Molecular identification of *Acanthamoeba*, *Naegleria fowleri* from various water sources, Egypt

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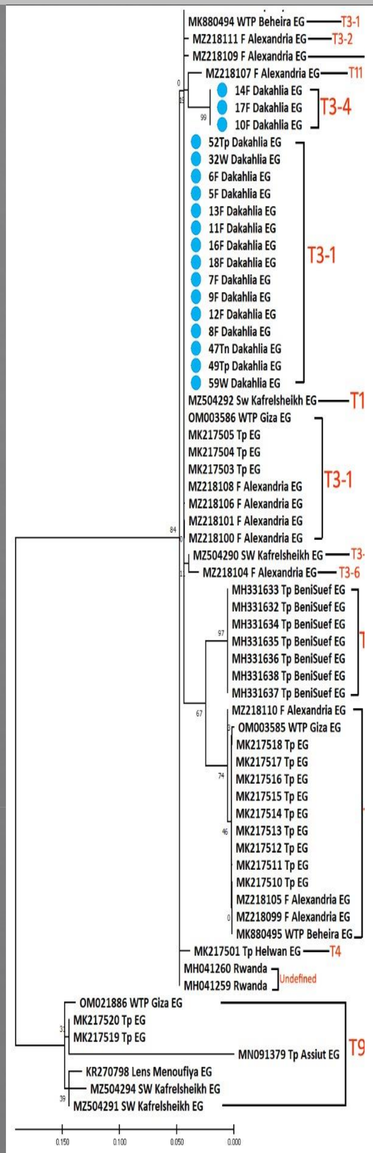
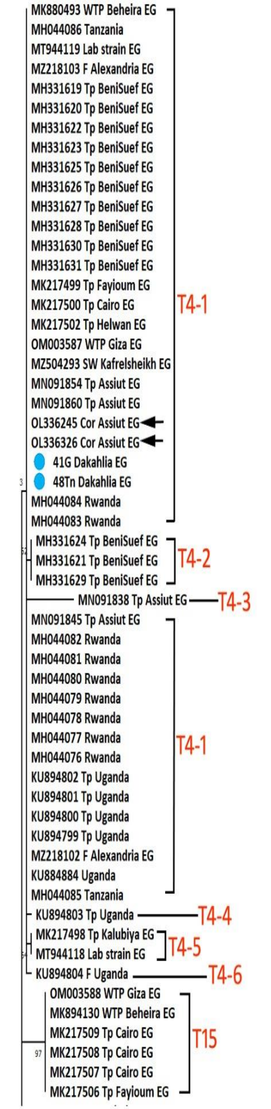
Introduction

- ✓ Water plays a significant role in the transmission of numerous pathogenic microorganisms. Water-borne pathogenic protozoan parasites including *Cryptosporidium spp., Giardia lamblia, Entamoeba histolytica, Blastocystis hominis* and free-living amoebae (FLA) as *Acanthamoeba* as well as *Naegleria spp.*
- ✓ *Acanthamoeba* can cause granulomatous amoebic encephalitis (GAE), whereas *N. fowleri*, is the causative agent of primary amoebic encephalitis (PAE). In addition, *Acanthamoeba* can cause a vision-threatening pathology (Acanthamoeba keratitis, AK) particularly in contact lens users.
- ✓ The objective was to detect the occurrence and to identify various genotypes of 2 potentially pathogenic waterborne protists (*Acanthamoeba* and *N. fowleri*) in water samples from various sources in Dakahlia governorate, Egypt. Comparisons have been made with earlier reports from Egypt and the Nile basin countries (whenever possible) to evaluate the potential water-associated threats to human health in Egypt.

Materials and Methods

- ✓ **Water sample collection**
- ✓ 190 water samples (10 litres each) were collected from various water sources in 5 different districts (Mansoura, Sandoub, Gedella, Mit-Mazah and Aga) in Dakahlia governorate
- ✓ **Water processing**
- ✓ **DNA extraction**
- ✓ using the DNeasy plant kits (Qiagen, Valencia, CA, USA) .
- ✓ **PCR amplification**
- ✓ Conventional PCR reactions were conducted to amplify *Acanthamoeba*, *Naegleria*, and *N. fowleri*
- ✓ **Sequencing**
- ✓ About 20positive bands of *Acanthamoeba* were incised, purified and sent for commercial sequencing (Colors lab, Cairo, Egypt).
- ✓ **Data analysis**
- ✓ To identify various patterns of epidemiology and genotyping for the tested protozoa in Egypt, electronic searches using various databases were conducted to collect all published articles on those protozoa in Egypt.. The collected sequences (including those of the present study) were aligned and used to construct the phylogenetic trees





Results

- ✓ ***Acanthamoeba*** **were molecularly detected in 38.7% from various sources including tap water, while *Naegleria spp.* were 9.6% samples from the Nile, of them 2 (3.2%) were identified as *N. fowleri*. The results of sequencing revealed the genotype T3 and T4 of *Acanthamoeba* .**
- ✓ **The results of earlier surveys from Egypt were combined with our current study, *Acanthamoeba* showed the highest mean prevalence (43.03%) with insignificant variations among various water sources. Finished water in drinking water treatment plants had lower prevalence in comparison to the raw water, but the filtration efficiency has not exceeded 60.0%. *Acanthamoeba* were found with the genotype T4 (the highly pathogenic type) was the most significantly identified type. A common T4 haplotype was found circulating in water from Egypt and 3 other countries (Tanzania, Rwanda, Uganda) located on the Nile basin. The Nile water has the greatest estimated mean prevalence of *Naegleria spp.* at 23.79%.**