

The mycobiome of the skin of patients with atopic dermatitis and healthy volunteers

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BACKGROUND & OBJECTIVE

Atopic dermatitis (AD) is one of the most common inflammatory skin diseases, in which fungi are believed to act as triggering factors. Therefore, it is crucial to assess the composition of skin mycoflora for a better understanding of the etiopathogenesis of AD.

The aim of the study was to explore the skin mycobioome of AD patients and healthy individuals by using culture-dependent and metagenomics, culture-independent methodologies.

METHODS

The study included 50 AD patients and 50 healthy individuals recruited between 2017 and 2019. Skin scrapings from elbows, necks and knees were collected with either a scalpel or OpSite dressings (Smith&Nephew Education; UK) (**Fig. 1**) in AD and healthy subjects, respectively. Culture-dependent species identification involved a battery of conventional phenotypic tests and PCR-based sequencing of the internal transcribed spacer (ITS) 1&2 regions (Jagielski et al., 2014, BMC Dermatol., 14:e3). Whereas, metagenomic sequencing, was performed directly on skin samples using ITS1-targeted primers, namely FungITS1 and FungITS2 (White et al., 1990, Mol. Ecol. 2:113-118).

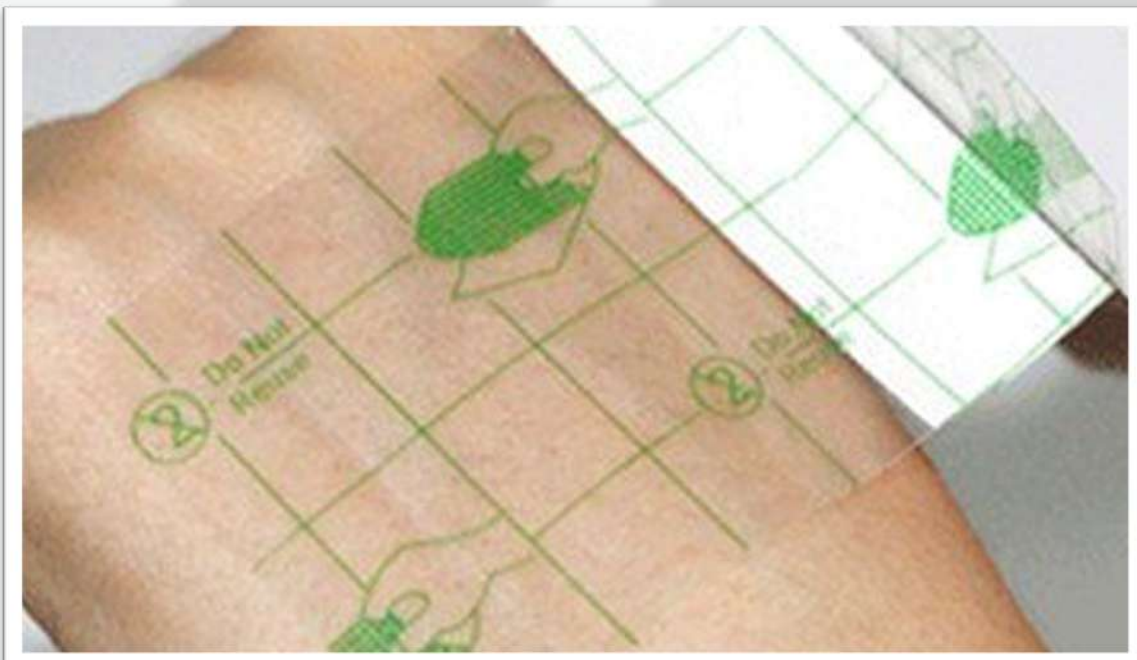


Fig.1 Sample collection. Material from healthy individuals was obtained with an OpSite dressing.

RESULTS

The overall positive culture rate was 44% for AD patients and 24% for healthy individuals. *Candida* spp. were recovered at the highest frequency (33.3%), followed by *Rhodotorula* spp. (21.6%) and *Malassezia* spp. (11.8%). Culture-based phenotypic and molecular (PCR-sequencing) methods used for species identification gave concordant results for 76.5% of the isolates cultured ($n=51$) (**Tab. 1**).

Tab.1. Species identification using the phenotypic and PCR-seq. based methods.
Disconcordand results are marked with grey.

Group	Phenotypic identification	PCR-seq. identification	% identity*	No. of isolates
AD patients	<i>Candida albicans</i>	<i>Candida albicans</i>	99.8-100%	3
	<i>Candida guilliermondii</i>	<i>Meyerozyma guilliermondii</i>	100%	3
	<i>Candida krusei</i>	<i>Pichia kudriavzevii</i>	100%	3
	<i>Candida lipolytica</i>	<i>Yarrowia lipolytica</i>	100%	1
	<i>Candida lusitanae</i>	<i>Clavispora lusitanae</i>	99.7%	1
	<i>Candida parapsilosis</i>	<i>Candida parapsilosis</i>	100%	1
	<i>Candida</i> sp.	<i>Candida zeylanoides</i>	100%	1
	<i>Cryptococcus uniguttulatus</i>	<i>Filobasidium uniguttulatum</i>	100%	1
	<i>Malassezia globosa</i>	<i>Malassezia globosa</i>	99.0-99.3%	2
	<i>Malassezia sympodialis</i>	<i>Malassezia sympodialis</i>	99.8-100%	3
	<i>Naganishia albid</i>	<i>Naganishia diffluens</i>	99.70-100%	4
	<i>Rhodotorula rubra</i>	<i>Rhodotorula mucilaginosa</i>	99.3-100%	9
	<i>Rhodotorula rubra</i>	<i>Rhodotorula diobovata</i>	99.7%	1
	<i>Rhodotorula</i> sp.	<i>Rhodotorula diobovata</i>	100%	1
	<i>Saccharomyces</i> sp.	<i>Nakazawaea holstii</i>	98%	1
	<i>Trichosporon beigelli</i>	<i>Cutaneotrichosporon dermatis</i>	100%	1
	<i>Wickerhamia fluorescens</i>	<i>Wickerhamia fluorescens</i>	99.4%	1
Healthy volunteers	<i>Acremonium</i> sp.	<i>Phialemonium</i> sp.	100%	1
	<i>Candida albicans</i>	<i>Candida albicans</i>	100%	3
	<i>Candida krusei</i>	<i>Pichia kudriavzevii</i>	100%	1
	<i>Kllockera japonica</i>	<i>Candida tropicalis</i>	100%	1
	<i>Malassezia sympodialis</i>	<i>Malassezia sympodialis</i>	100%	1
	<i>Pichia methanolica</i>	<i>Ogataea methanolica</i>	99.5%	1
	<i>Saccharomyces cerevisiae</i>	<i>Saccharomyces cerevisiae</i>	100%	1
	<i>Sporobolomyces</i> sp.	<i>Sporoblomyces roseus</i>	99.6%	1
	<i>Sterigmatomyces</i> sp.	<i>Cutaneotrichosporon curvatus</i>	100%	1
	<i>Trichiphyton cutaneum</i>	<i>Trichosporon domesticum</i>	99.8%	1
	<i>Trichosporon mucoides</i>	<i>Trichosporon montevidense</i>	100%	1
	<i>Zygosaccharomyces rouxii</i>	<i>Saccharomyces cerevisiae</i>	99.6%	1

*First hit according to BLAST Refseq ITS database (<https://www.ncbi.nlm.nih.gov/refseq/>).

Tab.2 Relative abundance of fungal classes and families in analyzed samples. Samples obtained from AD patients and healthy individuals are in grey- and cream-colored columns, respectively. The shortcuts in taxa names indicate taxa with „Incertae sedis” description („ls”) or taxa that could not be specified at presented taxonomic level („ni”).

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CONCLUSIONS

In conclusion, a higher positive culture rate, interpersonal diversity of the mycoflora, and a clear predominance of specific taxa were observed in AD patients when compared with healthy individuals.

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