

INVESTIGATION OF SUBTILISIN GENES IN DERMATOPHYTES ISOLATED FROM HUMAN DERMATOPHYTOSIS IN ARDABIL, NORTHWEST OF IRAN

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ABSTRACT : Keratinase enzymes are important virulence factors that play critical roles at the invasive stage of dermatophyte infection. In the present study, we evaluate the presence of genes encoding subtilisins (*SUB*) in four dermatophyte species includes that isolated from human dermatophytosis. Clinical specimens obtained from patients suspected of dermatophytosis were subjected to direct examination and culture. PCR technique using panfungal primers targeting the ITS region of the rDNA gene was used to confirm the identity of dermatophyte isolates. Finally, specific primers were used to determine the presence of *SUB* gene families in clinical isolates were evaluated. The prevalence of dermatophytosis in suspected patients was 13.7%. *Tinea corporis* (37.1%) was the predominant type of dermatophytosis. Totally, the difference reflected the low distribution of *SUB1* (50%) and *SUB5* (54.2%). In *T. mentagrophytes*, all isolates have *SUB2*, *SUB3*, *SUB4*, *SUB6* and *SUB7*. As well as 100% of *E. floccosum* strains have *SUB2* and *SUB7*. The most frequent *SUB* gene in *M. canis* isolates were *SUB3* (75%). In *T. rubrum* *SUB1* was not detected in any of isolates but *SUB2*, *SUB5* and *SUB7* were more prominent. In conclusion, the possession of *SUB* genes by different dermatophytes species armed the fungi with virulence factors needed to invade keratinized tissue and cause dermatophytosis. However, the low profile of some *SUB* genes in our clinical isolates indicates that not all *SUB* genes are involved in the pathogenesis of dermatophytosis. The characterization of proteins coded by *SUB* genes remains crucial to providing useful data that may disclose the contributory role of *SUB* genes in dermatophytes pathogenesis.

Key words : Dermatophytosis, Tinea, virulanve, subtilisin, polymerase chain reaction, Iran.

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INTRODUCTION

Dermatophytes are a group of molds that invade keratinized tissues, such as hair, skin, and nails of humans and animals causing spectrum of clinical conditions known as dermatophytosis (ringworm or tinea). They have a worldwide distribution and by the newly proposed classification, they comprise more than 50 species under seven genera (*Trichophyton*, *Epidermophyton*, *Nannizzia*, *Microsporum*, *Lophophyton*, *Arthroderma* and *Paraphyton*) (de Hoog *et al*, 2017). Transmission of dermatophytosis can be via direct contact with infected persons (anthropophilic), animals (zoophilic) or environmental soil (geophilic) (Richardson and Warnock,

2012). Clinical presentation of these infections is known as a 'tinea' and its variants include tinea corporis, tinea capitis, tinea pedis, tinea manum, tinea cruris, tinea barbae, tinea faciei, and tinea unguium (Degreef, 2008). Although, molecular mechanisms of dermatophyte–host interaction are still not fully explored, the capacity of dermatophytes to secrete protease enzymes that hydrolyze host keratin tissues of nail, hair, and stratum corneum of host skin is well known (Kaplan *et al*, 2020). Several proteases have already been isolated from various species of dermatophytes and showed keratinolytic, elastinolytic, and/or collagenolytic activities (Tsuboi *et al*, 1989 and Abdel-Rahman, 2001). Subtilisin-like proteases (*SUB*) are the group of endoproteases including keratinase found in