Characterization of the Skin Mycobiome in Patients with Atopic Dermatitis

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Background Patients with atopic dermatitis (AD) are known to be vulnerable to various infections of microbiome due to comprised skin barrier. Even though mycobiome, the skin fungal community, has key roles in immune-priming frontiers, studies referring to skin mycobiome in AD are restrictive yet.

Objectives This study aimed to comparatively analyze the overall skin mycobiome between patients with AD and healthy individuals in the Korean population. We also aimed to elucidate the role of *Malassezia* in pathophysiology of AD.

Methods Skin swab samples from the antecubital fossae of 8 patients with AD and 8 healthy controls were analyzed. Using sequencing method followed by direct DNA extraction and molecular PCR, taxonomic compositions of fungi at stepwise level ranks were analyzed. The phylogenic marker used was internal transcribed spacer 2 regions of DNA.

Results According to diversity analyses using Shannon diversity index (SDI), patients with AD were shown to have more diverse fungi than healthy controls at genus and species level.

Fig. 1. Diversity analyses using SDI at phylum (A), genus (B), and species (C) level

Circular dots and square dots represent SDIs of samples from AD and HC, respectively. AD, atopic dermatitis; HC, control

Malassezia globosa and *Malassezia restricta* were prevalent in all samples across both study groups. However, *Malassezia slooffiae*, *Malassezia obtusa* and *Malassezia yamatoensis* were identified only in the samples from AD group, while *Malassezia furfur* was detected more frequently in the healthy controls.

Fig. 2. Relative abundance of *Malassezia* species

Fig. 3. Diversity analysis on *Malassezia* species using SDI

The difference of mean SDIs of the *Malassezia* components between 2 groups was not significant, in contrast that the difference existed in terms of overall fungal species level.

Conclusion We detected a tendency of higher intra- and inter-personal skin fungal diversities in AD populations compared with healthy populations. Simultaneously, non-*Malassezia* diversity was more noticeable in AD populations. Although this study was limited by the small sample size, it would be a preliminary study, contributing to set up the database of skin mycobiome in patients with AD.

References

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