

Functional Enrichment Analysis and Antimicrobial Resistance Identification of Protozoan Naegleria Genome Through Insilco Approach (Karachi Strain Nf001)

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ABSTRACT

Objective: A brain eating ameba is in warm fresh water and soil (Nadeem *et al.*, 2023) known as Naegleria fowleri. There are different strains of N.Fowleri, the only human infecting Naegleria is fowleri (Herman *et al.*, 2021). The novelty of this research was to examine the resistance of a strain of N. fowleri from Pakistan to drugs, target genes and determine its annotations through genome analysis insilico.

Methods: The genome sequence strain NF001 (Tayyab *et al.*, 2023) was compared to the genomes of other strains. A phylogenetic analysis on Naegleria nucleotide sequences was done by MEGA. For the further investigation of potential loci that can be associated with AMR, the genome of N. fowleri was compared to the PubMLST database and ResFinder tool was employed, but no resistance genes were detected in CARD and ResFinder. AMR identification predict by FGENSESH 2.6. Protein to protein interaction (PPI) analyze by String and KEGG mapper database using the GO ID file.

Result: we developed pairwise distribution and employed tools, to efficiently evaluate our data. In addition, we conducted molecular typing by utilizing the species identification (species ID) for the Naegleria Fowleri genomic sequence to identify a match with bacteria (BACT000019) and HCM1_116. No resistance genes were detected in the Naegleria organism using a minimum threshold of 98% and a minimum length requirement of 60%. By ResFinder, prediction analysis for target genes using the FGENSESH software, applied to a Genome NF001 strain identified, Sequence Length: 19,822 base pairs., Predicted Genes: 8 genes, with 3 in the positive chain and 5 in the negative chain., Predicted Exons: 8 exons, also distributed across the chains similarly. Positions of predicted genes and exons: Variant 1 from 1.

Keywords: Naegleria Fowleri, phylogenetic tree, Molecular typing, Genomics, MEGA, Antimicrobial resistance, Machine learning algorithms.

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