THE SKIN MYCOBIOME IN PATIENTS WITH ATOPIC DERMATITIS AND HEALTHY INDIVIDUALS

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INTRODUCTION

Atopic dermatitis (AD) is a complex chronic inflammatory disease in which fungi are believed to act as aggravating factors. Thus, analysis of the composition of skin mycobiota is crucial for a better understanding of the etiology of AD.

METHODS

The study included 49 AD patients (24 woman, 25 men; mean age: 31.8 ± 13.1) and 50 healthy individuals (39 woman, 11 men; mean age: 37.8 ± 14.3) recruited between 2017 and 2019 at the Department of Dermatology, Venereology and Allergology, Wroclaw Medical University. Samples from the creases of the elbows (AD patients with acute skin lesions on elbows, n = 44 and all healthy individuals) or neck/knee bending (AD patients with no acute lesions on elbows, with lesions on neck/knee bending; n = 6) were collected with either a scalpel (AD subjects) or OpSite dressings (Smith & Nephew Education; UK) (healthy individuals; Fig. 1). DNA was isolated using GeneMATRIX Environmental DNA & RNA Purification Kit (EurX, Poland). Metagenomic sequencing was performed using primers FungITS1 and FungITS2 (Fig. 2), as described previously (Fraczek et al., 2017, J Allergy Clin Immunol. 9:39) at the DNA Sequencing and Oligonucleotide Synthesis Laboratory, Polish Academy of Science.

RESULTS

A total of 61 and 44 (considering the abundance above 1% within samples) various taxonomic fungal families were found on the skin of AD patients and healthy individuals, respectively. In both groups, the most abundant were fungi of Trichosporonaceae, Cladosporiaceae, Debaryomycectaceae, Malasseziaceae and Saccharomycetales. Among patients with AD, five families, i.e. Cladosporiaceae, Debaryomycectaceae, Malasseziaceae, Saccharomycetales and Botryosphaeraceae were represented at a higher frequency, when compared with healthy individuals. On the contrary, among healthy subjects Thermoascomycetes family was overrepresented.

CONCLUSIONS

This study provides an important insight into the fungal composition of the skin of AD patients. A higher interpersonal diversity of the mycobiota, and a clear predominance of specific taxa was observed in AD patients when compared with healthy individuals.

This work was supported by the «Iuventus Plus» grant from the Polish Ministry of Science and Higher Education (0258/IP1/2016/74)