

Title: In silico characterization of cell wall genes with a tandem repeats involved with fungal infection in *Trichophyton rubrum*

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Trichophyton rubrum infect human keratinized tissue (skin, nails and, rarely, hair) and is the most common etiological agent of dermatophytoses worldwide. The transcriptome profile of *T. rubrum* after growth on keratin substrates was analysed using a microarray custom slide containing 6,091 sequences. Using the Dermatophyte Tandem Repeat Database (DTRDB) we identified a gene encoding an adhesin-like protein with a tandem repeat sequence. Tandem repeats are adjacent DNA sequences of 2-200 nucleotides in length and some tandem repeats are involved in the pathogenicity of microorganisms. These repetitive DNA sequences are found in different classes of fungal proteins, especially those involved in cell adhesion, a determinant factor for the establishment of fungal infection. The aim of this work was the functional and in silico characterization of two genes encoding cell wall protein with a tandem repeats sequence from *T.rubrum* GenBank Database. The functional analysis of protein sequences was carried out using the InterPro software package and gene expression was carried out by quantitative RT- PCR. *In silico* analysis showed that the two proteins contains at least 10 domains potentially involved with fungal adhesion. Moreover, the proteins contains 8 conserved common domains: cytoplasmic domain, non cytoplasmic domain, signal peptide, signal peptide C region, signal peptide H region, signal peptide N region, signal P-TM and transmembrane region. The expression of two adesins TERG_08771 (fold change 2.33) and TERG_05644 (fold change 1.42) was also induced during the *T. rubrum* growth in minimum medium added keratin for 24h, suggesting its role in fungal-host interactions.

Key words: cell wall, infection, keratin, *T. rubrum*, tandem repeats,

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