

Antimicrobial Resistance of Naegleria Infections Using the Naegleria Genome and Bioinformatics Tools

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ABSTRACT

Monitoring the surveillance of infections and their phylogeny can help determine the nature of any organism species. Antibiotic resistance is also a common practice these days for public health and practitioners. This infection is mostly applicable in research with veterinary medicine, the environment, pharmaceutical firms, and private laboratories. Particularly those that work with organizations that undertake diagnoses, research, or observation. Online Bioinformatics tools are freely accessible and beneficial these days. Some of the major tools are useful in helping predict the outset of the disease. A current rise in global warming has led to the invasion of many microorganisms. The thermotolerant amoeba is a free-living organism that can survive in extreme temperatures. Naegleria can be found in moist soil and waters all over the world and they replicate in the warmer months when the temperature rises. As a result infecting the central nervous system via the neuroepithelium, resulting in a deadly infection that shows similarity with acute bacterial meningitis. This research was conducted to identify evolutionary relationships of strains having similarity to the genome of the Naegleria organism. Documented outbreaks of this infection are reported in recreational waters around the country. To establish a phylogenetic relationship, a total of 21 sample isolates were obtained from NCBI and analyzed by MEGA. A comparison of sequences from Naegleria and other species was also performed using PubMLST. For finding any resistance genes present in the organism we use the resfinder tool. The result computes by examining the genetic content of protozoans and finding their evolutionary relationships will help us identify their similarity. Using molecular typing technique with online tools can be used to identify whether these strains have similarity with other organisms. Our results proved to have gaps in the alignment and no resistance being present in the protozoa. This research placed emphasis on how to figure out where outbreaks are coming from and whether they have resistance to antibiotics. In context to the future it can also be helpful to figure out if Naegleria can develop resistance as these species are dangerous and can cause major illnesses. Molecular evolutionary research, as well as enormous amounts of sequence information, has made the research and development of antimicrobial resistance determinants approachable in an academic context.

Keywords: Naegleria Fowleri, Antimicrobial Resistance, Mega Software, Bioinformatics.

INTRODUCTION

Naegleria fowleri is a primary amoeba that survives on free living water and soils [1]. Naegleria fowleri may lead to a deadly cause which is primary amoebic meningoencephalitis also referred to as PAM [2]. People who swim, dive, or water ski in freshwater are at risk. Researchers focus is now on global warming due to the spread of N. fowleri in Pakistan [3]. Naegleria fowleri enters the brain olfactory bulb causing severe inflammation which result in death [4]. Because multiple genera of amoebae present in the same ecological area are morphologically similar, it is challenging to correctly identify Naegleria fowleri [5]. There is an urgent need for new medication developments that have rapid onset, are effective, safe, and permeable to the brain. Genes

can be identified globally using genomics, either fully or by identifying known protein domains that advance the possibility of molecular characterization. A comparative genomics approach can be used to obtain and search for the strains that set pathogens in the creation of medicines, vaccines, and diagnostics.

OBJECTIVES

The objectives of this research was to conduct a comparative genomic analysis of *Naegleria* and its strains to find their similarity and evaluate to see if the strains have developed resistance.

METHODOLOGY

The data collection was performed using this NCBI database. *Naegleria fowleri* genome (JX827422.1) Fasta file was used to blast the sequences and obtain the results. For many types of microbiological genomic data, NCBI constitutes primary experimental information. Blast Analysis was being done to obtain highly similar sequences to the sequences available in the database of the NCBI. 33 strains were selected from the blast results and their aligned Fasta file was used to observe the phylogenetic relationship in the mega software for this purpose. MEGA is an application software package that can be used to estimate evolutionary distances, reconstruct phylogenetic trees, and compute fundamental statistical values from genomic species. Mega was beneficial in identification of similarity in species with relation to its own relative strains. The UPGMA tree in mega was used to build the phylogenetic tree of *Naegleria* species as shown in figure 1.

RESULTS AND DISCUSSION

The Bacterial Isolate Genome Sequence Database (BIGSdb) program, which contributes the PubMLST databases, addresses the issue relating to molecular typing [6]. A comparison of sequences from *Naegleria* and other species strains was performed, and the results revealed gaps in the alignment as shown in Figure 2. Resfinder is a bioinformatics pipeline for identifying AMR genes and mutations and providing in silico predictions of organism’s phenotypes. This tool aggregates data from four functional meta-genomics research against 23 antimicrobials to find resistance genes. The result reveal no resistance genes being present in the *Naegleria* organism.

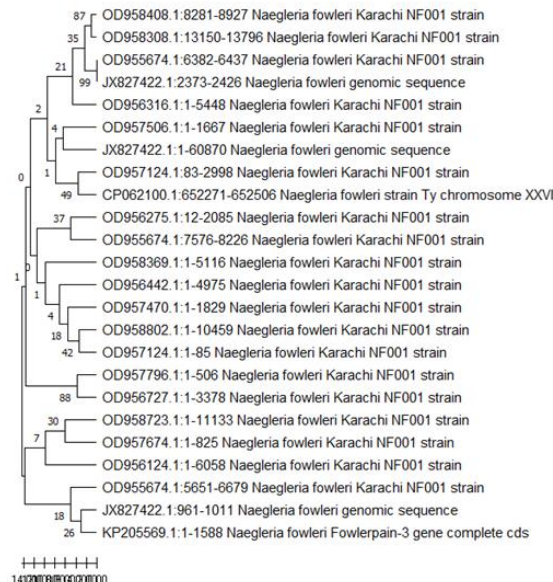


Figure 1. shows the phylogenetic trees of strains constructed with MEGA.

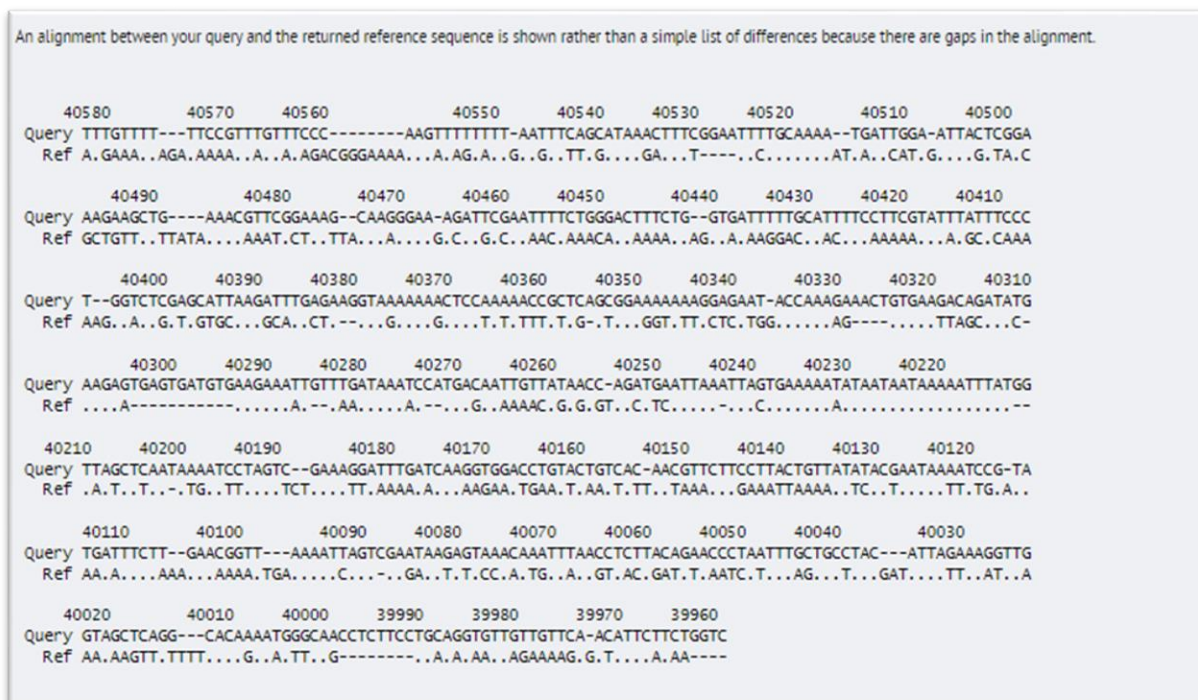


Figure 2. A comparison of sequences from Naegleria and other species strains was performed, and the results revealed gaps in the alignment

CONCLUSION

In conclusion AMR occurs when resistance genes are present in microorganisms undergo and they undergo random resistance over time. Antimicrobials as a result are used in practically all modern medical technologies to treat or prevent pathogens and infections. Our findings show that no resistance genes are found in Naegleria strains. It should be extended that in the future these strains could develop resistance.

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