Archives of Razi Institute, Vol. 77, No. 5 (2022) 1737-1740

DOI: 10.22092/ARI.2022.359398.2414

Original Article

Comparison of Skin Bacteria between Psoriasis Patients and Healthy Control

Ali Abd, S[1 *], Alsaffar, J. M. J[1], Agop, A. K[1], Kadhem, E, J[2]

1. Biotechnology Department, College of Science, University of Baghdad, Baghdad, Iraq
2. Ministry of Industry, Ibn Sina Research Center, Baghdad, Iraq

Received 2 June 2022; Accepted 22 June 2022
Corresponding Author: samah.abd.1985@gmail.com

Abstract

Psoriasis is an autoimmune, persistent, inflammatory skin illness that is influenced by a variety of circumstances. Psoriasis etiology is strongly linked to bacteria, particularly those in the pharynx and skin. This research intended to deepen our understanding by elucidating the connection between the skin microbiome and psoriasis to improve therapeutic balance using probiotics, antimicrobials, and even topical microbiota transplantation. In this work, the culture-dependent approach is utilized to compare the skin microbiomes of psoriatic and healthy individuals. On brane-heart infusion agar, swabs from 60 psoriasis patients in the flare-up stag and 40 healthy controls were cultured and grown for 48 hours. The resultant colonies were then subcultured and purified to produce a single pure colony. Using Macconkey agar for preliminary colony identification, Vitek then characterized the purified colonies. The results revealed substantial bacterial species and phyla variations between psoriatic patients and healthy controls. In addition, increased rates of opportunistic infections *Pseudomonas stutzeri* and *Staphylococcus pseudintermedius* were detected in psoriatic patients' normal skin and lesions.

Keywords: Psoriasis, Skin Microbiome, Dysbiosis

1. Introduction

Psoriasis is an autoimmune, chronic inflammatory skin condition that causes the rapid growth of skin cells, resulting in the formation of thick, scaly skin plaques. According to the annual figures of the World Health Organization, over 100 million people worldwide suffer from psoriasis (1). The skin is the primary barrier between humans and their environment. Our skin is our primary contact with the outside world. The skin's microbiome contains a diverse population of bacteria, most of which are harmless commensals that guard against pathogenic organisms and train the innate and adaptive immune systems. By boosting the expression of antimicrobial peptides and creating biofilms, the immune response of keratinocytes can be enhanced (2). Therefore, alterations to the microbial ecology of the skin could affect the skin's ability to resist infection. Numerous inflammatory and autoimmune diseases have been related to the skin microbiome (3, 4), indicating that it plays an essential role in maintaining health.

2. Materials and Methods

2.1. Subjects

Sixty patients with chronic plaque psoriasis, consisting of 39 females and 21 males, and forty healthy controls, consisting of 27 females and 13 males, participated in this study at the Department of Dermatovenereology, Al-Yarmouk educational hospital in Baghdad. Patients with other immunological

illnesses and those receiving biological or chemical treatment were eliminated. All patients were selected at the commencement of their symptoms. The average age of patients was 34.90 1.80 years, while that of healthy controls was 33.05 1.80 years.

2.2. Sampling

Swabs were taken from both control and psoriatic patients from the olecranon (elbow); psoriatic sites were also sampled in psoriatic patients. Briefly, swab samples were taken from a 2 x 2 cm area using flocked swabs (FLOQSwabsTM, COPAN Diagnostics Inc., United States).

2.3. Culture Media Preparation

According to the manufacturer's guidelines, brain heart infusion and Macconkey agar were produced. The medium was cooled to 50–45 °C before being placed into sterile Petri dishes. All swabs were spread on the agar plate for brain-heart infusion. The plates were then incubated at 37°C for 48 h. After incubation, the separated colonies were subjected to additional purification and subculture. Using Macconkey agar, preliminary identifications of each isolate were made.

2.4. Bacterial Identification

The Vitek 2 compact (bioMérieux Inc. USA) system was used for identification, with GP ID REF21342 (identification-Gram-positive bacteria) and GN ID REF21341 (identification-Gram-negative bacteria) cards. The manufacturer's instructions were followed in every step of the testing process.

2.5. Statistical Analysis

The mean and standard error of the mean were calculated using IBM SPSS version 28.0. Furthermore, the probability was tested using the student T-test. The probability was calculated via Pearson's chi-square test for nonparametric data.

3. Results

The results of bacterial identification based on biochemical tests in both healthy (normal skin) and psoriatic patients (regular and lesions) revealed that the most prevalent species in healthy skin were *Staphylococcus aureus* (95%), *Staphylococcus epidermidis* (72.5%), and *Staphylococcus hominis* (50%). In contrast, in psoriatic patients, the most prevalent species were *Staphylococcus epidermidis* (5%), followed by *Staphylococcus aureus* (45%) and *Micrococcus luteus* (39%). In comparison, the bacterial species in lesional skin were *Micrococcus luteus* (56%), *Staphylococcus aureus* (43.3%), and *Pseudomonas stutzeri* (36.6%); the percent of other bacteria species shown in figure 1. The results showed differences in dominant species and the frequency percentage for the same species between the compared groups. Besides, higher frequencies of the opportunistic pathogens *Pseudomonas stutzeri* and *Staphylococcus pseudintermedius* in normal skin and lesions in patients compared to healthy normal skin. The results showed differences in dominant species and the frequency percentage for the same species between the compared groups. Besides, higher frequencies of the opportunistic pathogens *Pseudomonas stutzeri*, *Corynebacterium jeikeium*, and *Staphylococcus pseudintermedius* in both normal skin and lesions in patients with this opportunistic species were absent in healthy normal skin in the control group.

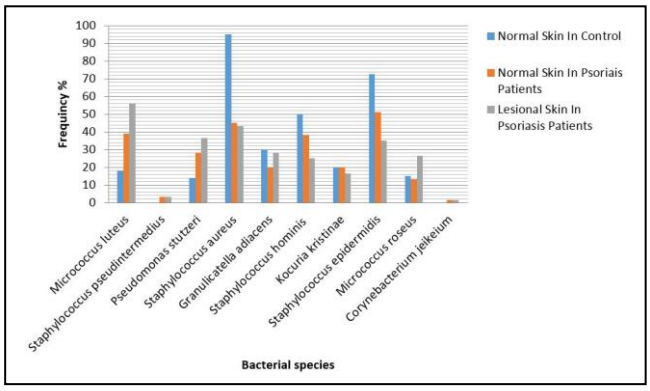

Figure 1. Bar chart declare the frequency % of skin bacteria species comparison between psoriatic patients' normal skin, lesional skin, and healthy skin in controls

At the phylum level, there was a significant (P<0.01) increase in Actinobacteria in lesional skin, but no significant difference recorded in Proteobacteria between controls and patients; additionally, there was a significant (P<0.01) decrease in firmicutes in both normal skin and lesions in psoriasis patients compared

to normal skin in controls. Moreover, this study shows that the dominant phyla in psoriatic skin were actinobacteria and firmicutes, as shown in figure 2.

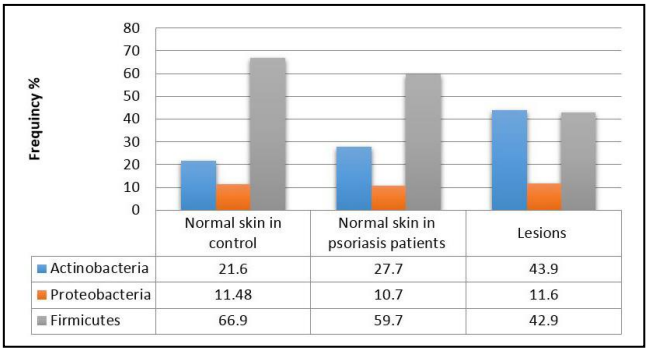

Figure 2. Bar chart declares the frequency % of skin bacteria phyla comparison between psoriatic patients and healthy control

4. Discussion

Compared to microbiome research dependent on 16s rRNA sequencing, our study is somewhat compatible with Alexseyenko and his collaborators. They determined that Actinobacteria and Firmicutes predominated in psoriatic lesions (3, 4). In contrast, Firmicutes ranked lower in the studies conducted by Assarsson, Duvetorp (5), (6, 7). Fahlen, Engstrand (8) discovered an increase in the number of proteobacteria in lesional skin, whereas Gao and his colleagues discovered a decrease (9). In contrast to our findings, Drago, De Grandi (6) found that Proteobacteria and Bacteroidetes were the most prevalent microbiome in psoriasis lesions. The breadth and depth of interactions between humans and microbes are astounding. Even the bacterial component, which has been the subject of the most research, is enormous. Despite the typical human body's 30 trillion cells, approximately 39 trillion bacteria cells inhabit it (10). Commensal bacteria use a variety of secreted compounds, antigens, metabolites, and toxins to communicate with their hosts. They can also interact with each other by competing for resources, making antibiotics and bacteriocins, encouraging horizontal gene transfer, and doing many other things that can be both helpful and harmful. Several investigations have discovered a connection between skin dysbiosis and some skin diseases, such as psoriasis (4), acne (11), wounds (12), and even atopy (13).

This study finds that the species and phylum levels of the skin microbiome of people living with psoriasis differ from those of healthy persons. This study showed that people with psoriasis have different levels of species and phylums in their skin microbiome than healthy people. This can disrupt the balance and homeostasis of the skin's symbiosis, leading to opportunistic pathogens activating the immune system. More research into how the skin microbiome is involved at the molecular level in the disease could help us understand skin diseases better and find new ways to treat them.

Authors' Contribution

Study concept and design: S. A. A.
Acquisition of data: J. M. J. A.
Analysis and interpretation of data: J. M. J. A.
Drafting of the manuscript: A. K. A.
Critical revision of the manuscript for important intellectual content: S. A. A.
Statistical analysis: E. J. K.
Administrative, technical, and material support: S. A. A.

Ethics

The study protocol was approved by the medical ethics board of the University of Baghdad, Baghdad, Iraq.

Conflict of Interest

The authors declare that they have no conflict of interest.

References

1. IM. M, B. L, SM. J. Global report on psoriasis. World Health Organization; 2016.
2. Wanke I, Steffen H, Christ C, Krismer B, Gotz F, Peschel A, et al. Skin commensals amplify the innate immune response to pathogens by activation of distinct

signaling pathways. J Invest Dermatol. 2011;131(2):382-90.

3. Alekseyenko AV, Perez-Perez GI, De Souza A, Strober B, Gao Z, Bihan M, et al. Community differentiation of the cutaneous microbiota in psoriasis. Microbiome. 2013;1(1):31.
4. Ganju P, Nagpal S, Mohammed MH, Nishal Kumar P, Pandey R, Natarajan VT, et al. Microbial community profiling shows dysbiosis in the lesional skin of Vitiligo subjects. Sci Rep. 2016;6:18761.
5. Assarsson M, Duvetorp A, Dienus O, Soderman J, Seifert O. Significant Changes in the Skin Microbiome in Patients with Chronic Plaque Psoriasis after Treatment with Narrowband Ultraviolet B. Acta Derm Venereol. 2018;98(4):428-36.
6. Drago L, De Grandi R, Altomare G, Pigatto P, Rossi O, Toscano M. Skin microbiota of first cousins affected by psoriasis and atopic dermatitis. Clin Mol Allergy. 2016;14:2.
7. Loesche MA, Farahi K, Capone K, Fakharzadeh S, Blauvelt A, Duffin KC, et al. Longitudinal Study of the Psoriasis-Associated Skin Microbiome during Therapy with Ustekinumab in a Randomized Phase 3b Clinical Trial. J Invest Dermatol. 2018;138(9):1973-81.
8. Fahlen A, Engstrand L, Baker BS, Powles A, Fry L. Comparison of bacterial microbiota in skin biopsies from normal and psoriatic skin. Arch Dermatol Res. 2012;304(1):15-22.
9. Gao Z, Tseng CH, Strober BE, Pei Z, Blaser MJ. Substantial alterations of the cutaneous bacterial biota in psoriatic lesions. PLoS One. 2008;3(7):2719.
10. Sender R, Fuchs S, Milo R. Revised Estimates for the Number of Human and Bacteria Cells in the Body. PLoS Biol. 2016;14(8):1002533.
11. Fitz-Gibbon S, Tomida S, Chiu BH, Nguyen L, Du C, Liu M, et al. Propionibacterium acnes strain populations in the human skin microbiome associated with acne. J Invest Dermatol. 2013;133(9):2152-60.
12. Gardner SE, Hillis SL, Heilmann K, Segre JA, Grice EA. The neuropathic diabetic foot ulcer microbiome is associated with clinical factors. Diabetes. 2013;62(3):923-30.
13. Kong HH, Oh J, Deming C, Conlan S, Grice EA, Beatson MA, et al. Temporal shifts in the skin microbiome associated with disease flares and treatment in children with atopic dermatitis. Genome Res. 2012;22(5):850-9.