

Molecular Characterization of *Acanthamoeba* species in Water Resources of Ordu Province in Turkey

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Aim of the study: The aim of this study was to perform the molecular identity of *Acanthamoeba* species in water samples collected from Ordu province in Turkey.

Material and Methods: The samples (roughly 500ml) were filtered by a cellulose nitrate membrane with a pore size of 0.45 µ. The filter was poured onto non-nutrient agar plates coated with *Escherichia coli*. DNAs were extracted and the occurrence of *Acanthamoeba* DNAs were tested by the genus-specific primer. Phylogenetic tree was drawn by comparing all data sets between our sequences and the small subunit (SSU) rRNA references sequences from GenBank by Bioedit and MEGA version 5.05.

Results: A total of 39 out of 75 samples (52%) were positive for *Acanthamoeba* species. The water samples from Ordu center (12/6), Ünye (18/10), Fatsa (24/12), Perşembe (21/11) were found positive for the contamination of *Acanthamoeba*. *Acanthamoeba* strains represented the members of sequence type 4 (T4) and T5 in the Neighbor-Joining (NJ), Maximum-Parsimony (MP) and Maximum-Likelihood (ML) trees. Phylogenetic tree showed that Haplotype-I was placed in the same lineage with *Acanthamoeba tringularis* with 96%, 98% and 95% bootstrap values in the NJ, ML and MP trees, respectively. Haplotype-II appeared to sister to *Acanthamoeba polyphaga* with 97%, 99% and 96% bootstrap values in the NJ, ML and MP trees, respectively. Haplotype-III was placed in the same lineage with *Acanthamoeba lenticulata*. This relation was supported with 96%, 85% and 95% bootstrap values in the NJ, ML and MP trees, respectively. This is the first study for the detecting of *Acanthamoeba* sp. in investigated area.

Keywords: *Acanthamoeba* sp., waterborne parasites, Ordu, (SSU) rRNA.