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Amino acid sequence analysis and molecular cloning of *Naegleria fowleri* proteins

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Naegleria fowleri is a thermophilic free-living amoeba that causes primary amoebic encephalitis (PAM) in humans, while *N. lovaniensis,* the morphologically identical species, is not. A two-dimensional (2-D) gel analysis was employed to compare total proteins in *N. fowleri* to those of *N. lovaniensis* in order to identify proteins that may link to its pathogenesis. Until now we have detected 63 protein spots in *N. fowleri* by means of N-terminal and/or internal amino acid sequences analyses. Due to lacking in the available genetic data of DNA of *N. fowleri*, it is sometime difficult to link information from the proteome analyses with information on DNA. In the present experiment, we partially cloned the genes of 2 protein spots, tentatively designated as #15(24.1kDa, pI6.5) and #35 (50.9 kDa, pI 16.7), that are specific to *N. fowleri* by means of degenerate PCR. The respective PCR products had approximately 250 bp and 400 bp in sizes. From the amino acid sequence predicted from the amplified DNA, #15 was identified with high confidence as thioredoxin peroxidase (22.3 kDa,Q6DV14) with 80% (54/67) homology. Similarly the predicted amino acid sequence of #35 showed 55% (67/120) homology to that of glutamate dehydrogenase (55.0kDa, Q54KB7).