

SEQUENCE ANALYSIS AND STRUCTURE PREDICTION OF THE COMPLETE PREPRO-FORM GROUP 1 ALLERGEN OF ADULT *DERMATOPHAGOIDES FARINAE* (HUGHES) (ACARI: PYROGLYPHIDAE) FROM CHINA

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ABSTRACT - The cDNA coding for group 1 allergen of adult *Dermatophagoides farinae* (Hughes) (Acari: Pyroglyphidae) from China was cloned, sequenced and expressed successfully. Sequence analysis showed the presence of an open reading frame containing 966 bp that encodes a protein of 321 amino acids. Through bioinformatics analyses, the hydrophobic protein was demonstrated to be likely extracellular, with a cleavage site between positions 18 and 19. Interestingly, homology analysis showed that the Der f 1 shared greater than 88% identity in amino acid sequence with Eur m 1 but only 77% with Der p 1. Phylogenetic analyses suggested that *D. farinae* was evolutionarily closer to *Euroglyphus maynei* (Cooreman) than to *Dermatophagoides pteronyssinus* (Trouessart), even though *D. pteronyssinus* and *D. farinae* belong to the same genus *Dermatophagoides*. A total of three cysteine peptidase active sites were found in the predicted amino acid sequence, including 127-138 (QGCGSCWAFSG), 267-277 (NYHAVNIV GYG) and 284-303 (YWIVRNSWDTTWGDSGYGYF). Moreover, secondary structure analysis revealed that Der f 1 from China contained an alpha helix (34%), an extended strand (17%), a beta turn (6%), and a random coil (43%). A simple three-dimensional model of this protein was constructed using SWISS- MODEL server.

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