

Study of Skin Micro Flora with Special Reference to Age and Gender

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ABSTRACT

This study examines the distribution and variation of skin microbiota across different body sites, ages and genders. We collected and analyzed bacterial samples from males and females aged 20-60 from five body regions (mouth, nose, ear, underarms, and skin). Results revealed distinct microbial profiles: *Micrococcus spp.* were predominantly found in males, while *Enterobacter spp.* were more common in females. Notable age-related shifts included an increase in *Corynebacterium* and *Streptococcus* in older males and *Citrobacter* and *Pseudomonas* in older females. These findings highlight the influence of factors such as moisture, pH and nutrition on skin microbiota and emphasize the need for gender-specific considerations in microbiome research. Understanding these microbial distributions is crucial for insights into skin health and disease and may inform future therapeutic and cosmetic applications.

Keywords: Normal human skin flora, Microbiome, Microbiota, Gender differences, Age changes, Bacterial communities, Skin health.

INTRODUCTION

The microorganisms called normal flora are those that live on the surface of living things, such as humans, animals and do not cause illness. The complicated human organ known as the skin works to keep moisture in and keep germs out. Additionally, it offers a habitat for certain human flora. The surface of normal skin on people is home to vast populations of bacteria. The gram- positive cocci and diphtheroid that make up the majority of the typical skin flora may act as a selective barrier to prevent the growth of potentially harmful organisms.

The skin is the largest organ in the human body making up over 16% of the total mass of the body. The skin is the human body's second largest micro-ecosystem, behind the stomach. Research has indicated that approximately 40 trillion adult skin microbes exist, making up 16% of all human symbiotic microorganisms. A survey has indicated that approximately 40 trillion adult skin microbes exist, making up 16% of all human symbiotic microorganisms (Guo *et al.*, 2023).

Microbes that make the resident flora: These bacteria can be discovered on the surface of the skin and below the surface cells of the stratum corneum. For example, the common resident flora of the skin is *Streptococci*, and the common resident flora of the mouth, or oral cavity is *Staphylococci*. Approximately 10¹³ are present within the human body's cells, and there are typically around 10¹⁴ organisms. Plant microbial life is normally steady and certain genera are administered to specific components of the frame at specific points in an men's and women's lives.

Normal flora has a big impact on immunity and inflammation. A person's skin usually contains a constant amount of bacteria on it; the survival of the bacteria and the extent of colonization are largely determined by the bactericidal activity of the skin, which is species-specific, as well as the environment to which the skin is exposed. The normal microbial flora in the mouth depends on the location (saliva, tongue, tooth enamel, gingival surface) and gingivo periodontal health status. Because of the skin's desiccation, gram-negative bacteria make up a very small portion of the skin's flora (Dangi *et al.*, 2021).

The microbiota begins to colonize during birth, and this colony's composition is determined by the mode of delivery (Chu *et al.*, 2017; Grice and Segre *et al.*, 2011). A large number of *Candida spp* are found on human skin, usually on the mucous membranes of the mouth. The four main bacterial phyla present on the skin are *Actinobacteria* (36-51%), *Proteobacteria* (11-16%), *Bacteroidetes* (6-9%), and *Firmicutes* (24-34%) are the three types of bacteria (Gallo *et al.*, 2017; Byrd *et al.*, 2018; McLoughlin *et al.*, 2021). Atopic dermatitis (AD) is a chronic inflammatory dermatosis that affects 2-10% of adults and 15-20% of children (Lunjani *et al.*, 2019). The makeup of the skin micro biome changes during puberty favoring

124 lipophilic skin species. Due to these differences the keratinized areas of the mouth have an order magnitude higher permeability than the skin. There is no need for a water barrier because the oral cavity is a moist environment in contrast to the skin. Non-keratinized epithelia cover the inside of the tongue, the buccal regions, the inside of the lip and the soft palate. Since most microorganisms grow best in the pH range of 6.5–7.5, this relatively low pH limits the range of bacteria that can thrive on the skin's surface (Wert *et al.*, 2020).

Due to its significance in skin health and disease as well as its possibilities for use in therapeutic and cosmetic applications, the human skin micro biome is an interesting topic (Byrd *et al.*, 2018). From a group of elderly women, more *Corynebacterium* bacteria and less *Cutibacterium* bacteria were recovered. Reduced sebum secretion is linked to a decrease in the prevalence of *Cutibacterium spp.* on the forehead, forearms and cheeks in the elderly. According to research by among the fungal species include 14 *Aspergillus*, *Epicoccum*, *Rhodotorula*, *Cryptococcus*, and *Malassezia spp.* are the most common fungus species, accounting for around 80% of the total fungal flora (Grice and Segre *et al.*, 2011; Sanford and Gallo *et al.*, 2013; Drełno *et al.*, 2016; Byrd *et al.*, 2018; Lunjani *et al.*, 2019; McLoughlin *et al.*, 2021; Rozas *et al.*, 2021). In pilosebaceous follicles, tiny mites known as *Demodex spp.* live (Boxberger *et al.*, 2021; Forton and De Maertelaer *et al.*, 2021).

MATERIALS AND METHODS

Sample Collection

Samples were collected from the five different parts of the body (mouth, nose, ear, underarms, and skin) of the male and female of the same body. The people were within the age group of 20–60 with no observable symptomatic disease. Since the study group consisted of healthy individuals, the usage of cosmetics was not taken into consideration when selecting participants. Instead, a sterile cotton swab was used to gather skin samples, which were then placed in a tube containing distilled water. Samples were collected from nine different regions of healthy male and female skin, making a total of ten samples. Cotton swabs should be in sterile condition with the help of laminar air flow or hot air oven or alcohol to avoid any type of contamination present on cotton swab. Samples were taken from moist areas of the skin that are conducive to bacterial development and colonization. A number and an alphabet corresponding to the sites chosen were used to code each sample.

RESULT AND DISCUSSION

In this study, we observed notable differences in the bacterial flora of body parts between genders and across age groups, highlighting distinct microbial community patterns. In males, *Micrococcus spp.* were consistently prevalent across various body sites and ages, particularly in the mouth and ear, suggesting a stable presence of these bacteria throughout male life stages. *Lactobacillus* was commonly found on the skin of younger males, indicating its role in skin health or pH regulation in this demographic. As males aged, the presence of *Corynebacterium* and *Streptococcus* increased, possibly reflecting age-related shifts in skin microbiota. Conversely, *Enterobacter* was infrequent in males, whereas *Staphylococcus* and *Acinetobacter* exhibited age-related variations in the urinary area, suggesting that bacterial composition in this region might be influenced by aging.

In females, a distinct microbial profile emerged. *Enterobacter* was notably more prevalent in the skin and mouth, with an increase in *Citrobacter* on the skin and *Pseudomonas* in the nose as age progressed. This suggests that the female microbiome adapts differently with age compared to males. Notably, the urinary area of older females was predominantly colonized by *E. coli*, diverging from the patterns seen in males, where *Enterobacter* and other organisms were more common. These findings indicate significant gender-specific variations in bacterial communities, which may be influenced by biological differences and age-related changes. Such variations could reflect diverse microbiome dynamics or host factors between sexes, emphasizing the need for gender-specific considerations in microbiome research and clinical application.

Table 1: Result from male and female sample of bacteria age (20 – 30)

S.NO.	TEST	CATALASE	CITRATE	UREASE	INDOLE	VP	MR	TRIPLE SUGAR	TRYPTIC	H ₂ S	STARCH
1.	<i>Lactobacillus</i>	-	+	-	-	-	+	ND	+	-	-
2.	<i>Micrococcus</i>	+	-	+	-	+	-	A/K	-	-	+
3.	<i>Streptococcus</i>	-	-	-	+	-	+	A/A	+	-	+
4.	<i>Micrococcus</i>	+	-	+	-	+	-	A/K	-	-	+
5.	<i>Staphylococcus</i>	+	+	+	-	+	+	A/A	+	-	-
6.	<i>Corynebacterium</i>	+	+	-	-	+	-	ND	+	+	-
7.	<i>Enterobacter aerogenes</i>	+	+	-	-	+	-	A/A GAS	+	-	-
8.	<i>Staphylococcus</i>	+	+	+	+	+	+	A/A	+	+	-

9. <i>Streptococcus</i>	-	-	-	INDOLE	VP	MR	A/A TRIPLE SUGAR	+	-	H ₂ S
10. <i>Acinetobacter</i>	+	+	-	+	-	-	A/A	ND	-	-

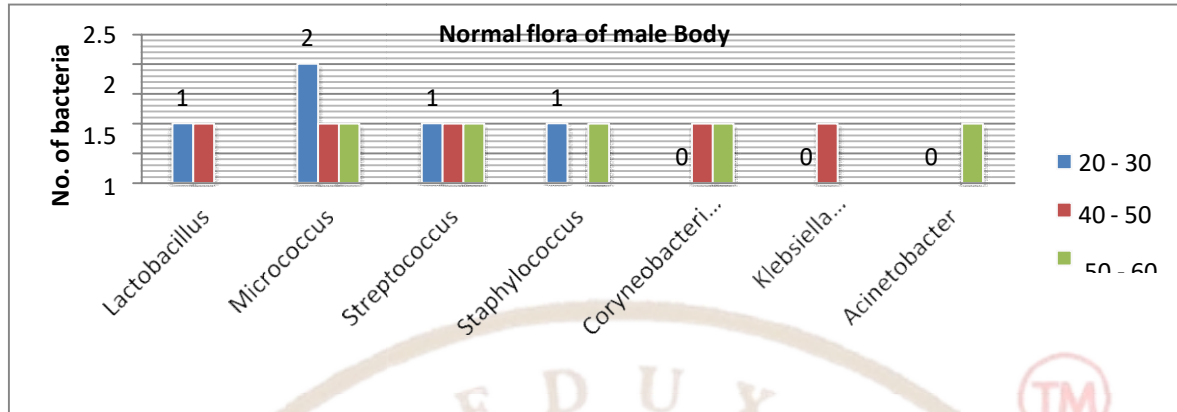
Table 2: Result from male and female sample of bacteria age (40 – 50)

S.NO.	TEST	CATALASE	CITRATE	UREASE	INDOLE	VP	MR	TRIPLE SUGAR	TRYPTIC	STARCH
1.	<i>Corynebacterium</i>	+	+	-	-	+	-	ND	+	++
2.	<i>Streptococcus</i>	-	-	-	+	-	+	A/A	+	-
3.	<i>Micrococcus</i>	+	-	-	-	+	-	A/K	-	+
4.	<i>Staphylococcus</i>	+	+	+	-	+	+	A/A	+	-
5.	<i>Acinetobacter</i>	+	+	-	+	-	-	A/A	ND	-
6.	<i>Citrobacter</i>	+	+	+	-	-	+	A/A Gas	-	++
7.	<i>Streptococcus</i>	-	-	-	+	-	+	A/A	+	-
8.	<i>Pseudomonas+ areuginosa</i>	+	+	-	-	-	-	A/A	+	+
9.	<i>Enterobacter aerogenes</i>	+	+	-	-	+	-	A/A Gas	+	-
10.	<i>E.coli</i>	+	-	-	+	-	+	A/A Gas	-	+

Table 3: Result from male and female sample of bacteria age (50 – 60)

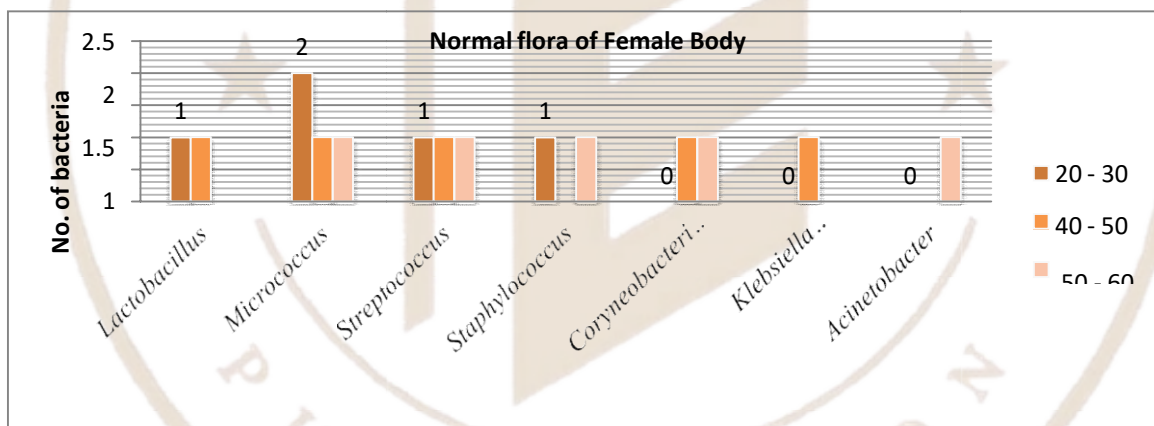
S.NO.	TEST	CATALASE	CITRATE	UREASE	INDOLE	VP	MR	TRIPLE SUGAR	TRYPTIC	H ₂ S	STARCH
1.	<i>Lactobacillus</i>	-	+	+	-	-	+	ND	+	-	-
2.	<i>Corynebacterium</i>	+	+	-	-	+	-	ND	+	+	+
3.	<i>Klebsiella pneumoniae</i>	+	+	+	-	+	-	A/A	-	-	-
4.	<i>Streptococcus</i>	-	-	-	+	-	+	A/A	+	-	-
5.	<i>Micrococcus</i>	+	-	-	-	+	-	A/K	-	-	+
6.	<i>Enterobacter aerogenes</i>	+	+	-	-	+	-	A/A Gas	+	-	-
7.	<i>Acinetobacter</i>	+	+	-	+	-	-	A/A	ND	-	-
8.	<i>Pseudomonas areuginosa</i>	+	+	-	-	-	+	A/A	+	+	+
9.	<i>Citrobacter</i>	+	+	+	-	-	+	A/A Gas	-	+	+
10.	<i>E.coli</i>	+	-	-	+	-	+	A/A Gas	-	-	+

Age	<i>Lactobacillus</i>	<i>Micrococcus</i>	<i>Streptococcus</i>	<i>Staphylococcus</i>	<i>Corynebacterium</i>	<i>Klebsiella pneumoniae</i>	<i>Acinetobacter</i>
20 - 30	1	2	1	1	0	0	0
40 - 50	1	1	1	0	1	1	0
50 - 60	0	1	1	1	1	0	1



Graph 1: Comparison of different age group of male bacteria

Age	Corynebacterium	Enterobacter	Staphylococcus	Streptococcus	Acinetobacter	Pseudomonasareuginosa	Citrobacter	E.coli
20 - 30	1	1	1	1	1	0	0	0
40 - 50	0	1	0	0	1	1	1	1
50 - 60	0	1	0	1	0	1	1	1



Graph 2: Comparison of different age group of female bacteria

CONCLUSION

Our study highlights distinct bacterial distributions between males and females, with *Micrococcus spp.* predominantly found in males and *Enterobacter spp.* more common in females across various age groups. The presence of these bacteria is influenced by factors

such as moisture, pH, and nutrition in different body regions. Our findings underscore the skin's role in fostering a diverse and regulated microbiota that helps protect against pathogenic organisms.

This research contributes to a deeper understanding of the complex interactions between skin bacteria, such as *Staphylococcus*, *Corynebacterium*, *Streptococcus*, and *Pseudomonas*, and their roles in skin health and disease. Future studies will benefit from exploring these relationships further, refining our knowledge of the skin microbiome and its impact on human health.

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