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Molecular identification and phylogenetic analysis of free-living amoeba in the water resources of Arak, Iran

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ABSTRACT

The aim of the present study was to detect free-living amoeba (FLA) in the water resources of Arak, Iran using molecular tools. A total of 154 samples were collected from different water supplies. Molecular analyses, sequencing, and phylogenetic study were conducted to confirm the species and genotypes of FLA. Fisher exact test was used to determine the significance. Of 154 water samples, 19 (12.3%) samples were tested positive for FLA. Three genotypes of *Acanthamoeba* including T4, subtype D, and T5 were identified among the isolates. The pathogenicity assay showed that the isolate of *Acanthamoeba* in drinking water was highly pathogenic. Three species of *Naegleria*, including *N. australiensis*, *N. pagei*, and *N. gruberi* were found among the samples. Six isolates of *Vermamoeba* were identified as *V. vermiformis*. Meanwhile, three other species including *Vannella* sp., *Vahlkampfia avara*, and *Stenamoeba polymorpha* were also recovered from the water samples. Statistical analysis showed a significant difference between the various water resources contaminated with FLA. This is the first study to reveal the presence of *S. polymorpha* in water sources in Iran. According to the findings of the present study, health officials should be beware of potential public health impacts of FLA in water resources.

Key words: Arak, FLA, genotype, Iran, phylogenetic study, Stenamoeba

HIGHLIGHTS

- Different species of Acanthamoeba, as well as Vermamoeba vermiformis, Naegleria australiensis, N. pagei, and N. gruberi were found in water resources.
- Three species of Vannella, as well as Vahlkampfia avara and Stenamoeba polymorpha were recovered from the water samples.
- This study is the first of its kind revealing the presence of *S. polymorpha* in Iran.

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