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# Microbes and Infection

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Original article

## cDNA representational difference analysis used in the identification of genes expressed by *Trichophyton rubrum* during contact with keratin

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### Abstract

Dermatophytes are adapted to infect skin, hair and nails by their ability to utilize keratin as a nutrient source. *Trichophyton rubrum* is an anthropophilic fungus, causing up to 90% of chronic cases of dermatophytosis. The understanding of the complex interactions between the fungus and its host should include the identification of genes expressed during infection. To identify the genes involved in the infection process, representational difference analysis (RDA) was applied to two cDNA populations from *T. rubrum*, one transcribed from the RNA of fungus cultured in the presence of keratin and the other from RNA generated during fungal growth in minimal medium. The analysis identified differentially expressed transcripts. Genes related to signal transduction, membrane protein, oxidative stress response, and some putative virulence factors were up-regulated during the contact of the fungus with keratin. The expression patterns of these genes were also verified by real-time PCR, in conidia of *T. rubrum* infecting primarily cultured human keratinocytes *in vitro*, revealing their potential role in the infective process. A better understanding of this interaction will contribute significantly to our knowledge of the process of dermatophyte infection.

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**Keywords:** *Trichophyton rubrum*; Representational difference analysis; Infection; Dermatophytoses

### 1. Introduction

Dermatophytoses are among the few fungal diseases that are directly communicable from person to person. Dermatophytes infect mainly healthy individuals, causing infections of keratinized structures, including the skin, hair, and nails [1]. Dermatophytes are not part of the normal human microbial flora. They are, however, particularly well adapted to infecting these tissues because, unlike most other microbial pathogens, they can use keratin as a source of nutrients [2].

*Trichophyton rubrum* is the most frequently isolated agent of dermatophytosis worldwide, accounting for approximately 80% of reported cases of onychomycosis [3]. Since 90% of the chronic dermatophyte infections are caused mainly by *T. rubrum*, this pathogen must have evolved mechanisms that evade or suppress cell-mediated immunity [4].

Despite its prevalence, little is known about the molecular basis of dermatophyte pathogenesis. Studies regarding the structure, expression, and regulation of the genes of *T. rubrum* have been relatively limited because of its unaggressive and non-life-threatening nature. In host–pathogen interactions, the gene expression of the pathogen is modulated by signals from the host, and knowing the pattern of expression may

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