High-throughput sequencing to explore the extrachromosomal plasmid rDNA of Naegleria fowleri AY27 genotype II: A human brain-eating Amoeba

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## Abstract

Naegleria fowleri is the only known Naegleria spp. that cause acute, fulminant, and rapidly fatal infection in the central nervous system of humans called primary amebic meningoencephalitis (PAM). We report a 28 years-old suspected PAM patient hospitalized in Karachi, Pakistan, with no earlier memoire of recreational activities but daily ritual ablution. Wet film observation of CSF showed amoebic trophozoites and confirmation of N. fowleri was done using Internal Transcribed Spacers detection method ((ITS-PCR). Clinical isolate of N. fowleri from patient CSF was sequenced for circular extrachromosomal ribosomal DNA (CERE - rDNA). The CERE contains 18S, 5.8S and 28S ribosomal subunits separated by internal transcribed spacers, 5 open reading frames (ORF's), and mostly repeat elements comprising 7268bp out of 15786bp (46%). A wide variety of variations and recombination events were observed. Finally, the ORF's that comprised of only 4 hypothetical proteins were modelled and screened against Zinc drug-like compounds. Two compounds [ZINC77564275 (ethyl 2-(((4-isopropyl-4H-1,2,4-triazol-3-yl)methyl)(methyl)amino)oxazole-4-carboxylate) and ZINC15022129 (5-(2-methoxyphenoxy)-[2,2'-bipyrimidine]-4,6(1H,5H)-dione)] were finalized as potential druggable compounds based on ADME toxicity analysis. We propose that the compounds showing least toxicity would be potential drug candidates after laboratory experimental validation is performed.

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