Acanthamoeba spp.

Subjects: Parasitology Contributor: Karolina Kot

Acanthamoeba spp. are free-living amoebas, which are widely distributed in soil, water, and air. They are capable of causing granulomatous amebic encephalitis, *Acanthamoeba* pneumonia, *Acanthamoeba* keratitis, and disseminated acanthamoebiasis.

Keywords: Acanthamoeba spp. ; free-living amoebas

1. Introduction

Acanthamoeba spp. are free-living amoebas (FLA) widely distributed in the environment, including soil, water, and air ^[1]. They are capable of causing cerebral (granulomatous amebic encephalitis, GAE) and extracerebral (*Acanthamoeba* keratitis, AK; *Acanthamoeba* pneumonia, AP; cutaneous acanthamoebiasis and disseminated acanthamoebiasis) life-threatening infections among humans ^[2]. *Acanthamoeba* spp. exist as an active (trophozoite) and dormant (cyst) forms. The cysts can abide and survive in various environments for years and transform into trophozoites under favorable environmental conditions ^[3].

Cerebral and extracerebral infections caused by *Acanthamoeba* spp. occur mostly among immunocompromised individuals, including HIV positive, organ transplant recipients, patients with chronic diseases, and those who undergo immunosuppressive therapy. Acanthamoebiasis has also been observed in immunocompetent individuals ^{[4][5]}. Despite low occurrence worldwide, the mortality rate of *Acanthamoeba* spp. infections is very high. The pathogenesis of acanthamoebiasis is not fully understood. *Acanthamoeba* spp. may invade through different ways, such as the respiratory tract or breaks in the skin, resulting in hematogenous dissemination to the brain ^[6]. *Acanthamoeba* spp. infections cases are often underdiagnosed and hence strong clinical suspicion along with laboratory technical expertise is required for early diagnosis and therapeutic intervention ^[7].

2. Biology of Acanthamoeba spp.

Acanthamoeba spp. exist in two distinct forms: an actively feeding and dividing trophozoite (15–45 μ m) and a dormant cyst stage (12–25 μ m) ^[8]. Both stages are infective to humans. Trophozoites of *Acanthamoeba* spp. actively feed on bacteria, yeast, algae and small organic particles. Cysts are formed after exposure to unfavorable environmental conditions, including changes in humidity, temperature, or environmental pH ^[4]. Cysts are resistant to many chemical and physical factors, including UV radiation, osmotic pressure, disinfectants, and antiseptics ^{[9][10]}. They can survive in the environment for more than 20 years ^[11].

3. Genome of Acanthamoeba spp.

Acanthamoeba species are identified based on the analysis of the diagnostic fragment 3 (DF3) region of the ribosomal DNA gene, designated *Acanthamoeba*-specific amplimer S1 (ASA.S1) ^[12]. DF3 encodes the highly variable stem 29-1 of the nuclear small subunit 18S rRNA gene ^[13]. *Acanthamoeba* genotypes are distinguished by a 5% or greater sequence difference between isolates ^{[14][15]}. To date, 22 sequence types have been identified, designated T1 through T22 ^[16]. However, Booton et al. ^[17], examining the DF3 subregion of ASA.S1 in the samples of T3 and T4 isolates, observed several unique sequences within T3 and T4 isolates. These sequences were designated T3/1–T3/5 and T4/1–T4/10 ^[17]. Due to the fact that different laboratories applied redundant numerical labels to identify different sequences, Fuerst and Booton ^[16] suggested new subtypes for the T4 genotype, which have been labeled T4A–T4F and T4Neff. The authors also described different sequences within T3 (labeled T3/01–T3/13), T5 (labeled T5/01–T5/15), T11 (labeled T11/01–T11/14), and T15 (labeled T15/01–T15/11). Types T2 and T6 are the most closely related pair of sequence types within *Acanthamoeba*, and these two types are considered as a supergroup in which five subtypes are formed: T2, T2/6A, T2/6B, T2/6C and T6 ^[16].

Among all genotypes, T4 is the most frequently isolated from nature, and it includes many pathogenic strains that have been associated with neurological and pulmonary acanthamoebiasis. It is assumed that T4 is characterized by increased virulence and increased resistance to chemotherapeutic agents ^[18]. The genotypes T1, T2, T4, T5, T10, T11, and T12 are the factors of granulomatous amebic encephalitis ^{[13][19]}, whereas T2, T4, T5, T16, and T18 may be the factors of *Acanthamoeba* pneumonia ^{[20][21][22][23]}.

4. Occurrence of Acanthamoeba spp. in the Environment

Acanthamoeba spp. are free-living protozoa that are widely distributed in the environment. Trophozoites and cysts of *Acanthamoeba* spp. with varying degrees of pathogenicity were found in the water, soil, and air samples. They occur in the rivers, seas, ocean sediments, lakes, ponds, hot springs, water sewage, swimming pools, rainwater, and even in mineral and bottled water ^[5]. In recent years, *Acanthamoeba* spp. have been isolated from tap water in Lithuania and city water in Iran ^{[24][25]}. In Poland, Derda et al. ^[26] isolated *Acanthamoeba* spp. from fountains, and Górnik and Kuźna-Grygiel ^[27] found the presence of pathogenic *Acanthamoeba* strains in natural recreational tanks and indoor as well as outdoor swimming pools. *Acanthamoeba* spp. strains were also isolated from potting soil, dust, air conditioning, dental units and dialysis stations ^[28]. Besides, amoebas were isolated from vegetables, fruits, mushrooms, but also from biological materials, such as swabs from the nasal mucosa, throat, and purulent secretions from the ear ^[26]. In Nigeria, the colonization of nasal mucosa by *Acanthamoeba* spp. was found in 24% of the studied participants ^[29]. The ubiquity of *Acanthamoeba* spp. is confirmed by the fact that 80% of the human population has natural IgG antibodies against *Acanthamoeba* spp. ^[30].

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