The Role of Fungi in Atopic Dermatitis



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KEYWORDS

• Atopic dermatitis • Malassezia spp • Sensitization

KEY POINTS

- Malassezia spp is a genus of lipophilic yeasts and the most common fungus on healthy skin.
- Malassezia spp. may contribute to skin inflammation and flares during the course of atopic dermatitis.
- Some Malassezia species release immunogenic proteins (allergens), that elicit an IgE response and react with skin immune cells.
- IgE-mediated sensitization to Malassezia spp. is common in atopic dermatitis patients but rare in healthy individuals.

INTRODUCTION

Atopic dermatitis (AD) is a chronic relapsing inflammatory skin disorder, characterized by intensely itchy eczema. The prevalence of AD has tripled within the last 3 decades, currently affecting up to 30% of children and 10% of adults in industrial countries. The pathogenesis of AD is not fully understood. Besides some other environmental factors, the skin microbiome—the community of microorganisms colonizing the skin—has been attributed a pathogenic role in AD. The altered skin colonization with microorganisms in AD patients versus healthy individuals has been extensively investigated for bacteria, in particular *Staphylococcus aureus*. These aspects are highlighted in the article, (See Sun and Ong's article, "Infectious Complications in Atopic Dermatitis", in this issue). Recently, microbiome research extended the possible pathogenic role of fungi in AD. This research has focused on the commensal lipophilic yeast *Malassezia* spp because (i) AD patients are more frequently sensitized to *Malassezia* spp than healthy individuals, and (ii) AD patients may benefit from an antifungal therapy that is effective against *Malassezia* spp. This research led to the

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publication of a plethora of studies on the possible role of Malassezia spp in the development and course of AD. Several studies applied culture or molecular methods such as polymerase chain reaction (PCR) to assess possible differences in the epidemiology of Malassezia spp skin colonization between healthy and diseased skin such as AD. However, these studies obtained variable results presumably owing to methodical inconsistencies such as skin sampling from inconsistent body sites and the use of different cultivation methods or PCR primers. Next-generation sequencing is a molecular method that has been recently introduced into skin microbiome research, because it gives information on skin microbial communities that is complementary to cultivation or PCR. As for the bacterial skin microbiome, next-generation sequencing revealed that the skin fungal microbiome is highly specific for a particular body site.² Therefore, comparing the prevalence of Malassezia spp between different body sites sampled in different studies will give unreliable results. Also, the epidemiologic studies used different culture media to detect Malassezia spp. The authors (Glatz M, unpublished data, 2014) and others have shown that different culture media favor the growth of particular Malassezia spp. 3-6 Therefore, the use of only one or a few types of culture media does not necessarily depict the whole spectrum of Malassezia spp present in a sample. Surprisingly, studies comparing healthy individuals and AD patients did not reveal a difference in the frequency of skin colonization with Malassezia spp between both groups.6 It therefore appears as a medical conundrum how Malassezia spp on the one hand seems to contribute to the pathogenesis of AD patients and on the other hand is a commensal on healthy skin. Recent research at least partially elucidated the possible pathogenetic role of *Malassezia* spp in AD.

EPIDEMIOLOGY

The skin is an ecosystem and harbors diverse and body site—specific microbial communities, which have been termed the skin microbiome. The phylogenetic profiling of the skin microbiome revealed that fungi are part of the normal skin flora at all body sites and comprise 1% to 22% of the phylogenetic composition of the skin microbiome. Malassezia spp almost exclusively comprises of the fungal flora of the healthy skin on most body sites. It is therefore the main eukaryotic member of the microbial flora of the skin. Malassezia spp is a genus of lipophilic yeasts (Fig. 1). Most of the Malassezia spp lack the genes for fatty acid synthase genes and therefore rely

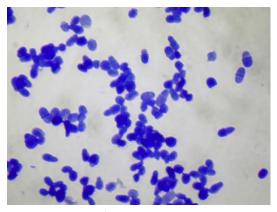


Fig. 1. *M sympodialis* culture isolated from a patient with AD, on *Malassezia* CHROM agar, grown for 72 hours at 32°C. (*From* Glatz M, Bosshard PP, Hoetzenecker W, et al. The role of Malassezia spp. in atopic dermatitis. J Clin Med 2015;4:1219; with permission.)

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