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<p style="text-align: center;"><b>TITLE</b></p> <p style="text-align: center;"><b>Isolation and molecular characterization of <i>Acanthamoeba</i> spp. from different environmental sources in Tabriz, northwest of Iran</b></p>	<p style="text-align: center;"><b>Behroz Mahdavi Poor<sup>1</sup>, *Abdolhossein Dalimi<sup>1</sup>, Fatemeh Ghafarifar<sup>1</sup>, Fariba Khoshzaban<sup>2</sup>, Jalal Abdolalizadeh<sup>3</sup></b></p> <ol style="list-style-type: none"><li>1. Department of Parasitology, Faculty of Medical Sciences, TarbiatModares University, Tehran, Iran</li><li>2. Department of Parasitology and Mycology, Faculty of Medical Sciences, Shabed University, Tebran, IR Iran.</li><li>3. Drug Applied Research Center, Tabriz University of Medical Sciences, Tabriz, Iran.</li></ol> <p style="text-align: center;"><b>* Corresponding author:</b> Dalimi_a@modares.ac.ir</p>
<p><b>Background:</b> The members of <i>Acanthamoeba</i> genus are among free-living amoeba (FLA) which could be a pathogenic parasite. The amoeba is a ubiquitous organism and has frequently isolated from wide variety of environmental samples.</p> <p><b>Materials and methods:</b> In this cross sectional study different natural and man-made habitats were evaluated for the presence of <i>Acanthamoeba</i> in Tabriz city from January to April 2016. Total of 74 samples were collected consisting of 16 dust samples of the eye hospital environments, 9 samples of hospital tap water, 8 soil samples, and 41 fixed and floating biofilm samples of swimming pools and hot tubs. All samples were cultured and screened for the presence of the amoebacyst or trophozoite. For molecular characterization, PCR and sequencing were conducted based on the genus specific fragment of 18S ribosomal RNA gene.</p> <p><b>Results:</b> <i>Acanthamoeba</i> spp. were microscopically detected in 2 (12.5%) dust samples, 6 (75%) soil samples, and 8 (19.5%) swimming pool and hot tub samples. The amoeba was not found in tap water samples. Out of 16 isolates, 12 were shown expected band in PCR amplification. Sequence analysis of 11 samples showed that isolated <i>Acanthamoeba</i> belonged to the T4 (82%) and T3 (18%) genotypes.</p> <p><b>Conclusion:</b> Because of the high prevalence rate of potentially pathogenic T4 genotype, it is necessary to pay more attention to the public health importance of the <i>Acanthamoeba</i> in the study area.</p>	