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Molecular Characterization of Subunit G of the Vacuolar ATPase in Pathogen Dermatophyte *Trichophyton rubrum*

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Abstract:

Trichophyton rubrum is an anthropophilic fungus causing up to 90% of chronic cases of dermatophytosis. Several properties of this fungus have been investigated so far. However, a few studies were carried out in the field of molecular biology of this fungus. In the present study, we tried to identify the subunit G of its vacuolar ATPase (V-ATPase). Pairs of 21 nt primers were designed from highly conserved regions of the V-ATPase subunit G genes in other fungi. Mentioned primers were utilized in PCR using isolated genomic DNA template as well as cytoplasmic RNA of *T. rubrum* and the PCR and RT-PCR fragments were then sequenced. About 469 nucleotides were sequenced which encoded a polypeptide with 119 amino acids. Nucleotide sequence comparison in gene data banks (NCBI, NIH) for both the DNA and its deduced amino acid sequence revealed significant homology with V-ATPase subunit G genes and proteins of other eukaryotic cells. The amino acid sequence of the encoded protein was about 84% identical to the sequence of V-ATPase subunit G from other fungi. In summary, we have cloned the first V-ATPase subunit G of dermatophytes and characterized it as a member of this gene family in other eukaryotic cells.

Keywords:

Fungal RNA , Fungal DNA

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