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Worldwide distribution of genotypes in *Acanthamoeba* keratitis: a systematic review

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Worldwide distribution of genotypes in *Acanthamoeba* keratitis: a systematic review.

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**Abstract**

*Acanthamoeba* spp. are among the most prevalent protozoa distributed in the world, causing diseases as *Acanthamoeba* keratitis, which is a painful and severe sight threatening corneal disease that in some cases can cause even blindness. In recent years, the prevalence of *Acanthamoeba* keratitis has rapidly increased, making it increasingly recognized as important for human health. This systematic review proposes to analyze the frequency of genotypes of the genus *Acanthamoeba* in keratitis cases around the world, as well as to analyze the types of samples collected and the identification methods used. Most cases were found in Asia and Europe. Undoubtedly, the T4 genotype was the most prevalent worldwide, followed by T3, T15, T11 and T5. Besides that, T4 genotype was also related to a greater number of species of *Acanthamoeba*. Given the differences in pathogenicity, virulence,

susceptibility to treatment and clinical outcomes between genotypes, genotyping of all isolates from cases of *Acanthamoeba* keratitis is essential to have a better correlation between *in vitro* and *in vivo* efficacy, resulting in better drug therapies and successful treatment in cases of this important ocular infection.

Keywords: free living amoebas, *Acanthamoeba* spp., keratitis, genotype

## **Introduction**

Free-living amoebae (FLA) of the genus *Acanthamoeba* are ubiquitously distributed in the nature (Siddiqui and Khan 2012). They can be isolated from practically all natural and artificial environments including soil, dust, water, air, medical equipment, lens fluids, air-conditioning and also in the nasopharyngeal mucosa of healthy individuals (Clarke and Niederkorn 2006; Nagyová et al. 2010a; Siddiqui and Khan 2012; Khezri et al. 2016; Tawfeek et al. 2016; Król-Turmińska and Olender 2017; Lass et al. 2017). *Acanthamoeba* spp. are among the most prevalent protozoa distributed in the world and are known as amphizoic organisms because they have the ability to exist both as free-living amoebae or as pathogenic and opportunistic parasites that often come into contact with humans, causing serious infections (Oddo 2006; Visvesvara et al. 2007; Lanocha et al. 2009).

Besides, they can cause infections by themselves, *Acanthamoeba* spp. are known to be “Trojan horses”, serving as hosts of a variety of pathogens microorganisms which may include viruses, protists and bacteria, may acting as a reservoir for maintaining and dispersing their endosymbionts in the environment (Greub and Raoult 2004; Berger et al. 2006; Siddiqui and Khan 2012).

As a parasite, *Acanthamoeba* can cause a clinical condition called granulomatous amebic encephalitis (GAE), which is an opportunistic, insidious and chronic infection of the

central nervous system characterized by relatively high mortality despite low incidence (Visvesvara et al. 2007; Visvesvara and Schuster 2008; Diaz 2010). These FLA can also cause several highly destructive disseminating infections concerning lungs, kidneys, liver, adrenal glands, heart, bones and skin, that can affect both immunocompromised and immunocompetent patients. However, the most common extracerebral infection caused by this amoeba is *Acanthamoeba* keratitis (AK) (Khan 2006; Ren and Wu 2010; Walochnik et al. 2015; Kot et al. 2018).

*Acanthamoeba* keratitis is a painful and severe sight threatening corneal disease that in some cases can cause even blindness. Unlike GAE, AK also occurs in immunocompetent individuals, as a result of poor hygiene in the care of contact lenses or after a corneal trauma (Visvesvara et al. 2007; Dart et al. 2009; Jercic et al. 2019). The clinical findings of AK include excruciating pain, considerable production of tears, photophobia, inflammation with redness, corneal abrasion and opacification, blurred vision, foreign body sensation, edema, stromal infiltration, epithelial loss, ring ulcers, cataract, glaucoma and even corneal perforation and vision loss if it's not treated aggressively and adequately (Khan 2006; Castrillón and Orozco 2013; Lorenzo-Morales et al. 2015). Meanwhile, the same symptoms can occur in bacterial, fungal and viral keratitis, making common the misdiagnosis, although the AK usually progresses slower than the others (Lorenzo-Morales et al. 2013). Besides that, cases of co-infection of *Acanthamoeba* spp. with fungi as *Fusarium* and *Candida* or bacteria as *Pseudomonas* have already been reported (Sharma et al. 2013; Nunes et al. 2016; Buchele et al. 2018).

In recent years, the prevalence of *Acanthamoeba* keratitis has rapidly increased, therefore it has become increasingly recognized as important in human health. The prevalence has increased due to availability of diagnostic methods that allow the differential diagnosis of other types of keratitis, as well as by the increase in the number of contact lens

(CL) users, which is the main risk factor for the disease (Khan 2006; Patel and Hammersmith 2008; Dart et al. 2009).

The number of contact lens users are growing every year worldwide and the number of AK cases has increased concomitantly with this number (Maycock and Jayaswal 2016). Currently, about 90% of patients diagnosed with AK are CL wearers, with reported rates between 1 to 33 cases per million. (Khan 2006; Visvesvara et al. 2007). Due to the fact that the amoeba gains access to the lens case through the air or tap water, AK infections related to CL are in most cases related to poor cleaning, overuse, swimming or sleeping with them. However, it is important to note that even patients who regularly disinfect the lens with multipurpose solution still can contract AK, since it has been shown that most commercially available cleaning solutions are ineffective against the protozoan (Kilvington et al. 2004; Hammersmith 2002; Shoff et al. 2008; Walochnik et al. 2015). One of the factors that can explain this situation is the biofilm formation after the contamination of contact lenses, which may enhance *Acanthamoeba* persistence on contact lens storage as well as providing nutrients for the amoeba, playing an important role in the pathogenesis of AK (Khan 2006). Other predisposing factors, even in users who don't wear contact lenses, include previous mechanical corneal trauma associated with the exposure of contaminated soil, water or vegetation (Jiang et al. 2006; Wesolowska et al. 2006; Lorenzo-Morales et al. 2015).

Diagnosis of AK is one of the most challenging corneal diseases to be diagnosed and is only often considered when there is a failure in the response to first line therapy for herpes simplex virus or bacterial/fungal keratitis. Besides that, diagnosis methods currently used are invasive because they require stromal biopsy or corneal scrapes, for example. Moreover, the sooner the disease is diagnosed, better are the chances of a successful prognosis (Dart et al. 2009; Page and Mathers 2013).

AK treatment is difficult and prolonged, becoming an extremely challenging problem due to the fact that there are no drugs specifically approved for this infection, so in general multiple antibacterial, antifungal and antiamoebic agents are used in combination to improve the results (Gokhale 2008; Wilhelmus et al. 2008; Juárez et al. 2018). It occurs because a lot of factors, including the wide range of virulence that the different genotypes of *Acanthamoeba* spp. show, make it almost impossible to establish a correlation between *in vivo* and *in vitro* drug activity efficacies. Beyond that, even after the clinical resolution, medications have to be used for a long time to prevent relapses, due to the fact that de cystic forms are extremely resistant (Kumar and Lloyd 2002; Astorga et al. 2011). In case of severe infection, corneal transplantation is the last therapeutic option when oral or topical treatments have failed (Kitzmann et al. 2009; Nguyen et al. 2010; Lorenzo-Morales et al. 2015). Among the measures that can be used to prevent the infection are educating lens wearers regarding the proper care of contact lenses and it's cases, using the appropriate disinfecting solutions, no overnight wear of CL and no showering or swimming with contact lenses, in order to avoid the contact with contaminated water (Visvesvara et al. 2007).

To avoid wrong treatments and early diagnosis, it is essential to know the pathogen. The life cycle of *Acanthamoeba* spp. consists in two stages, an actively feeding and reproduction trophozoite and a latent cyst stage, with minimal metabolic activity (Siddiqui and Khan 2012; Lorenzo-Morales et al. 2015). The trophozoites of *Acanthamoeba* spp. exhibit prominent vacuoles and typical acanthopodia, which are fine and spine-like structures on their surface. Their size is normally around 12–35 µm in diameter, but it can vary significantly between isolates, due to the many different genotypes and species (Khan 2006; Visvesvara et al. 2007; Costa et al. 2010). As a result of unfavourable environmental conditions as desiccation, changes in pH and temperature, increased osmolarity or hypo-osmolarity and food deprivation, the encystment occurs. Briefly, the trophozoite

becomes a cyst metabolically inactive, that has a double wall composed of an endocyst and ectocyst both containing cellulose (Marciano-Cabral and Cabral 2003; Munguía 2005; Siddiqui et al. 2012; Costa et al. 2010; Martín-Pérez et al. 2017). It allows the organism to survive extreme conditions, retaining its pathogenic properties for long periods of time in hostile environments, which justifies why AK treatment is so difficult, because *Acanthamoeba* encysts when the environment becomes unfavorable due to the medications. Both cysts and trophozoites can adhere to the surface, including soft or rigid CL and contact lens cases, allowing them to invade the eye tissues (Khan and Tareen 2003; Marciano-Cabral and Cabral 2003; Siddiqui and Khan 2012).

In an attempt to organize the increasing number of isolates belonging to the *Acanthamoeba* genus, Pussard and Pons (1977) initially classified the species based on morphological features of the cysts. Then, *Acanthamoeba* spp. were divided into three different morphological groups (I-III), according to their cyst shape of ectocyst and endocyst as well as the size. This methodology made it possible to differentiate more than 24 species of *Acanthamoeba* (Khan 2006; Visvesvara et al. 2007; Kłopotcka et al. 2009; Fuerst et al. 2015; Derda et al. 2016). Most AK infections are caused by representatives of group II, but some isolates belonging to the group III have also been described as causative agents of the disease. Among the species of *Acanthamoeba* that cause AK, the most prevalent are *Acanthamoeba polyphaga* and *A. castellanii*, although *A. culbertsoni*, *A. rhyodes*, *A. griffini*, *A. quina* and *A. lugdunensis* have also been described as causing the infection (Clarke and Niederkorn 2006; Visvesvara 2010; Lorenzo-Morales et al. 2015). Nevertheless, the classification based on morphology criteria is currently considered ambiguous and unreliable because species morphology may change according to the culture conditions, resulting in variations in cyst morphology, which is a very important characteristic for species identification. Moreover, several studies have demonstrated inconsistencies in cyst

morphology of the same isolate, indicating that morphological identification should not be used alone for the identification of species, requiring the use of molecular techniques (Khan 2006; Castrillón and Orozco 2013). To avoid these problems, nowadays molecular classification methods have been generated, which are usually classified on the basis of the nuclear small subunit 18S ribosomal RNA full gene sequence (Rns), which allows the differentiation of *Acanthamoeba* spp. into 22 genotypes (T1-T22) and encompass all the *Acanthamoeba* isolates found so far (Corsaro et al. 2015; Fuerst and Booton 2015; Corsaro et al. 2017; Taher et al. 2018).

Several studies across the world suggest that the predominant genotype in both keratitis and non-keratitis samples, has been the T4 genotype. Meantime, T2, T3, T5, T6, T8, T9, T11, T13, and T15 genotype species have also been isolated from patients with AK. Therefore, most genotypes known to date have at least once been involved with the disease in humans, although in the best of our knowledge, there are no studies that have taken global cases into account jointly, but analyzed regionally (Khan et al. 2002; Maghsood et al. 2005; Iovieno et al. 2010; Booton et al. 2009; Risler et al. 2013; Walochnik et al. 2014).

Molecular techniques, especially sequencing of 18S rRNA genes are increasingly being used for *Acanthamoeba* genotyping. The sequences obtained are compared to *Acanthamoeba* reference strains sequences, through multiple alignments with all available 22 genotypes, with the model assumption of a <5% sequence dissimilarity within them (Visvesvara et al. 2007; Lorenzo-Morales et al. 2015). Besides that, PCR-based methods have been developed for the rapid and useful detection of *Acanthamoeba*, which have good sensitivity and specificity (Schroeder et al. 2001; Fraser et al. 2012). Genotypic classification can be achieved by exploiting the inter-strain variations in the 18S ribosomal RNA (rRNA) subunit (Rns) sequence. The complete Rns gene exceeds 2000 nucleotides, then a fragment within the Rns gene named as “*Acanthamoeba* specific amplimer (ASA.S1)” with 423 to 551



bp is used for genotyping *Acanthamoeba* spp. (Schroeder et al. 2001; Booton et al. 2002; Zhao et al. 2010). The region ASA.S1 includes a conserved region named as ‘stem 29-1’ and a highly variable sequence called diagnostic fragment 3 (DF3) that has around 240 nucleotides and is widely used for *Acanthamoeba* genotyping. It’s important to note that the literature frequently refers the region of the gene identified by the amplicon ASA.S1 as the JDP, due to the fact that it is amplified using primers JDP1 and JDP2 (Stothard et al. 1998; Schroeder et al. 2001).

This systematic review proposes to analyze if the frequency of genotypes in the genus *Acanthamoeba* in cases of keratitis is the same in different geographic regions around the world, as well as analyzing the types of sample collection and the methods of identification of *Acanthamoeba* used, given its importance for the development of future specific drugs through better correlation between *in vitro* activity and *in vivo* efficacy, as well as for the improvement of diagnostic techniques, resulting in a better prognosis for patients with keratitis.

## **Materials and methods**

This systematic review has been conducted by searching on the database sources including PubMed, Science Direct, Scielo and Google Scholar for articles in English. No restrictions were placed on study date, therefore, articles were found between 2002 and 2020. The keywords used combined in our search strategy were “*Acanthamoeba*”, “keratitis” and “genotype”. All studies that estimated the genotypes of *Acanthamoeba* spp. in samples from patients with keratitis all around the world were included in this review.

Studies with samples other than samples from patients with keratitis or paraphernalia of contact lenses from patients with keratitis were excluded. Articles that do not have the country where the samples were collected or the genotype of the isolates were also excluded.

All required data such as number of cases, type of sample collected, genotype, molecular biology method employed, primers used, pairwise sequence identities, species of *Acanthamoeba*, collection country and year of the study were extracted from each of the eligible articles and entered into Microsoft Excel software.

## **Results**

Altogether, 2.934 papers were addressed based on four databases including PubMed, Science Direct, Scielo and Google Scholar. Of these, 97 papers were used in the current study, as they met the previously selected inclusion and exclusion criteria.

Our study collected data on the number of published articles that contained cases of keratitis caused by *Acanthamoeba* spp. and the respective genotypes and year of publication. Thereafter, the number of publications per year can be observed according to the Figure 1, where it's possible to see that the first publication took place in the year 2002 (Booton et al. 2002).

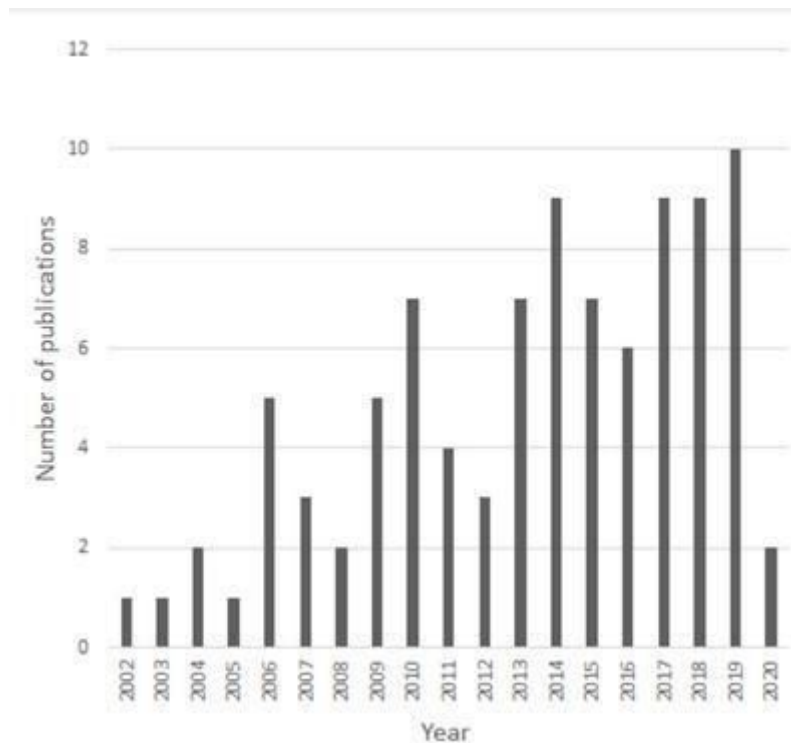


Figure 1: Number of publications per year of cases of *Acanthamoeba* keratitis that indicate the genotype of the isolate.

Regarding to the type of sample collected in each study, it is possible to observe that the most diverse samples were collected. Corneal scrapes were the most collected, followed by contact lens samples. However, most authors used more than one type of sample in their studies, associating corneal scrapings with corneal biopsies, contact lenses, corneal swabs, contact lens paraphernalia (lens maintenance solution, lens case), and these associations can be seen in detail in Table 1. Besides that, unusual samples were collected and used in only one study each, as corneal button (Zhao et al. 2010), vitreous fluid (Khairnar et al. 2011) and amniotic membrane (Sharifi et al. 2010), which is a graft used for treatment of corneal epithelial defects. Some studies did not specify the type of sample collected, using only terms such as “symptomatic keratitis human patients” or “corneal samples”. Six of the studies did not contain information about the sample collected.

Table 1: Details of the samples collected in each study and their respective references

| Type of sample collected | References   |
|--------------------------|--|
| Corneal scrapings        | Sharma et al. 2004; Zhang et al. 2004; Spanakos et al. 2006; Ertabaklar et al. 2007; Xuan et al. 2007; Ozkoc et al. 2008; Booton et al. 2009; Iovieno et al. 2010; Nagyová et al. 2010b; Niyyati et al. 2010; Nuprasert et al. 2010; Kliescikova et al. 2011; Lorenzo-Morales et al. 2011; Takaoka-Sugihara et al. 2012; Arnalich-Montiel et al. 2013b; Duarte et al. 2013; Buerano et al. 2014; Chomicz et al. 2014; Ghamilouie et al. 2014 a; Ghamilouie et al. 2014 b; Chomicz et al. 2015; Koltas et al. 2015; Behera et al. 2016; Padzik et al. 2016; Tawfeek et al. 2016; Baltaza et al. 2017; Padzik et al. 2017; Alves et al. 2018; Baltaza et al. 2018; Buchele et al. 2018; Fabres et al. 2018; Possamai et al. 2018; Taher et al. 2018; Bahreini et al. 2019; Baltaza et al. 2019; Omaña-Molina et al. 2019; Orosz et al. 2019; Tananuvat et al. 2019; Alver et al. 2020; Prithiviraj et al. 2020 |

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| Contact lens   | Jeong et al. 2007; Omaña-Molina et al. 2013; Heredero-Bermejo et al. 2015; Martín-Pérez et al. 2019   |
| Corneal scrapings, contact lenses  | Yera et al. 2008; Dendana et al. 2013; González-Robles et al. 2014; Abedkhozasteh et al. 2015; Hajjalilo et al. 2016; Omaña-Molina et al. 2016; Casero et al. 2017; Scheid and Balczun 2017 |
| Corneal scrapings, corneal biopsies  | Maghsood et al. 2005; Yera et al. 2007; Gatti et al. 2010; Arnalich-Montiel et al, 2014   |
| Corneal scrapings, contact lenses and contact lens paraphernalia                                     | Booton et al. 2002; Mubareka et al. 2006; Lorenzo-Morales et al. 2007; Niyiyati et al. 2009; Antonelli et al. 2018; Esboei et al. 2020  |
| Corneal scrapings and corneal button   | Zhao et al. 2010  |
| Corneal scrape, biopsies and/or cotton swabs, contact lenses and contact lens paraphernalia          | De Jonckheere 2003; Di Cave et al. 2009; Ledee et al. 2009; Risler et al. 2013; Del Chierico et al. 2016; Chegeni et al. 2019; Jercic et al. 2019   |
| Corneal scrapings and swabs, contact lens and contact lens paraphernalia (lens case, lens solutions) | Abe and Kimata 2010; Di Cave et al. 2014; Wagner et al. 2016  |
| Corneal and eye scrapings, corneal biopsy,   | Sharifi et al. 2010; Khairnar et al. 2011   |

|  |   |
|--|---|
| eye and corneal swabs, contact lens and it's solutions, vitreous fluid and amniotic membrane |   |
| Symptomatic keratitis human patients, corneal samples  | Paterson et al. 2011; Rahman et al. 2013; Niyyati and Dodanghe 2015; Rocha-Cabrera et al. 2015; Fu-Chin et al. 2017; Martín-Pérez et al. 2017; Nakaminami et al. 2017; Sant'Ana et al. 2017; Li et al. 2019 |
| No information   | Arnalich-Montiel et al. 2013a; Mirjalali et al. 2013; Rahman et al. 2013; Nakagawa et al. 2015; Megha et al. 2018; Niyyati et al. 2018  |

Regarding to the methods used, it is possible to infer that the vast majority of articles used the conventional PCR technique for the identification of *Acanthamoeba* isolates. However, other methodologies have been used, such as Real-time polymerase chain reaction (Nakagawa et al. 2015; Antonelli et al. 2018), RT polymerase chain reaction (RT-PCR) (Fu-Chin et al. 2017), triplex quantitative real-time polymerase chain reaction (qPCR) assay (Scheid and Balczun 2017), PCR-RFLP (Ghamilouie et al. 2014 b), real-time FRET PCR (Orosz et al. 2019), multiplex PCR (Sharma et al. 2004), and real-time fluorescence resonance energy transfer polymerase chain reaction (Orosz et al. 2018). In addition, some studies have associated methodologies, such as conventional PCR and Real-time PCR (Koltas et al. 2015), cDNA-AFLP and real time RT-PCR (Abedkhozasteh et al. 2015), besides conventional PCR e MALDI-TOF (Megha et al. 2018). JDP1 and JDP2 are the most widely used primer set, used in fifty studies. This primer set is utilized for PCR amplification of the

Rns amplicon ASA.S1 of 18S rRNA, which encodes the highly variable DF3 region. However, some studies used different combinations of primers, such as 5'-NTR and VP1 (Orosz et al. 2018; Orosz et al. 2019), CRN5-1137 and E528F-1492R (Martín-Pérez et al. 2017), 892C and JDP2 (Behera et al. 2016), SSU1 and SSU2 (Ertabaklar et al. 2007), YKF2 and JDF2 (Rahman et al. 2013), SSU2F and JDP2 (Risler et al. 2013) and also eukaryote-specific primers CRN5 and 1137, which amplify the GTSA.B1 (Possamai et al. 2018, Nagyová et al. 2010a).

The ideal percentage of similarity between isolates and genotypes sequences of databases is higher than 95%, considering that each genotype is similar, with few differences, we need to be sure of the result. In the studies analyzed, most articles comply with this suggestion. Meanwhile, many articles did not even contain this information and others had similarity values between 95 and 97%.

In the studies analyzed, genotyped cases of keratitis caused by *Acanthamoeba* spp. were found on 4 continents, being Asia, America, Europe and Africa. Genotyped *Acanthamoeba* isolates were found in 31 countries around the world, in 8 countries in Asia, 7 in America, 14 in Europe and 2 in Africa. In addition, two of the studies did not specify the country where the samples were collected, calling them ‘‘North America’’ and ‘‘Southern Africa’’, referring only to the continent. No studies pertaining to the continent Australia have been found so far.

The total number of genotyped cases of amoebic keratitis caused by *Acanthamoeba* spp. found worldwide is equal to 878. Of these, were found 373 in Asia, 197 in America, 268 in Europe and 40 in Africa. The total number of cases per genotype in each continent can be seen in Figure 2. In this same figure, we can see that the T4 genotype is the most prevalent and Asia is the continent where there are more cases of this genotype.

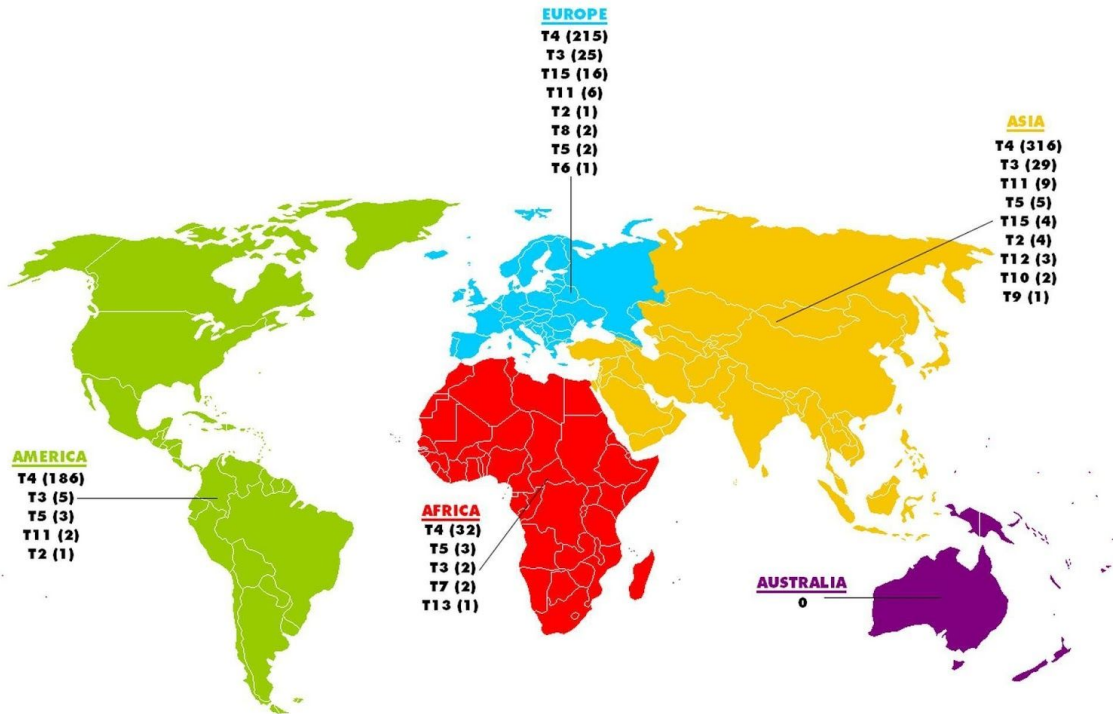


Figure 2: Relationship between cases of amoebic keratitis caused by *Acanthamoeba* spp. with their respective continents and genotypes found. In parentheses, the number of cases of each genotype can be seen.

In Figure 3 it is possible to observe that, undoubtedly, the T4 genotype is the most prevalent worldwide, corresponding to 749 of the total 878 cases. In addition, the prevalence of each genotype and the respective number of cases (in parentheses) were: T3 (61), T15 (20), T11 (17), T5 (13), T2 (6), T12 (3), T7 (2), T8 (2), T10 (2), T6 (1), T9 (1) and T13 (1). Besides that, it's possible to see that genotypes T1, T14, T16, T17, T18, T19, T20, T21 and T22 were not found to cause AK.



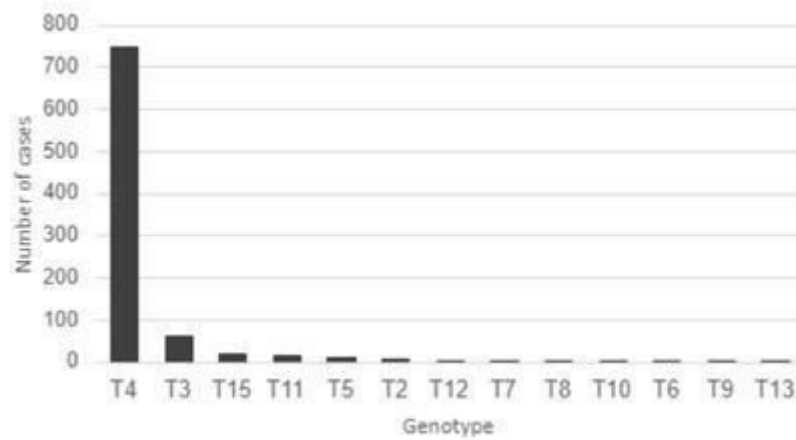


Figure 3: Absolute number of worldwide cases of *Acanthamoeba* keratitis and their respective genotypes.

In more detail, Table 2 shows the number of cases of each genotype in the different countries in each continent and their respective references.

Table 2: Countries where cases of keratitis were found on each continent and their respective genotypes. The number of cases for each genotype can be found in parentheses.

| Continent   | Genotypes  | References   |
|-------------|--|--|
| <b>Asia</b> |  |  |
| China       | T4 (55) T3 (2)                                     | Booton et al. 2002; Zhang et al. 2004; Zhao et al. 2010; Li et al. 2019            |
| India       | T4 (66), T11 (4), T12 (3), T10 (2), T5 (2), T3 (1) | Sharma et al. 2004; Behera et al. 2016; Megha et al. 2018; Prithiviraj et al. 2020 |

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|-------------|---|--|
| Iran        | T4 (90), T3 (5), T11 (5),<br>T2 (3), T9 (1) | Niyyati et al. 2009; Niyyati et al. 2010; Mirjalali et al. 2013; Ghamilouie et al. 2014a; Ghamilouie et al. 2014b; Abedkhojasteh et al. 2015; Maghsood et al. 2015; Niyyati and Dodanghe 2015; Hajjalilo et al. 2016; Niyyati et al. 2018; Bahreini et al. 2019; Chegeni et al. 2019; Esboei et al. 2020 |
| Japan       | T4 (61), T3 (6), T5 (2)                     | Abe and Kimata 2010; Takaoka-Sugihara et al. 2012; Rahman et al. 2013; Nakagawa et al. 2015; Nakaminami et al. 2017  |
| Korea       | T4 (9)                                      | Jeong et al. 2007; Xuan et al. 2007  |
| Philippines | T4 (1)                                      | Buerano et al. 2014  |
| Taiwan      | T4 (2)                                      | Fu-Chin et al. 2017  |
| Thailand    | T4 (5), T5 (1)                              | Nuprasert et al. 2010; Tananuvat et al. 2019   |
| Turkey      | T4 (27), T3 (15), T15 (4),                  | Ertabaklar et al. 2007;  |

|  |        |  |
|--|--------|--|
|  | T2 (1) | Ozkoc et al. 2008; Koltas et al. 2015; Alver et al. 2020 |
|--|--------|--|

### America

|               |                          |  |
|---------------|--------------------------|--|
| Argentina     | T4 (10)                  | Casero et al. 2017   |
| Brazil        | T4 (22), T3 (1), T5 (1)  | Duarte et al. 2013; Sant'Ana et al. 2017; Alves et al. 2018; Buchele et al. 2018; Fabres et al. 2018; Possamai et al. 2018 |
| Canada        | T4 (29)                  | Mubareka et al. 2006; Khairnar et al. 2011   |
| Chile         | T4 (73), T11 (2), T2 (1) | Jercic et al. 2019   |
| Mexico        | T4 (4), T3 (2)           | Omaña-Molina et al. 2013; González-Robles et al. 2014; Omaña-Molina et al. 2016; Omaña-Molina et al. 2019;                 |
| United States | T4 (35), T3 (2), T5 (1)  | Booton et al. 2009, Ledee et al. 2009  |
| Venezuela     | T4 (13)                  | Wagner et al. 2016   |
| North America | T5 (1)                   | Iovieno et al. 2010  |

### Europe

|                |   |  |
|----------------|---|--|
| Austria        | T6 (1)                                      | Blaschitz et al. 2006  |
| Belgium        | T4 (15)                                     | De Jonckheere 2003   |
| Czech Republic | T4 (3), T3 (1)                              | Nagyová et al. 2010b;<br>Kliescikova et al. 2011   |
| England        | T4 (1)                                      | Paterson et al. 2011   |
| France         | T4 (33), T3 (3), T2 (1), T5<br>(1), T11 (1) | Yera et al. 2007; Yera et al.<br>2008; Risler et al. 2013  |
| Germany        | T4 (1)                                      | Scheid and Balczun 2017  |
| Greece         | T4 (4), T5 (1)                              | Spanakos et al. 2006   |
| Hungary        | T4 (6), T8 (2)                              | Orosz et al. 2018; Orosz et<br>al. 2019  |
| Italy          | T4 (68), T15 (14), T3 (12),<br>T11 (1)      | Di Cave et al. 2009; Del<br>Gatti et al. 2010; Di Cave et<br>al. 2014; Chierico et al.<br>2016; Antonelli et al. 2018  |
| Poland         | T4 (31)                                     | Chomicz et al. 2014;<br>Chomicz et al. 2015; Padzik<br>et al. 2016; Baltaza et al.<br>2017; Padzik et al. 2017;<br>Baltaza et al. 2018; Baltaza<br>et al. 2019 |

|          |                                      |   |
|----------|--------------------------------------|---|
| Slovakia | T4 (3), T15 (1)                      | Nagyová et al. 2010b  |
| Spain    | T4 (40), T3 (8), T11 (3)             | Lorenzo-Morales et al. 2007;<br>Lorenzo-Morales et al. 2011;<br>Arnalich-Montiel et al.<br>2013a; Arnalich-Montiel et<br>al. 2013b; Arnalich-Montiel<br>et al, 2014;<br>Heredero-Bermejo et al.<br>2015; Rocha-Cabrera et al.<br>2015; Martín-Pérez et al.<br>2017; Martín-Pérez et al.<br>2019 |
| Sweden   | T4 (10), T3 (1), T11 (1),<br>T15 (1) | Sharifi et al. 2010   |

### **Africa**

|                 |                                    |   |
|-----------------|------------------------------------|---|
| Egypt           | T4 (27), T5 (3), T3 (2), T7<br>(2) | Tawfeek et al. 2016; Taher<br>et al. 2018 |
| Tunisia         | T4 (5)                             | Dendana et al. 2013                       |
| Southern Africa | T13 (1)                            | Grün et al. 2014                          |

This systematic review showed that the T4 genotype, the most prevalent, besides being responsible for the largest number of cases worldwide, is also related to a greater number of species of *Acanthamoeba*. In addition, it can be seen in Table 3 that the same species is related to different genotypes. For example, *A. castellani* and *A. palestinensis* belong to genotype T4 and T2 each, *A. culbertsoni* belong to genotype T4 and T10 and *A. hatchetti* belong to genotype T4, T6 and T11. However, it is important to note that most articles do not have the identification of *Acanthamoeba* species.

Table 3: *Acanthamoeba* species related to each genotype and their respective references.

| Genotypes | Species  | References   |
|-----------|--|--|
| T4        | <i>A. castellani</i> , <i>A. polyphaga</i> , <i>A. palestinensis</i> , <i>A. culbertsoni</i> , <i>A. triangularis</i> , <i>A. rhysodes</i> , <i>A. royreba</i> , <i>A. quina</i> , <i>A. hatchetti</i> | Maghsood et al. 2005; Spanakos et al. 2006; Ertabaklar et al. 2007; Xuan et al. 2007; Ozkoc et al. 2008; Di Cave et al. 2009; Sharifi et al. 2010; Omaña-Molina et al. 2013; Di Cave et al. 2014; Ghamilouie et al. 2014b; Koltas et al. 2015; Omaña-Molina et al. 2016; Casero et al. 2017; Baltaza et al. 2017, Fu-Chin et al. 2017; Nakaminami et al. |

|    |  |   |
|----|--|---|
|    |  | 2017; Padzik et al. 2017; Sant'Ana et al. 2017; Baltaza et al. 2018; Megha et al. 2018; Taher et al. 2018; Baltaza et al. 2019; Omaña-Molina et al. 2019; Prithiviraj et al. 2020   |
| T2 | <i>A. castellani; A. palestinensis</i> | Maghsood et al. 2005; Alver et al. 2020   |
| T3 | <i>A. griffini</i>                     | Maghsood et al. 2005; Sharifi et al. 2010; Di Cave et al. 2014; González-Robles et al. 2014; Heredero-Bermejo et al. 2015; Koltas et al. 2015; Omaña-Molina et al. 2016; Megha et al. 2018; Taher et al. 2018; Martín-Pérez et al. 2019 |
| T5 | <i>A. lenticulata</i>                  | Spanakos et al. 2006; Ledee et al. 2009; Iovieno et al. 2010; Rahman et al. 2013; Megha et al. 2018; Taher et al. 2018  |

|     |                                    |  |
|-----|------------------------------------|--|
| T6  | <i>A. hatchetti</i>                | Blaschitz et al. 2006, Megha et al. 2018   |
| T7  | <i>A. astronyxis</i>               | Tawfeek et al. 2016  |
| T11 | <i>A. stevensoni, A. hatchetti</i> | Sharifi et al. 2010; Lorenzo-Morales et al. 2011; Hajjalilo et al. 2016; Prithiviraj et al. 2020 |
| T10 | <i>A. culbertsoni</i>              | Behera et al. 2016   |
| T15 | <i>A. jacobsi</i>                  | Di Cave et al. 2009; Sharifi et al. 2010; Koltas et al. 2015; Di Cave et al. 2014                |

## Discussion

As a result of their ubiquity, the cosmopolitan protozoa of the genus *Acanthamoeba* pose a risk to human health, due to their ability of being inside the host or in the environment. Studies are still needed in order to elucidate the pathogenesis of AK and other diseases caused by this free-living amoeba, for improvement of diagnostic techniques and medications with specific therapeutic targets.

Our study shows that in the last 20 years there has occurred a crescent increase in the number of articles containing the genotyping of *Acanthamoeba* isolates causing keratitis, especially in the last decade. Nevertheless, unfortunately the pandemic of Sars-Cov-2 caused the number of publications to decrease almost as it did twenty years ago, which is obviously an exception to the upward trend. Several factors are related to the increase in the number of



AK cases worldwide every year, such as the widespread use of contact lenses for vision correction or cosmetic purposes and better diagnostics, therefore becoming an emerging disease (Panjwan 2010; Astorga et al. 2011). However, we believe that the number of cases is still underreported and, in addition, not all diagnosed cases are genotyped. Although there are several studies with genotyping in certain countries, to the best of our knowledge did not exist until the present moment a single study that listed all of these cases, thus providing a worldwide idea of the frequency of these genotypes in AK.

Various sample collection methods have been shown to be effective for the isolation of *Acanthamoeba* spp. causing keratitis, such as corneal scraping, corneal biopsies and corneal smears, as well as collections of contact lenses and their accessories, such as lens cases and solutions for lenses. However, our study shows that the most chosen samples for the isolation of *Acanthamoeba* were the corneal scrape and contact lenses of patients with keratitis.

Although our review shows that several different techniques can be used for the diagnosis of *Acanthamoeba*, it also shows that a very useful molecular technique used for the detection and genotyping of *Acanthamoeba* spp. is the Polymerase Chain Reaction (PCR) and that this is the methodology used in the vast majority of studies, with rare exceptions. The method is usually performed through amplification of the fragment of the 18S rRNA gene using the JDP1 (5'-GGCCCAGATCGTTTACCGTGAA-3') and JDP2 (5'-TCTCACAAGCTGCTAGGGAGTCA-3') primers (Schroeder et al. 2001; Lorenzo-Morales et al. 2015).

Nevertheless, other sets of PCR primers would also provide genotype identification, since the amplicon ASA.S1 did not appear to distinguish between all sequence types. The genotype specific amplicon B1 (GTSA.B1) has proven to be accurate in identifying the

different genotypes (Fuerst et al. 2015), having been chosen in two studies (Nagyová et al. 2010b; Possamai et al. 2018).

The detection of *Acanthamoeba* genotypes in keratitis patients can also be performed using real-time PCR assay. This method allows an accurate and rapid diagnosis (Visvesvara et al. 2007; Corsaro et al. 2015; Maycock and Jayaswal 2016), then several studies have also reported its use alone (Nakagawa et al. 2015; Fu-Chin et al. 2017; Antonelli et al. 2018) or in association with other methodologies, as the conventional PCR (Koltas et al. 2015) or cDNA-AFLP (Abedkhojasteh et al. 2015). Furthermore, one study (Sharma et al. 2004) used a multiplex real-time PCR assay, that has been newly used and developed for the detection of FLA. In addition to enabling simultaneous detection of *Acanthamoeba* and other FLA of the genres *Naegleria* and *Balamuthia* in the same human specimen, it also allows the detection of 10 different genotypes of *Acanthamoeba* at the same time, which could facilitate the laboratory routine in genotyping isolates (Qvarnstrom et al. 2006; Goldschmidt et al. 2009). Another method used in one article (Ghamilouie et al. 2014b) that has been shown to be effective and sensitive is the Restriction Fragment Length Polymorphism (RFLP), which is the phylogenetic analysis of mitochondrial DNA, allowing understanding about the relationships among different *Acanthamoeba* strains (Kong et al. 2002; Schuster and Visvesvara 2004; Fuerst et al. 2015). In the last years, a method called Matrix-assisted Laser Desorption-ionization Time-of-flight MS (MALDI-TOF MS) has been improved for different microorganisms including protists. It has been used not only for identifying but also to establish strain differences based on biomarkers fingerprints that are characteristic protein patterns. Among the advantages, it is possible to mention that it is a practical and rapid method, enabling identification of amoeba in 15 minutes (Moura et al. 2003a; Moura et al. 2003b). However, this methodology still needs to be improved for the diagnosis of

*Acanthamoeba*, because there are still divergences between the results obtained by it and by conventional PCR (Megha et al. 2018).

Our study shows that, when analyzing all genotyped cases of AK, there are 749 cases genotyped as T4, which corresponds to 85,31% of the total number of cases reported worldwide. In addition, the T4 genotype was the most prevalent on all continents where cases of keratitis were found, which suggests that even in different countries, isolates with this genotype may have similar pathogenic properties. It is known that an important initial step in the pathogenesis of AK is the adherence to corneal epithelial cells that is strongly related to expression of mannose binding protein. This mannose binding protein in T4 genotype appears to bind more tightly to the membrane surface of host cells, making this genotype more cytotoxic than others, culminating in a greater number of infections (Hurt et al. 2003; Garate et al. 2006; Ledee et al. 2009; Noorjahan 2010). Besides that, exposure to mannose generates liberation of a low molecular weight protease called MIP133, which has the ability to cause cytolytic effect to corneal epithelial cells (Hurt et al. 2003; Garate et al. 2006; Ledee et al. 2009; Noorjahan 2010). As a result, it is suggested that T4 is the most virulent genotype and owner of properties that enhance its transmissibility, given its greatest environmental distribution (Maghsoud et al. 2005; Ledee et al. 2009). Therefore, the highest mannose binding protein expression in T4 genotype could be an effective specific target for new therapeutic approaches that would serve as a treatment for the vast majority of cases of amoebic keratitis.

In addition to T4, our study shows that the second most prevalent genotype is T3, with 61 reported cases, followed by T15 with 20 cases, T11 with 17 and T5 with 13. Other genotypes were also reported as keratitis causing, although less frequently, as T2 (6 cases), T12 (3 cases), T7, T8 and T10 (2 cases each). In addition, the T6, T9 and T13 genotypes also caused *Acanthamoeba* keratitis, with one case each. It is also possible to observe that the

distribution of frequencies between genotypes in the four continents where cases of AK were found is very similar. Related to T3, it was the second most prevalent genotype in three of the four continents where the AK cases were reported. The exception occurred in Africa, where the T5 genotype was the second most prevalent. However, it is important to note that the diagnosis of AK is difficult, and the vast majority of diagnosed cases are not genotyped. Furthermore, our study clearly showed that there is a difference in the number of genotyped cases between the continents, with the African continent having the lowest number of cases and Asia the largest, probably on account of financial resources. Even so, the genotypic distribution of cases reported worldwide so far has been described in our study.

Although the T4 genotype is the most prevalent, genotyping of all isolates from cases of *Acanthamoeba* keratitis is essential, due to the fact that scientific literature shows that infections caused by non-T4 genotypes are more aggressive. Besides, the outcomes are extremely unfavorable (Iovieno et al. 2010; Sharifi et al. 2010). Moreover, more resistance to multipurpose contact lens cleaning solutions are related to non-T4 genotypes, as T3 and T5 (Shoff et al. 2007), besides a worse response to medical therapy, longer delays to diagnosis when compared with T4 genotype and greater need for surgical intervention, that is, worse clinical outcomes (Arnalich-Montiel et al. 2014).

Our study made it possible to observe that although *A. castellani* and *A. polyphaga* be the species whose genotype is T4 in most isolates, other species were part of this genotype, such as *A. culbertsoni*, *A. triangularis*, *A. rhyodes*, *A. royreba*, *A. quina*, and *A. hatchetti*. In addition, *A. castellani* and *A. palestinensis* were also related to T2 genotype and the T3 genotype were only related to *A. griffini*. That is, the classification of *Acanthamoeba* in species and genotypes still needs to be improved, so that these relationships are more clearly understood. Besides that, we agree with a recent study (Corsaro 2020), which says that the identification of *Acanthamoeba* would currently have a clearer organization, due to the fact

that the classification using only morphology was once appropriate, but today it is cause for confusion, relating several species to the same genotype.

It is also important to mention that there is still no single effective treatment that can be used in cases of AK, so novel therapeutics are needed in order to totally eliminate both amoeba life forms, that is, trophozoites and cysts. It is important to remember that cysts are very resistant and related to the recurrence of infection. Given the differences in pathogenicity, virulence, susceptibility to treatment and clinical outcomes between genotypes, genotyping is a path to be taken so that we have a better correlation between *in vitro* and *in vivo* efficacies, resulting in better drug therapies and successful treatment in AK cases.

In conclusion, *Acanthamoeba* genotyping is very important not only for taxonomic purposes and understanding the geographical distribution of species, but also for clinical and epidemiological studies, understanding the pathogenesis and clinical outcomes of this infection. The scientific literature shows that non-T4 genotypes produce worse symptoms and have poorer response to medical therapy than genotype T4 (Arnalich-Montiel et al. 2014), although more than 85% of *Acanthamoeba* keratitis cases have been linked with T4 genotype, which is why it's supposedly the most virulent. AK remains a challenging disease to diagnose and treat, so further studies should be conducted in order to elucidate what makes some genotypes more pathogenic than others. This information would also play a fundamental role in providing more reliable diagnosis and novel therapeutic strategies.

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**Conflict of interest**

The authors declare that they have no conflict of interest.

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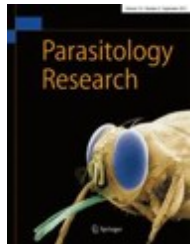


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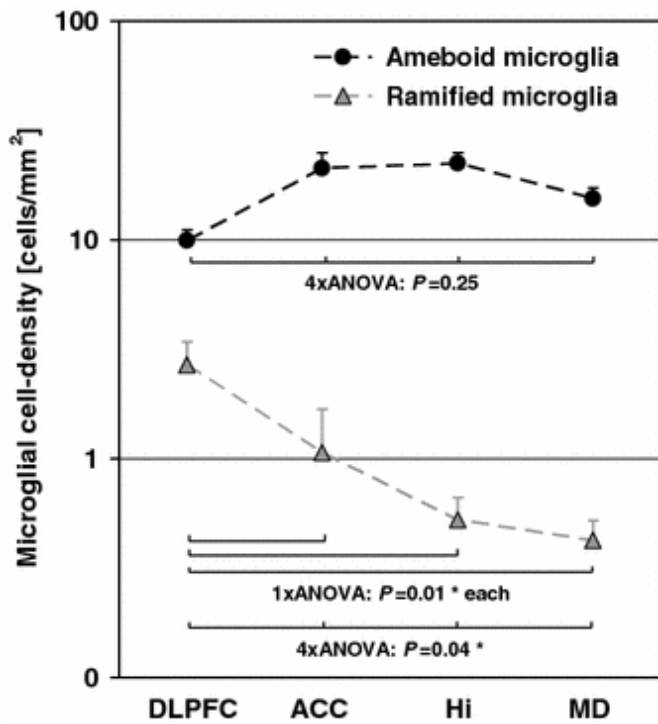
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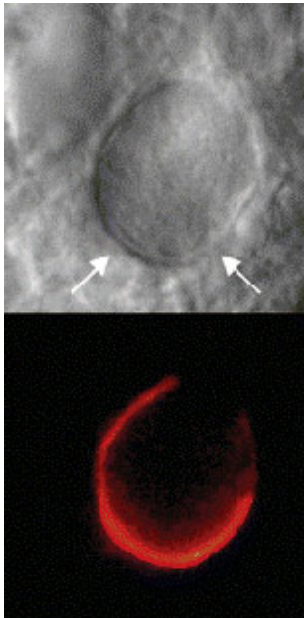
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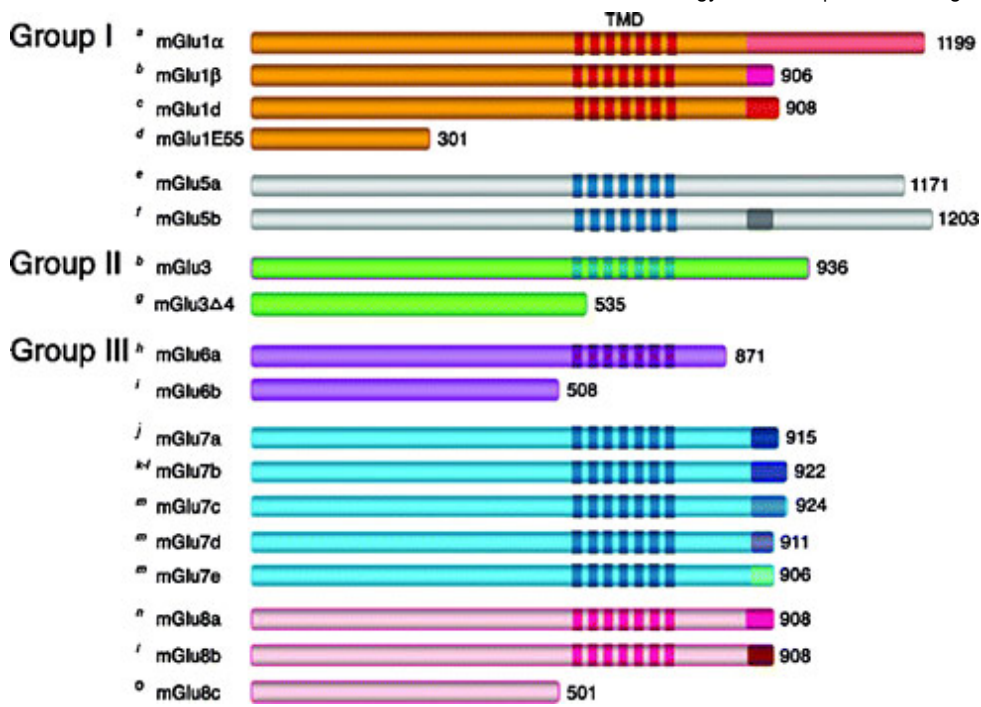
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When reporting a study that involved human participants, their data or biological material, authors should include a statement that confirms that the study was approved (or granted exemption) by the appropriate institutional and/or national research ethics committee (including the name of the ethics committee) and certify that the study was performed in accordance with the ethical standards as laid down in the 1964 Declaration of Helsinki and its later amendments or comparable ethical standards. If doubt exists whether the research was conducted in

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- This study was performed in line with the principles of the Declaration of Helsinki. Approval was granted by the Ethics Committee of University B (Date.../No. ...).
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- This research study was conducted retrospectively from data obtained for clinical purposes. We consulted extensively with the IRB of XYZ who determined that our study did not need ethical approval. An IRB official waiver of ethical approval was granted from the IRB of XYZ.
- This retrospective chart review study involving human participants was in accordance with the ethical standards of the institutional and national research committee and with the 1964 Helsinki Declaration and its later amendments or comparable ethical standards. The Human Investigation Committee (IRB) of University B approved this study.

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## Informed consent

All individuals have individual rights that are not to be infringed. Individual participants in studies have, for example, the right to decide what happens to the (identifiable) personal data gathered, to what they have said during a study or an interview, as well as to any photograph that was taken. This is especially true concerning images of vulnerable people (e.g. minors, patients, refugees, etc) or the use of images in sensitive contexts. In many instances authors will need to secure written consent before including images.

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### **Consent to Participate**

For all research involving human subjects, freely-given, informed consent to participate in the study must be obtained from participants (or their parent or legal guardian in the case of children under 16) and a statement to this effect should appear in the manuscript. In the case of articles describing human transplantation studies, authors must include a statement declaring that no organs/tissues were obtained from prisoners and must also name the institution(s)/clinic(s)/department(s) via which organs/tissues were obtained. For manuscripts reporting studies involving vulnerable groups where there is the potential for coercion or where consent may not have been fully informed, extra care will be taken by the editor and may be referred to the Springer Nature Research Integrity Group.

### **Consent to Publish**

Individuals may consent to participate in a study, but object to having their data published in a journal article. Authors should make sure to also seek consent from individuals to publish their data prior to submitting their paper to a journal. This is in particular applicable to case studies. A consent to publish form can be found

[here. \(Download docx, 36 kB\)](#) ↓

### **Summary of requirements**

The above should be summarized in a statement and placed in a 'Declarations' section before the reference list under a heading of 'Consent to participate' and/or 'Consent to publish'. Other declarations include Funding, Conflicts of interest/competing interests, Ethics approval, Consent, Data and/or Code availability and Authors' contribution statements.

Please see the various examples of wording below and revise/customize the sample statements according to your own needs.

#### Sample statements for "**Consent to participate**":

Informed consent was obtained from all individual participants included in the study.

Informed consent was obtained from legal guardians.

Written informed consent was obtained from the parents.

Verbal informed consent was obtained prior to the interview.

#### Sample statements for "**Consent to publish**":

The authors affirm that human research participants provided informed consent for publication of the images in Figure(s) 1a, 1b and 1c.

The participant has consented to the submission of the case report to the journal.

Patients signed informed consent regarding publishing their data and photographs.

#### Sample statements if identifying information about participants is available in the article:

Additional informed consent was obtained from all individual participants for whom identifying information is included in this article.

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Images will be removed from publication if authors have not obtained informed consent or the paper may be removed and replaced with a notice explaining the reason for removal.

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## **Research involving animals, their data or biological material**

The welfare of animals (vertebrate and higher invertebrate) used for research, education and testing must be respected. Authors should supply detailed information on the ethical treatment of their animals in their submission. For that purpose they may use the [ARRIVE](#) checklist which is designed to be used when submitting manuscripts describing animal research.

For studies involving client-owned animals, authors must also document informed consent from the client or owner and adherence to a high standard (best practice) of veterinary care.

Authors are recommended to comply with:

- The International Union for Conservation of Nature (IUCN) [Policy Statement on Research Involving Species at Risk of Extinction](#) and consult the [IUCN red list index of threatened species](#).
- [Convention on the Trade in Endangered Species of Wild Fauna and Flora](#)

When reporting results authors should indicate:

- ... that the studies have been approved by a research ethics committee at the institution or practice at which the studies were conducted. Please provide the name of ethics committee and relevant permit number;
- ... whether the legal requirements or guidelines in the country and/or state or province for the care and use of animals have been followed.

Researchers from countries without any legal requirements or guidelines voluntarily should refer to the following sites for guidance:

- [The Basel Declaration](#) describes fundamental principles of using animals in biomedical research
- [The International Council for Laboratory Animal Science](#) (ICLAS) provides ethical guidelines for researchers as well as editors and reviewers
- The [Association for the study of Animal Behaviour](#) describes ethical guidelines for the treatment of animals in research and teaching
- The [International Association of Veterinary Editors' Consensus Author Guidelines on Animal Ethics](#) provide guidelines for authors on animal ethics and welfare

Researchers may wish to consult the most recent (ethical) guidelines available from relevant taxon-oriented professional societies.

If a study was granted exemption or did not require ethics approval, this should also be detailed in the manuscript.

### Summary of requirements

The above should be summarized in a statement and placed in a 'Declarations' section before the reference list under a heading of 'Ethics approval'.

*Examples of statements to be used when ethics approval has been obtained:*

- All procedures involving animals were in compliance with the European Community Council Directive of 24 November 1986, and ethical approval was granted by the Kocaeli University Ethics Committee (No. 29 12 2014, Kocaeli, Turkey).
- All procedures performed in the study were in accordance with the ARVO Statement for Use of Animals in Ophthalmic Vision and Research. The ethical principles established by the National Institutes of Health Guide for the Care and Use of Laboratory Animals (NIH Publications No. 8523, revised 2011) were followed. The research protocol was approved by the Ethics Committee on Animal Use (Protocol No. 06174/14) of FCAV/Unesp, Jaboticabal.
- This study involved a questionnaire-based survey of farmers as well as blood sampling from their animals. The study protocol was assessed and approved by Haramaya University, research and extension office. Participants provided their verbal informed consent for animal blood sampling as well as for the related survey questions. Collection of blood samples was carried out by veterinarians adhering to the regulations and guidelines on animal husbandry and welfare.
- All brown bear captures and handling were approved by the Ethical Committee on Animal Experiments, Uppsala, Sweden (Application C18/15) and the Swedish Environmental Protection Agency in compliance with Swedish laws and regulations.
- The ethics governing the use and conduct of experiments on animals were strictly observed, and the experimental protocol was approved by the University of Maiduguri Senate committee on Medical Research ethics. Proper permit and consent were obtained from the Maiduguri abattoir management, before the faecal samples of the cattle and camels slaughtered in this abattoir were used for this experiment.

*Examples of statements to be used when no ethical approval is required/exemption granted:*

- No approval of research ethics committees was required to accomplish the goals of this study because experimental work was conducted with an unregulated invertebrate species.
- As the trappings of small mammals were conducted as part of regular pest control measures in accordance with the NATO Standardized Agreement 2048 "Deployment Pest and Vector Surveillance and Control ", no approval by an ethics committee was required.
- All experiments have been conducted as per the guidelines of the Institutional Animal Ethics Committee, Department of Zoology, Utkal University, Bhubaneswar, Odisha, India. However, the insect species used in this study is reared for commercial production of raw silk materials, as a part of agro-based industry. Therefore, use of this animal in research does not require ethical clearance. We have obtained permission from the office of Research officer sericulture, Baripada, Orissa, India for the provision of infrastructure and support for rearing of silkworm both in indoor and outdoor conditions related to our study to promote sericulture practices.

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|                             | EMBL Nucleotide Sequence Database (ENA) |
| DNA and RNA sequencing data | NCBI Trace Archive                      |

dbSNP

dbVar

European Variation Archive (EVA)

dbGAP

The European Genome-phenome Archive (EGA)

Worldwide Protein Data Bank (wwPDB)

Biological Magnetic Resonance Data Bank (BMRB)

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