prediction of microbial type

We used PICRUSt2 to predict the functional content of the microorganisms and to determine whether the differences in skin aging indices by microbial type are related to the functions of the microorganisms (Figure 4 and Table 3(c)). A total of 34 pathways showed significant results, with approximately 10 pathways each appearing significantly for types C, B, and O, and no prominent pathways for type CB.

Type C and type B are similar in that the prominent pathways belong to metabolism, but the detailed functional content is different between the two types. Type C had many pathways related to carbohydrate and lipid metabolism, while type B had pathways related to the biodegradation of xenobiotics and pathways related to DNA repair. In type O, pathways belonging to cellular processes were prominent, specifically, pathways related to bacterial cell growth and death, such as the cell cycle, meiosis, and apoptosis, as well as pathways related to cell motility, such as flagella assembly. These pathways were mainly predicted from the *Neisseriaceae* (F) family, which is abundant in type O.

4 | DISCUSSION AND CONCLUSION

The skin microbiome has a significant impact on skin aging due to its close interaction with the skin. There is evidence that the skin microbiome can predict age of host better than the gut microbiome,¹⁵ highlighting the strong link between aging and the skin microbiome.

Although many studies suggested age-related microbes, it is not necessarily the case that these microorganisms are directly related to skin health. For example, *C. acnes* was frequently found on the skin of young individuals, but an abundance of *C. acnes* does not necessarily indicate young and healthy skin. However, after adjusting for age, we found that the relative abundance of *Cutibacterium* showed a positive association with skin aging characteristics. This means that when comparing people of the same age, those with more *Cutibacterium* exhibited more aging-related characteristics such as wrinkles and pigmentation. This phenomenon also applies to comparisons of skin properties between microbial types. Type C, which is composed of subjects with a high proportion of *Cutibacterium*, included many young people. If we compare the skin features of type C without age correction, it showed relatively low values of wrinkles and pigmentation. However, this pattern arises because both *Cutibacterium* and skin aging traits are each affected by actual age. Since the two factors are related to age, the analysis reveals an indirect negative correlation between them, even though in reality, there is a positive correlation. Therefore, to avoid age-induced misunderstandings, age-adjusted residuals were used for comparison when assessing associations between aging traits and microbial types. As seen in the results section, after age adjustment, wrinkles and pigmented spots were relatively higher in type C.

According to the results section, type C exhibited more severe signs of aging, while type B showed less severe aging. These findings suggest a negative association between skin microbial diversity and skin aging, which is in line with the general trend of the association between microbial diversity and health indicators.³ However, it is

not enough to explain skin aging based solely on microbial diversity. In response, we examined functional potentials of skin microbiome and compared them to identify valuable explanations for the association between microbial types and skin aging characteristics.

Type C exhibited many distinct metabolic pathways, including carbohydrate and lipid metabolism. Variations in nutrient utilization by the skin microbiota could be attributed to differences in metabolism-associated genes observed between types. Types C and O shared the common features of high sebum and porphyrin. However, type C had a higher potential for microbial utilization of sebum compared to other skin types, as it is enriched in genes related to lipid metabolism. *Cutibacterium*, which is abundant in type C skin, secretes lipase that can alter sebum composition and harm hair follicle walls, leading to reactive oxygen species production and inflammation.¹⁶ Moreover, free fatty acids produced by lipase can have several negative effects on the skin, such as inducing inflammation or promoting bacterial cell adhesion.^{17,18}

On the contrary, type O had a higher genetic potential related to cellular processes, such as cell growth, death, and motility, than metabolic-related genes. Since these characteristics differed from those of type C, they can be explained the differences in skin features between types C and O. However, since type O was a group of all subjects dominated by microorganisms other than *Cutibacterium*, it is challenging to conclude that high cellular activity and low metabolic potential are microbial traits common to all type O subjects. As the interpretation of functional potential is limited to possibilities, further studies are necessary to clarify the functional relationship between microbial types and skin phenotypes.

In summary, we developed a classification model for skin microbial types based on two major indicators Shannon index and the relative abundance of *Cutibacterium*. Our analysis showed significant associations between skin characteristics and the classification of microbial types, particularly *Cutibacterium*, which has the potential to impact skin aging. Notably, by adjusting for age, we were able to examine the associations between microorganisms and skin health deterioration more clearly. Our classification system offers a simple and intuitive way to explain skin phenomena, making it useful not only for dermatology but also for the cosmetic industry.

While our proposed classification method is user-friendly, it has some limitations. The criteria for classification can vary depending on the study population, and the types of classification need to be further subdivided based on the study's objectives. As mentioned earlier, the associations between microbial types and skin aging patterns do not imply causality. Moreover, the taxonomic resolution achieved by targeting the 16S rRNA gene with short-read sequencing was limited to the genus level, as compared to the higher resolution provided by entire gene sequencing.¹⁹

In our study, we specifically focused on the microbial community of the cheek, known for its relatively high sebum content compared to other skin sites. While the facial skin microbiota includes not only bacteria but also fungi and viruses, bacteria were found to be more

abundant and influential in sebaceous regions compared to fungi or viruses in other skin sites.²⁰ However, considering the potential interactions between bacteria and fungi in relation to skin health, further investigations into the interplay between these microorganisms are required. Advanced research techniques, such as shotgun metagenomics or internal transcribed spacer sequencing for fungal DNA, could be utilized to explore the interactions and underlying mechanisms between bacteria and other microorganisms, providing a comprehensive examination of their associations.

Despite its limitations, our study provides valuable insights into the relationships between skin microbial diversity, *Cutibacterium* abundance, and skin aging through a new classification method of skin microbial types. We found a significant correlation between sebum, one of the skin characteristics, and both microbial diversity and *Cutibacterium*. While environmental factors can impact the composition of the skin microbiome, the skin characteristics were measured and swab samples were collected within a week of individuals residing in Seoul, Korea, who shared similar environmental conditions in our analysis. Therefore, it is likely that the observed correlations between sebum and microbial features are maybe primarily influenced by host physiological factors, independent of other environmental influences. A previous research on the development of artificial sebum and sweat media revealed that the specific concentrations of sweat and sebum exerted a notable influence on the composition of the microbial community, primarily due to variations in nutrient availability for each microorganism.²¹ *Cutibacterium*, in particular, metabolizes sebum components to support its own growth²² and regulate the growth of other microbes.²³ Consequently, modulating sebum production has the potential to induce changes in the defined microbial types within our study.

Lifestyle factors such as BMI, dietary intake, smoking, and alcohol consumption have also showed associations with the skin microbiome.²⁴ Additionally, the changes in microbial composition and diversity by therapeutic methods including phototherapy,²⁵ topical treatment for acne,²⁶ and the use of basic cosmetic products²⁷ have also been investigated. Subsequent studies on lifestyle factors and therapeutic methods, therefore, can serve as a valuable basis for suggesting personalized skincare guides based on distinct skin microbiome types. Such determinants will contribute to a deeper understanding of the skin microbiome and their potential role in promoting overall skin health.

AUTHOR CONTRIBUTIONS

Yunkwan Kim, Joong-Gon Shin, and Nae Gyu Kang are involved in the conceptualization and project administration. Seo-Gyeong Lee, Hye Lim Keum, Ki-Nam Gu, Jung Yeon Seo, and Hae Jung Song were included in the analysis and visualization. Joong-Gon Shin, Seo-Gyeong Lee, and Jung Yeon Seo were involved in data collection and preparation. Seo-Gyeong Lee, Hye Lim Keum, Hae Jung Song, and Yunkwan Kim wrote the original drafts. Sangseob Leem, Hae Jung Song, Yunkwan Kim, Ki-Nam Gu, Seon Mi Lee, Woo Jun Sul, and Nae Gyu Kang were involved in writing the reviews and editing.

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CONFLICT OF INTEREST STATEMENT

All authors have no conflict of interest to declare.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are available from the corresponding author upon reasonable request.

ETHICS STATEMENT

This study was approved by the institutional review board at the LG H&H Research center in Seoul, South Korea. All research was conducted in accordance with relevant guidelines and regulations. Participants were fully informed of the study and provided written consent after reading the research protocol (LGHH-20191024-AB-01).

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