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Comparison between cosmetic and non-cosmetic users among the group of medical students to find the effect of cosmetics on their facial flora

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ABSTRACT

Human skin is a complex ecosystem with various microenvironmental conditions and thus, the presence of resident microbial flora prevents colonization by pathogens. Some cosmetics like skin peels are known to cause deeper exfoliation of the skin and causes loss of skin flora. So, in the present study, the attempt was to find out the effect of cosmetics that are applied to the face on resident flora of the face of medical students who are exposed to the hospital environment. Out of 120 subjects, 60 were cosmetic users and 60 were non-cosmetic users. Swabs were collected from the face of subjects after washing the face with soap and water and processed using standard techniques. The colonies were counted, identified and statistically analyzed. The isolated colonies were Coagulase Negative *Staphylococcus (CoNS)*, *Staphylococcus aureus*, *Micrococcus* species, gram-negative bacilli and *Corneybacterium* species from both the groups. It was found that regular cosmetics users 12(20%) yielded less isolates of CoNS as compared to non-cosmetic users 42(70%). It was found that the use of cosmetics thus decreases the normal resident flora of the skin, but larger studies with more subjects are needed to confirm the present result.

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INTRODUCTION

Human skin is the front line of defense against external infectious or toxic substances and is an environmental habitat that various bacteria, viruses, yeast and fungi can colonize. Human skin is a complex ecosystem with various microenvironmental conditions and thus, microbial skin communities are very diverse and complex (Lee *et al.*, 2018). The presence of resident microbial flora, which has evolved to survive and fill a niche, prevents colonization by pathogens and possible interference though ”bacterial interference” (Geo *et al.*, 2007).

Skin structures such as hair follicles, sebaceous glands, epocrine and apocrine sweat glands, as well as subepidermal skin compartments, provide distinct biological niches that are colonized by their own unique skin resident flora. Most of these skin microbes are harmless or commensal organisms that play essential roles in inhibiting colonization by pathogenic microbes or modulating innate and adaptive immune systems (Holland and Bojar, 2002).

Some cosmetics like skin peels are known to cause deeper exfoliation of the skin resulting in a breakin barrier effect and thus cause loss of skin flora. Cosmetics products that use poor quality ingredients that have not been regulated can lead to skin discoloration. Continuing use of cosmetics, which has certain preservatives, leads to alter the pH of the skin surface by either decreasing or increasing the resident microbial flora (Dayan and Wertz, 2011). The risk for this event is of concern and it is important to monitor the effect of cosmetics, whether it is good, bad, or neutral. So, in the present study, the attempt was to find out the effect of cosmetics that are applied to the face like foundation, powders, moisturizers and creams on resident flora of the face of medical students who are exposed to the hospital environment.

MATERIALS AND METHODS

It is a cross-sectional study involving medical students studying at Saveetha Medical College, Chennai, India, aged between 19 to 25 years, conducted in the year 2019 for the duration of three months.

The institutional ethics committee, along with the informed consent of the subjects, has been obtained for the study. The subjects were divided into two groups, those who do not use cosmetics and who use cosmetics. Those who occasionally use cosmetics and who do not belong to the above age groups were excluded. Only the cosmetics usually use on the face like foundation, powders, moisturizers and creams were considered (Lalitha and Prasadarao, 2015). Firstly, the subjects were made to wash their face with soap and water to remove the superficial environmental flora. The collection of sample starts with swabbing a sterile cotton swab which was dipped in 1 ml of peptone water on both the cheeks covering an area of approximately 1×1 inches (Ikpoh *et al.*, 2012). The swab material was transferred to the vials containing peptone water. Tenfold serial dilutions of the samples were made and 100μl of the diluted sample was spread over the surface of Trypticase soy agar, Mac Conkey´s agar and blood agar. The plates were incubated at 37°c overnight; the colonies on Trypticase soy agar were counted and multiplied by the dilution factor. The colonies on Mac Conkey´s agar and blood agar were identified by standard methods. Methicillin-resistant *Staphylococcus aureus*(MRSA) was determined by using 30μg cefoxitin disc as per CLSI guidelines (Collee and Miles, 2012; NCCLS, 2015). *S.aureus* with a zone of $\leq$21mm was considered as MRSA.

Statistical Analysis

Statistical analysis was done using the Chi-square method and p<0.05 was considered as statistically significant.

RESULTS AND DISCUSSION

The study was done on 120 medical students, out of which 96 were female and 24 were male students.

On analyzing the correlation between gender and the normal facial flora, it was found that both the gender yielded mostly gram-positive cocci 81(67.5%) followed by gram-negative bacilli 8(6.66%) and gram-positive bacilli 4(3.33%)which is shown in Table 1.

Twenty-seven samples yielded negligible growth. It was found that most of the students who were regular cosmetics users 25(41.67%) shows negligible growth than those of non-cosmetic users 2(3.33%).

On analyzing the types of flora, it was found that both regular cosmetic users and who do not use cosmetics yielded the following type of bacteria Coagulase-negative *staphylococci(CoNS)* 54(45%), *Staphylococcus aureus* 10(8.33%), *Micrococcus* species 17(14.17%) which were gram-positive cocci. CoNS were more frequently isolated from those who do not use cosmetic 42(70%) in comparison to those of regular cosmetic users12(20%) and the difference was statistically significant(p=<0.001. *S.aureus* and micrococci species were isolated more in cosmetic users comparing to non-cosmetic users. *S.aureus* isolated was found to be MRSA (10%) and Methicillin sensitive *S.aureus*(MSSA)(3.33%) in cosmetic users, whereas all are MSSA (3.33%) in non-cosmetic users. (Table 2)

The gram-negative bacilli isolated was found to be non-fermentors (6.67%). The gram-positive bacteria isolated were found to be *Corynebacterium* species and more in cosmetic users comparing to non-cosmetic users. (Table 2)

As reported in many previous studies, increased skin hydration values and skin roughness has been observed for facial cheeks skin after the use of cosmetics (Lee *et al.*, 2018). The bacterial diversity increased significantly with the use of basic cosmetics, suggesting that the use of cosmetics might cause an increase in bacterial diversity by the input of diverse cosmetic components onto the facial skin. Staphylococcus epidermis is one of the most important skin resident flora, which is not usually pathogenic but can cause infection to immune-compromised individuals, followed by *Staphylococcus aureus* in small numbers, anaerobic organisms like *Peptostreptococcus*, gram-negative bacilli like *Neisseria, Propionibacterium* and CoNS (Grice *et al.*, 2008). In this study, similar organisms were isolated.

Many review articles explained the effects of cos-

Table 1: Correlation between the number of students showing the growth of the various bacteria and gender

Bacteria isolated	Gender		p-value
	Female (n=96)%	Male (n=24)%	
Negligible growth	24(25%)	3(12.5%)	0.189
Coagulase negative Staphylococcus	38(39.58%)	16(66.66%)	0.017
S.aureus	9(9.38%)	1(4.17%)	0.408
Micrococcus species	15(15.62%)	2(8.33%)	0.359
Gram negative bacilli (non-fermentor)	7(7.29%)	1(4.17%)	0.583
Corneybacterium species	3(3.13%)	1(4.17%)	0.799

Table 2: Correlation between the number of students showing the growth of the various bacteria and the use of cosmetics on the face

Bacteria isolated	Cosmetic usage		p-value
	Regular (n=60)%	Non cosmetic users(n-60)%	
Negligible growth	25(41.67%)	2(3.33%)	<0.001
Coagulase negative Staphylococci	12(20%)	42(70%)	<0.001
S.aureus	8(13.33%)	2(3.33%)	0.047
Micrococcus	6(10%)	11(18.34%)	0.190
Gram negative bacilli(non-fermentor)	6(10%)	2(3.33%)	0.143
Corneybacterium species	3(5%)	1(1.67%)	0.309

metics on normal flora. A study shows the use of tropical products influencing the balance of microflora depending on the nature of the skin by studying the skin anatomy, nutrients and hydration of various types. Another study revealed the use of cosmetics as the protection factor from exterior environmental factors such as wind, UV exposure, etc. They showed that cosmetics maintain the skin water content and transepidermal water loss (TEWL), thus aid as a helping hand of the skin.

Another study shows that the use of prebiotics can provide a gentle and sustainable alternative to undirected antibacterial ingredients (Bockmühl *et al.*, 2007).

A review article talks about CoNS, a dominant normal flora of the skin acting as the first line of defense by producing peptides toxic to other organisms such as *S.aureus* and Group A *Streptococcus* (GAS *S.pyogenes*) (Cogen *et al.*, 2008). As CoNS was isolated less in cosmetic users comparing to non-cosmetic users, this point may be of concern as they act as the first line of defense against pathogenic organisms like *S.aureus.*

CONCLUSION

CoNS was less frequently isolated from regular cosmetic users in comparison to those who do not use cosmetics. As the study was done on a medical student, who was exposed to the hospital environment, lots of MRSA was expected and it was found that regular cosmetics users isolates were mostly MRSA. So they are the transient carriers, which is pathogenic in immunocompromised individuals. It was found that the use of cosmetics thus decreases the normal resident flora of the skin, but larger studies with more subjects are needed to confirm the present result.

Conflict of Interest

The authors declare that they have no conflict of interest for this study.

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REFERENCES

Bockmühl, D., Jassoy, C., Nieveler, S., Scholtyssek, R., Wadle, A., Waldmann-Laue, M. 2007. Prebiotic Cosmetics: An Alternative to Antibacterial Products. *International Journal of Cosmetic Science*, 29(1):63–64.

Cogen, A. L., Nizet, V., Gallo, R. L. 2008. Skin microbiota: a source of disease or defence? *British Journal of Dermatology*, 158(3):442–455.

Collee, J. G., Miles, R. 2012. Mackie & McCartney Practical Medical Microbiology. 14th Edition. pages 131–150.

Dayan, N., Wertz, P. W. 2011. Innate Immune System of Skin and Oral Mucosa: Properties and Impact in Pharmaceutics, Cosmetics, and Personal Care Products. 276.

Geo, F. B., Karen, C. C., Sb, J., Stephen, A. M. 2007. Jawetz, Melnick & Adelberg's Medical Microbiology: 24th Edition. *Sultan Qaboos University Medical Journal*, pages 197–201.

Grice, E. A., Kong, H. H., Renaud, G., Young, A. C., Bouffard, G. G., Blakesley, R. W., Wolfsberg, T. G., Turner, M. L., Segre, J. A. 2008. A diversity profile of the human skin microbiota. *Genome Research*, 18(7):1043–1050.

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.

Ikpoh, L., Udoekong, J., Iyam, N., S 2012. Comparative studies on the effect of locally made black soap and conventional medicated soaps on isolated human skin microflora. *World Journal of Microbiology and Biotechnology*, 2(4):533–537.

Lalitha, C., Prasadarao, P. V. 2015. Antimicrobial Efficacy of Preservatives used in Skin Care Products on Skin Micro Biota. *International Journal of Science and Research (IJSR)*, 4(6):366–369.

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. . *Microbiology Open*, 7(2):e00557.

NCCLS 2015. Performance standards for antimicrobial disk susceptibility testing; 25th Informational Supplement M100-S25. *National Committee for Clinical Laboratory Standards. Wayne, PA, USA*, 35(3):67.