



A Review of the Prevalence and Diagnostic Points of *Cryptosporidium* Species in Immunocompromised and Healthy Human Samples in Iran

Soudabeh Etemadi^{1,2*}, Omid Raiesi³, Muhammad I. Getso⁴, Vahid Raissi⁵, Hosnie Hoseini⁶

¹Department of Medical Parasitology and Mycology, Faculty of Medicine, Zahedan University of Medical Sciences, Zahedan, Iran.

²Infectious Disease and Tropical Medicine Research Center, Research Institute of Cellular and Molecular Sciences in Infectious Diseases, Zahedan University of Medical Sciences, Zahedan, Iran.

³Department of Parasitology, School of Allied Medical Sciences, Ilam University of Medical Sciences, Ilam, Iran.

⁴Department of Medical Microbiology and Parasitology, College of Health Sciences, Bayero University Kano, PMB 3011 Kano, Nigeria.

⁵Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran.

⁶Department of Laboratory Sciences, Zahedan Branch, Islamic Azad University, Zahedan, Iran.

Abstract

Cryptosporidium species are important intestinal pathogens with widespread distribution in humans and other hosts. Whereas the parasite causes acute and self-limiting gastroenteritis in people with healthy immune systems, many reports on this infection around the world are limited to people with defective or suppressed immune systems who suffer from a persistent and deadly infection. Using laboratory-serological and molecular methods for the detection of *Cryptosporidium* species in immunocompromised and healthy human samples, recent studies in Iran indicated that the prevalence of *Cryptosporidium* species in different samples varied between 0 to 14%. The samples in Iranian studies included human fecal and diarrheic samples from diarrheic children, patients with gastroenteritis, immunocompromised individuals, and people in contact with livestock. Furthermore, some species were reported based on molecular studies including *Cryptosporidium parvum* and *Cryptosporidium hominis*. Some studies have also reported *Cryptosporidium meleagridis*. In this review study, data were collected regarding the prevalence of cryptosporidiosis in high-risk individuals such as children and immunocompromised individuals. The results revealed that the higher prevalence of *C. parvum* in Iranian studies in the last 10 years may be attributed to the transmission of infection from animal sources.

Keywords: *Cryptosporidium* species, Health human samples, Immunocompromised individual, Diarrheic children, Iran

*Correspondence to

Soudabeh Eetemadi,
Department of Medical
Parasitology and Mycology,
Faculty of Medicine,
Zahedan University of
Medical Sciences, Zahedan,
Iran.
Tel: 054-33438487
Email: ssetemadi@gmail.
com



Received: June 19, 2021, Accepted: September 29, 2021, ePublished: December 30, 2021

Introduction

Cryptosporidium is a protozoan parasite of the phylum Apicomplexa that infects the margins of the gastrointestinal tract epithelial microvilli in a wide range of vertebrate hosts including humans (1). *Cryptosporidium* infection (cryptosporidiosis) is recognized as acute and self-limiting gastroenteritis in people with healthy immune systems, while it is regarded as a persistent and life-threatening infection in people with defective immune systems (2). It is estimated that millions of cases occur annually in developing and underdeveloped countries. This parasite is a critical factor in endemic infections, traveler's diarrhea, and epidemics (3). Frequent patterns of the disease are described based on age, season,

geographical location, and routes of transmission (4).

Cryptosporidiosis is more dominant among young children in developing countries that causes severe diarrhea similar to cholera (5, 6). Different species of *Cryptosporidium* can infect humans and a wide range of animals. In addition, the widespread occurrence of parasitic oocysts in the environment facilitates the acquisition of human infection in different ways (6). Person-to-person transmission may play a major role in the spread of *Cryptosporidium* infection in children and elderly populations, especially in kindergartens and nursing homes (7).

Cryptosporidium is transmitted feco-orally via ingestion of water or food contaminated by parasite oocysts (8)

which are physically and chemically resistant, can survive in the environment for a long time, and are insensitive to water chlorination (9-10).

***Cryptosporidium* Species Isolated From Humans**

Cryptosporidium parvum

Cryptosporidium parvum is one of the most frequently reported species among mammals and was initially identified in mice. The oocyst of this species is smaller than that of *Cryptosporidium muris* and, its habitat is usually the small intestine. More than 150 mammalian species have been identified as hosts of *C. parvum* and other similar parasites. Molecular characterization of the parasite has shown the occurrence of various genotypes with different base sequences and infectivity. DNA of some of the genotypes is now known as a distinct species such as *C. hominis* and *C. parvum* as human class II and I genotypes, respectively (11).

Other genotypes of the parasite are found in mice, pigs, marsupials, monkeys, mice, and mink. Currently, most researchers suggest that a species isolated from mammals is called *C. parvum* (11).

Cryptosporidium hominis

Although *Cryptosporidium* species that infect humans have previously been referred to as *C. parvum*, a human genotype (genotype 1) or genotype H has recently been identified as well. Thus, in recent years, studies conducted on biological and molecular differences, have categorized the human *Cryptosporidium* under a separate species called *C. hominis* (12, 13). These studies have not only demonstrated wide biological genetic differences between *C. hominis* and *C. parvum* (bovine genotype or genotype II) but also evidenced that the human species are antigenically more stable than the bovine species (13).

Cryptosporidium meleagridis

Stages of parasite growth were observed on the epithelial cells of the distal third of the small intestine of turkeys (14). A child with diarrhea in Mazandaran province of Iran was identified to be infected by *C. meleagridis*. In this study, it was found that the last two species (i.e., *C. parvum* and *C. meleagridis*) potentially had a shared transmission between humans and animals (15).

C. meleagridis is spherical and measures 4.6 by 5.2 μm with sporozoites, but it is not easily detectable inside the oocyst. The disease is associated with diarrhea, but the mortality rate is low. The parasite completes its entire life cycle on the surface of the intestinal epithelium and does not seem to invade host tissues (16).

Further studies have indicated that, in addition to turkeys, other birds such as chickens and parrots are susceptible to infection induced by *C. meleagridis*. Likewise, molecular studies have shown that *C. meleagridis* is a species distinct from other species and is

the third most common *Cryptosporidium* parasite found in humans (17, 18).

Important Predisposing Factors for Cryptosporidiosis Age

In tropical and temperate countries, *Cryptosporidium* is an important agent causing diarrhea in children. The effect of age may be related to the immune status of the young host and the infectivity of the *Cryptosporidium* species. Epidemiological studies have shown that cryptosporidiosis reaches the peak at two extremes of age. The first is under five years old and the second one occurs in adulthood (twenty to forty years old), which can be due to their occupational contacts (19).

Individual Immune System

As previously stated, cryptosporidiosis is a self-limiting gastrointestinal disorder in people with healthy immunity, while it causes persistent and life-threatening diarrhea in people with immunodeficiency (primary or secondary). Suppression of the immune system for any reason will increase the likelihood of cryptosporidiosis (20).

Other predisposing factors associated with cryptosporidiosis include weather, season, travel, occupation, contact with the animals, nutritional status, and personal health status (21).

Importance of Diagnostic Points

Similar to most intestinal parasites, *Cryptosporidium* is detected by microscopic examination of the stool. Stool samples are usually stored in 10% formalin. Fresh samples are also used for direct examination, but bear an increased risk of infecting the examiner (22).

Care should be taken when using stool preservatives, for example, polyvinyl alcohol interferes with staining techniques and is usually not recommended. Frozen stool samples and 2.5% potassium dichromate can be used for enzyme-linked immunosorbent assay (ELISA) and for preserving this parasite in stool samples, respectively (23).

Direct diagnosis of this parasite using a microscope is extremely challenging due to its wide spectrum of hosts and discrepancies in its oocyst size compared to other parasites transmitted feco-orally (24).

Cryptosporidium can be found elsewhere in the body that is suitable for parasite development, such as respiratory epithelium. However, the main site of the parasite is the surface of the small intestinal epithelium, causing recurrent and chronic diarrhea as well as diarrhea interspersed with constipation. Therefore, stool and sputum examination are the more preferred ways to diagnose the parasite. However, factors such as small size, transparency, and similarity of the parasite oocyst with other similar parasites make it impossible for direct examination to be considered as a gold standard test (25, 26).

Diagnostic Methods

Direct Stool Test Method

In this method, the parasite oocyst, which has been obtained by reliable methods of concentration (e.g., Shitter), is detected by a phase-contrast microscope or bright background (27).

Concentration Methods

Floatation

This method includes the Shitter method or floatation by sugar-water and the use of various salts (i.e., chloride, ZnSo₄, and NaCl), which are less sensitive and specific than the Shitter method. Further, they prevent the oocyst wall from rapid crystallization during the direct detection and diagnosis of parasites (28).

Sedimentation

Some references consider the formalin-ether deposition method to be a better option than the shitter floatation method (29). Nevertheless, Pal et al assume that the use of formalin-ethylacetate can reduce the number of oocysts, and the sediment obtained in this method due to having additional materials must be painted by appropriate painting techniques (30).

Smear Staining Methods

Two points are important to be considered in this method: First, the type of sample used (direct or concentrated), and second, the type of smear staining. In the case of the samples, direct, concentrated, or deposited samples can be used depending on the type of work.

- Kinyoun's acid-fast
- Modified acid-fast (Figure 1)
- Fluorescent acid-fast stains such as auramine-rhodamine: This method is faster with higher sensitivity than acid-fast (31).

Histopathological Method

This was the first test to detect the *Cryptosporidium* parasite in intestinal tissues. The cell forms of the parasite turn into purple with hematoxylin-eosin staining. Tissues become available only after invasive procedures, and organisms are not always detected on biopsies (32).

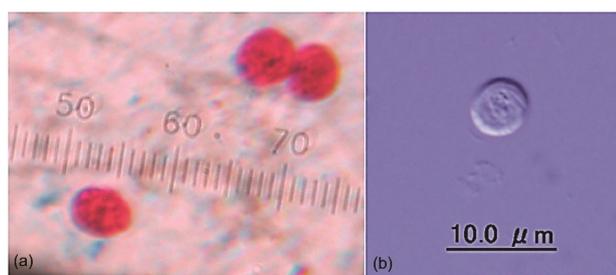


Figure 1. *Cryptosporidium parvum* Oocyte Size ($4.5 \times 4.2 \mu\text{m}$) by the Modified Acid-fast Staining Method and (b) *Cryptosporidium hominis* (6.5×4.7). Note. The size of oocysts varies in different species of parasites.

Serological Method

This method employs immunofluorescent tests based on monoclonal antibodies (copro-antigen-copro antibodies) that are specific to *Cryptosporidium* oocysts. The sensitivity of this method is 10 times greater than that of acid-fast dyeing methods. The direct immunofluorescence method using monoclonal antibodies is currently regarded as the gold standard test for fecal samples. The rate of parasite antigen detection using commercial kits in the form of ELISA and immunochromatographic tests is increasing. The ELISA tests are designed with high sensitivity and specificity (25).

Cryptosporidium Culture

Technically, the cultivation of *Cryptosporidium* faced some challenges in the past, but significant progress has been made in recent years. Today, the asexual stages of the parasite can be produced in antimicrobial systems (33).

Molecular Methods

The inability to identify and differentiate *Cryptosporidium* at the species and subspecies level delimits our knowledge of natural history, epidemiology, and the risk of zoonosis. Assessing the risks of water and food contamination by oocysts for public health is considered compounded (31). Given the new findings from the *Cryptosporidium* strains and their apparent similarities, this point becomes more evident and even more important when discussing *Cryptosporidium*. It is required to identify this parasite in terms of species, genotype, and its relationship with the age of the host via molecular pathways (34). Furthermore, the small size of oocysts in different species of *Cryptosporidium* with an extremely thin line demarcating their characteristics makes us realize the importance of using molecular methods (34, 35).

Currently, the use of such molecular methods as polymerase chain reaction (PCR), PCR-Restriction fragment length polymorphism (RFLP), nested-PCR, and DNA hybridization to detect *Cryptosporidium* parasites is increasing. These methods have higher sensitivity and specificity than the microscopic methods (36, 37).

The application of these methods is especially important in diagnosing clinical and environmental samples with low parasite numbers, detecting species differences and the genetic relationship between *Cryptosporidium* parasites, and examining the relationship between *Cryptosporidium* and other Apicomplexa. These methods are also used in epidemiological studies and geographical diversity of parasites (38). The details of which are provided in Table 1 (39-60).

Discussion

The aim of this study was to examine the prevalence and diagnostic points of *Cryptosporidium* species in immunocompromised and healthy human samples

Table 1. Detection of *Cryptosporidium* spp. in Humans in Iran During 2010-2020

Diagnostic Method (s)	Sample Size and its Characteristics	Positive Samples (%) Species <i>Cryptosporidium</i>	Area of Study	Reference
ELISA method	176 immunocompromised patients (children and adults with malignancy, kidney recipients, and HIV ⁺)	9 (5.1%) <i>Cryptosporidium</i> spp.	In the south-west of Iran	(39)
Modified acid-fast staining method	Diarrheic children	23/184 (12.5%) <i>Cryptosporidium</i> spp.	Isfahan	(40)
Direct method, acid-fast Staining, and auramine phenol fluorescence	420 stool samples from gastroenteritis patients	0 (0%) <i>Cryptosporidium</i> spp.	Western cities of Mazandaran province, Northern Iran	(41, 42)
Microscopic by MZN staining, PCR, and nested-PCR (18S ribosomal RNA)	850 human fecal samples	29 (3.41%) <i>C. parvum</i> and <i>C. hominis</i>	Rural area in the south of Iran	(43)
MZN technique and GP60 PCR-sequencing	794 diarrheic children	19 (2.40%) 17 (<i>C. parvum</i>) 2 (<i>C. hominis</i>)	Pediatrics hospital in Tehran, Iran	(44)
ZN acid-fast staining and nested PCR-RFLP (TRAP-C2 gene)	469 children less than 12 years	12 (2.5%) 10 (<i>C. parvum</i>) 1 (<i>C. hominis</i>) 1 (mix infection)	Pediatrics medical centers in Gazvin provinces	(45)
MZN staining technique	36 humans in the horse farms	2 (5.5%) <i>Cryptosporidium</i> spp.	Tabriz area	(46)
MZN staining	62 humans	9/62 (14.5%) <i>Cryptosporidium</i> spp.	Rural areas in Khuzestan, Southwest of Iran	(47)
Cold MZN staining method	237 humans (in contact with livestock)	6 (2.5%) <i>Cryptosporidium</i> spp.	Hamadan District	(48)
MZN method and PCR	2510 stool samples from children with diarrhea	30 (1.19%) <i>Cryptosporidium</i> spp.	Pediatric hospitals in Tehran	(49)
Acid-fast staining, auramine phenol fluorescence, and PCR-RFLP by SSU rRNA gene	348 patients with gastroenteritis	8 (2.3%) <i>C. parvum</i> or <i>C. hominis</i>	Mazandaran Province, Northern Iran	(50)
Modified acid-fast staining and PCR-RFLP	390 fecal samples (immunocompromised individuals and children)	16 cases (4.1%) 11 (<i>C. parvum</i>) 4 (<i>C. hominis</i>) 1 (<i>C. meleagridis</i>)	Southwest of Iran	(51)
Ziehl-Neelsen acid-fast and sequence analysis (gp60) gene	547 diarrheic children	27 (4.94%) 27 (<i>C. parvum</i>)	Gonbad Kavoos, Iran	(52)
PCR-RFLP (18S rRNA, SSU-rRNA gene)	113 diarrheic children	2 (1.76%) <i>C. parvum</i>	Hospitalized in Tabriz Pediatric Hospital	(53)
MZN, direct fluorescent-antibody, and nested-PCR assay	2,510 fecal samples from diarrheic children (under 12 years old)	30 (1.19%) <i>Cryptosporidium</i> spp.	Pediatric hospitals in Tehran, Iran	(54)
MZN	200 fecal samples from children	18 (9.7%) <i>Cryptosporidium</i> spp.	Hospitals in Zabol, Southeast Iran	(55)
MZN staining, PCR, and sequenced for phylogenetic analysis (SSU rRNA (18S gene))	132 children with cancer undergoing chemotherapy	5 (3.8%) <i>C. parvum</i>	Hospital of Tabriz University of Medical Sciences, Northwest of Iran	(56)
Acid-fast method, the UDG-LAMP assay	120 AIDS patients (volunteering APs)	13 (10.83%) <i>Cryptosporidium</i> spp.	Communicable Disease Control Center of Khorramabad, Iran	(57)
nested-PCR-RFLP (18S rRNA gene)	250 HIV/AIDS patients	27 (10.8%) <i>Cryptosporidium</i> spp. (70.38%) <i>C. parvum</i> (25.92%) <i>C. hominis</i> (3.7%) <i>C. meleagridis</i>	Southwest of Iran	(58)
Microscopic examination, acid-fast staining, nested-PCR-RFLP, and sequences analysis (18S RNA gene)	764 children aged <10 years with diarrheal disease	7 (0.91%) microscopic examination and acid-fast staining 2 (0.26%) sequences analysis <i>C. parvum</i>	Zahedan, Iran	(59)
Acid-fast (AF), PCR, and ELISA	221 diarrheal stool samples of children.	7 (3.2%) <i>C. parvum</i>	Urmia, northwest of Iran.	(60)

Note. ELISA: Enzyme-linked immunosorbent assay; HIV: Human immunodeficiency virus; PCR: Polymerase chain reaction; RFLP: Restriction fragment length polymorphism; MZN: Modified Ziehl-Neelsen; AIDS: Acquired immunodeficiency syndrome; UDG-LAMP: Uracil DNA glycosylase-supplemented loop-mediated isothermal amplification.

in Iran, and studies conducted in the last decade were reviewed accordingly.

The existence of different methods of transmission and the intricate zoonotic relationship of this parasite makes the epidemiology of cryptosporidiosis a complex entity. Investigating the prevalence of cryptosporidiosis through molecular tools helps in better understanding the risk factors, sources of the infection, epidemiology, transmission, and determination of specific host-species relationships (61).

In most of the above-mentioned studies, stool samples were first examined by the formalin-ether concentration method, and then, after microscopic examination, the modified acid-fast staining would be performed if the test was likely to be positive. Preparation of direct smears from stool or use of formalin-ether precipitate to prepare modified Ziehl-Neelsen staining smear is a common protocol for the microscopic detection of *Cryptosporidium* oocytes. However, this method requires a skilled technician to distinguish *Cryptosporidium* oocytes from yeasts and other cyclospora. Further, this method requires a considerable number of oocytes in the stool for better sensitivity. Therefore, there is a need to use a combination of the modified Ziehl-Neelsen staining method and molecular methods to get the best results (49).

In some studies that used molecular methods, after confirmation by staining, the parasite DNA was extracted from the stool samples using a kit for molecular tests. Most molecular studies performed in Iran used PCR, nested-PCR-RFLP, and sequences analysis methods. These studies applied ribosomal 18SsRNA genes, GP60, and TRAP-C2. Most of these studies used the nested-PCR method and the ribosomal 18SsRNA gene sequence methods, which can detect low-count parasites in samples. These methods are recommended to be used in cryptosporidiosis epidemiological studies, environmental studies, and water resources testing (43).

Sharbatkhori et al used the gp60 gene to determine the significant genetic heterogeneity between *C. parvum* and *C. hominis* in this gene and found different families in both species (52).

Some of the studies in Iran used ELISA and direct fluorescent-antibody serology methods and evidenced that molecular methods are more sensitive and specific compared to staining and serology methods. Moreover, one study in Iran used the uracil DNA glycosylase-supplemented loop-mediated isothermal amplification technique based on the target gene S-adenosyl methionine synthetase from *Cryptosporidium* gene to detect *Cryptosporidium* species in human immunodeficiency virus (HIV)-positive patients. This study tried to eliminate false-positive results following contamination (57).

The obtained results from various studies indicated that *C. parvum* and *C. hominis* accounted for 90% of human infections in most areas, and some studies reported *C.*

meleagridis (62).

The prevalence of *Cryptosporidium* species varies around the world, and the distribution of the species may also vary within a country. Studies on human samples demonstrated the predominance of *C. parvum*, *C. hominis*, and *C. meleagridis*, suggesting that their cycle frequency and routes of disease transmission are higher than that of other species. Therefore, it is possible to target appropriate routes for the transmission and spread of the parasite and control and prevent the spread of this parasite using appropriate strategies specifically aimed at sources of infection (63).

In most Iranian studies, children and immunocompromised adults were most susceptible to the parasites which can be mainly attributed to poor hygiene and weakened immune systems. Subsequently, the growing size of these sub-populations indicated an increased risk of infection in the community. Therefore, it is recommended that safety points, as well as healthcare and hygiene principles be well observed in dealing with sources of infection, especially in children. Further, the lack of effective treatment for this parasite necessitates focusing attention on the principles of parasite prevention and control as well as sources of the infection. Some important points highlighted by most of these studies include the health status of the community and sources of infection (e.g., consumable water) as factors affecting the prevalence (64).

No definitive treatment and proper treatment protocol have yet been proven for the disease. Thus, prevention seems to be the main factor to control this disease, especially in immunocompromised individuals since the development and clinical manifestations of cryptosporidiosis are affected by the individual's level of immunity (65).

Cryptosporidiosis appears with severe and, sometimes, fatal symptoms in children and immunocompromised individuals (66). In some reports, immunodeficiency is the most common risk factor for cryptosporidiosis in humans (39). However, the ability of many protozoan parasites to invade and cause disease in children and immunocompromised individuals, as well as the difficulty to distinguish *Cryptosporidium* parasites from other pathogenic protozoans via direct microscopic examination are the factors that pronounce the importance of molecular methods, especially parasite genotyping, in parasite identification (67).

Molecular research-based epidemiological studies allow researchers to gain a better understanding of the parasite transmissibility and pathogenicity pathogenic in humans, animals, and environmental samples (68).

Moreover, the use of molecular methods is highly useful in evaluating the common potential of humans and animals for infection by different species of *Cryptosporidium* (63).

More than 35 *Cryptosporidium* genotypes have so far been identified, some of which have recently been recognized as new species. Human infection by several species of *Cryptosporidium* has also been reported. Different species of *Cryptosporidium* are morphologically indistinguishable from each other while being genomically heterogeneous. Therefore, using molecular methods, especially genotyping, is essential to find out the origin of human or animal infections (69).

The results of this study indicated that due to the importance of cryptosporidiosis in people, especially in HIV patients, the need for conducting more studies has arisen in this field. In addition, it is important to identify and select other high-risk individuals who have defective immune systems.

Conclusion

In this review article data were collected regarding the prevalence of cryptosporidiosis in high-risk individuals such as children and immunocompromised individuals. The results revealed that the higher prevalence of *C. parvum* in Iranian studies in the last 10 years may indicate the transmission of infection from animal sources.

Conflict of Interest Disclosures

The authors declare no conflict of interests.

Acknowledgements

The authors express their appreciation and gratitude to all those who have directly or indirectly contributed to this project.

Ethical Statement

Ethical standards were observed for the review article.

Authors' Contributions

SE contributed to the study design, concept, and edition of the manuscript. OR and VR wrote the manuscript and collected the data, and finally MIG and HH edited the manuscript.

Funding/Support

No funding.

Informed Consent

The study was a review and thus required no informed consent from the participants.

References

- Silva FM, Lopes RS, Araújo-Junior JP. Identification of *Cryptosporidium* species and genotypes in dairy cattle in Brazil. *Rev Bras Parasitol Vet.* 2013;22(1):22-8. doi: 10.1590/s1984-29612013005000010.
- Clark EL, Blake DP. Genetic mapping and coccidial parasites: past achievements and future prospects. *J Biosci.* 2012;37(5):879-86. doi: 10.1007/s12038-012-9251-1.
- Shirley DA, Moonah SN, Kotloff KL. Burden of disease from cryptosporidiosis. *Curr Opin Infect Dis.* 2012;25(5):555-63. doi: 10.1097/QCO.0b013e328357e569.
- Jagai JS, Castronovo DA, Monchak J, Naumova EN. Seasonality of cryptosporidiosis: a meta-analysis approach. *Environ Res.* 2009;109(4):465-78. doi: 10.1016/j.envres.2009.02.008.
- Brook E, Hart CA, French N, Christley R. Prevalence and risk factors for *Cryptosporidium* spp. infection in young calves. *Vet Parasitol.* 2008;152(1-2):46-52. doi: 10.1016/j.vetpar.2007.12.003.
- Abu Samra N, Thompson PN, Jori F, Freaun J, Poonsamy B, du Plessis D, et al. Genetic characterization of *Cryptosporidium* spp. in diarrhoeic children from four provinces in South Africa. *Zoonoses Public Health.* 2013;60(2):154-9. doi: 10.1111/j.1863-2378.2012.01507.x.
- Kotloff KL, Nataro JP, Blackwelder WC, Nasrin D, Farag TH, Panchalingam S, et al. Burden and aetiology of diarrhoeal disease in infants and young children in developing countries (the Global Enteric Multicenter Study, GEMS): a prospective, case-control study. *Lancet.* 2013;382(9888):209-22. doi: 10.1016/s0140-6736(13)60844-2.
- Skotarczak B. Progress in the molecular methods for the detection and genetic characterization of *Cryptosporidium* in water samples. *Ann Agric Environ Med.* 2010;17(1):1-8.
- Yoder JS, Beach MJ. *Cryptosporidium* surveillance and risk factors in the United States. *Exp Parasitol.* 2010;124(1):31-9. doi: 10.1016/j.exppara.2009.09.020.
- Mirzaie F, Zibaei M, Mohaghegh MA, Raissi V. Investigation of soil contamination with *Cryptosporidium* spp. oocysts in different regions of Yazd, Central Iran. *Int J Enteric Pathog.* 2019;7(1):23-6.
- Putignani L, Menichella D. Global distribution, public health and clinical impact of the protozoan pathogen *Cryptosporidium*. *Interdiscip Perspect Infect Dis.* 2010;2010. doi: 10.1155/2010/753512.
- Fayer R, Santín M, Trout JM. *Cryptosporidium ryanae* n. sp. (Apicomplexa: Cryptosporidiidae) in cattle (*Bos taurus*). *Vet Parasitol.* 2008;156(3-4):191-8. doi: 10.1016/j.vetpar.2008.05.024.
- Ryan UM, Monis P, Enemark HL, Sulaiman I, Samarasinghe B, Read C, et al. *Cryptosporidium suis* n. sp. (Apicomplexa: Cryptosporidiidae) in pigs (*Sus scrofa*). *J Parasitol.* 2004;90(4):769-73. doi: 10.1645/ge-202r1.
- Meamar AR, Rezaian M, Rezaie S, Mohraz M, Kia EB, Houpt ER, et al. *Cryptosporidium parvum* bovine genotype oocysts in the respiratory samples of an AIDS patient: efficacy of treatment with a combination of azithromycin and paromomycin. *Parasitol Res.* 2006;98(6):593-5. doi: 10.1007/s00436-005-0097-4.
- Ghaffari S, Kalantari N. Molecular analysis of 18S rRNA gene of *Cryptosporidium* parasites from patients living in Iran, Malawi, Nigeria and Vietnam. *Int J Mol Cell Med.* 2012;1(3):153-61.
- Power ML, Ryan UM. A new species of *Cryptosporidium* (Apicomplexa: Cryptosporidiidae) from eastern grey kangaroos (*Macropus giganteus*). *J Parasitol.* 2008;94(5):1114-7. doi: 10.1645/ge-1508.1.
- Xiao L, Fayer R, Ryan U, Upton SJ. *Cryptosporidium* taxonomy: recent advances and implications for public health. *Clin Microbiol Rev.* 2004;17(1):72-97. doi: 10.1128/cmr.17.1.72-97.2004.
- Pedraza-Díaz S, Amar C, McLauchlin J. The identification and characterisation of an unusual genotype of *Cryptosporidium* from human faeces as *Cryptosporidium meleagridis*. *FEMS Microbiol Lett.* 2000;189(2):189-94. doi: 10.1111/j.1574-6968.2000.tb09228.x.
- Desai NT, Sarkar R, Kang G. Cryptosporidiosis: an under-recognized public health problem. *Trop Parasitol.* 2012;2(2):91-8. doi: 10.4103/2229-5070.105173.
- Certad G, Viscogliosi E, Chabé M, Cacciò SM. Pathogenic mechanisms of *Cryptosporidium* and *Giardia*. *Trends Parasitol.* 2017;33(7):561-76. doi: 10.1016/j.pt.2017.02.006.
- Cacciò SM, Chalmers RM. Human cryptosporidiosis in

- Europe. Clin Microbiol Infect. 2016;22(6):471-80. doi: 10.1016/j.cmi.2016.04.021.
22. Bern C, Ortega Y, Checkley W, Roberts JM, Lescano AG, Cabrera L, et al. Epidemiologic differences between cyclosporiasis and cryptosporidiosis in Peruvian children. Emerg Infect Dis. 2002;8(6):581-5. doi: 10.3201/eid0806.01-0331.
 23. Ahmed SA, Karanis P. Comparison of current methods used to detect *Cryptosporidium* oocysts in stools. Int J Hyg Environ Health. 2018;221(5):743-63. doi: 10.1016/j.ijheh.2018.04.006.
 24. Al-Dahhan IN, Zghair ZR. Isolation of *Cryptosporidium* spp. from rabbits in Baghdad city, Iraq. Plant Arch. 2020;20(Suppl 2):2911-4.
 25. Ezzaty Mirhashemi M, Zintl A, Grant T, Lucy FE, Mulcahy G, De Waal T. Comparison of diagnostic techniques for the detection of *Cryptosporidium* oocysts in animal samples. Exp Parasitol. 2015;151-152:14-20. doi: 10.1016/j.exppara.2015.01.018.
 26. Cunha FS, Peralta RH, Peralta JM. New insights into the detection and molecular characterization of *Cryptosporidium* with emphasis in Brazilian studies: a review. Rev Inst Med Trop Sao Paulo. 2019;61(3):e28. doi: 10.1590/s1678-9946201961028.
 27. Ghazy AA, Abdel-Shafy S, Shaapan RM. Cryptosporidiosis in animals and man: 2. Diagnosis. Asian J Epidemiol. 2015;8(4):84-103. doi: 10.3923/aje.2015.84.103.
 28. Dorostcar Moghaddam D, Azami M. Isolation of *Cryptosporidium* oocysts and sporozoites using discontinuous sucrose and isopycnic Percoll gradients. Iran J Basic Med Sci. 2005;8(1):18-24. [Persian].
 29. Xiao L, Ryan UM, Graczyk TK, Limor J, Li L, Kombert M, et al. Genetic diversity of *Cryptosporidium* spp. in captive reptiles. Appl Environ Microbiol. 2004;70(2):891-9. doi: 10.1128/aem.70.2.891-899.2004.
 30. Pal M, Tafese W, Tilahun G, Anberber M. Cryptosporidiosis: an emerging food and waterborne protozoan disease of global significance. Beverage & Food World. 2016;43(1):43-5.
 31. Jirků M, Valigurová A, Koudela B, Krížek J, Modrý D, Slapeta J. New species of *Cryptosporidium* Tyzzer, 1907 (Apicomplexa) from amphibian host: morphology, biology and phylogeny. Folia Parasitol (Praha). 2008;55(2):81-94.
 32. Carey CM, Lee H, Trevors JT. Biology, persistence and detection of *Cryptosporidium parvum* and *Cryptosporidium hominis* oocyst. Water Res. 2004;38(4):818-62. doi: 10.1016/j.watres.2003.10.012.
 33. Lacharme L, Villar V, Rojo-Vazquez FA, Suárez S. Complete development of *Cryptosporidium parvum* in rabbit chondrocytes (VELI cells). Microbes Infect. 2004;6(6):566-71. doi: 10.1016/j.micinf.2004.02.016.
 34. Fall A, Thompson RC, Hobbs RP, Morgan-Ryan U. Morphology is not a reliable tool for delineating species within *Cryptosporidium*. J Parasitol. 2003;89(2):399-402. doi: 10.1645/0022-3395(2003)089[0399:minart]2.0.co;2.
 35. Morgan U, Weber R, Xiao L, Sulaiman I, Thompson RC, Ndiritu W, et al. Molecular characterization of *Cryptosporidium* isolates obtained from human immunodeficiency virus-infected individuals living in Switzerland, Kenya, and the United States. J Clin Microbiol. 2000;38(3):1180-3. doi: 10.1128/jcm.38.3.1180-1183.2000.
 36. McLauchlin J, Amar CF, Pedraza-Díaz S, Mieli-Vergani G, Hadzic N, Davies EG. Polymerase chain reaction-based diagnosis of infection with *Cryptosporidium* in children with primary immunodeficiencies. Pediatr Infect Dis J. 2003;22(4):329-35. doi: 10.1097/01.inf.0000059402.81025.cd.
 37. Kaushik K, Khurana S, Wanchu A, Malla N. Evaluation of staining techniques, antigen detection and nested PCR for the diagnosis of cryptosporidiosis in HIV seropositive and seronegative patients. Acta Trop. 2008;107(1):1-7. doi: 10.1016/j.actatropica.2008.02.007.
 38. Gile M, Warhurst DC, Webster KA, West DM, Marshall JA. A multiplex allele specific polymerase chain reaction (MAS-PCR) on the dihydrofolate reductase gene for the detection of *Cryptosporidium parvum* genotypes 1 and 2. Parasitology. 2002;125(Pt 1):35-44. doi: 10.1017/s0031182002001786.
 39. Balouty Dehkordy A, Rafiei A, Alavi S, Latifi S. Prevalence of *Cryptosporidium* infection in immunocompromised patients, in south-west of Iran, 2009-10. Iran J Parasitol. 2010;5(4):42-7.
 40. Saneian H, Yaghini O, Yaghini A, Modarresi MR, Soroshnia M. Infection rate of *Cryptosporidium parvum* among diarrheic children in Isfahan. Iran J Pediatr. 2010;20(3):343-7.
 41. Nahrevanian H, Assmar M. Cryptosporidiosis in immunocompromised patients in the Islamic Republic of Iran. J Microbiol Immunol Infect. 2008;41(1):74-7.
 42. Nahrevanian H, Azarinoosh SA, Esfandiari B, Ziapoor SP, Shadifar M, Amirbozorgy G, et al. Current situation of *Cryptosporidium* and other enteroparasites among patients with gastroenteritis from western cities of Mazandaran province, Iran, during 2007-2008. Gastroenterol Hepatol Bed Bench. 2010;3(3):120-5. doi: 10.22037/ghfbb.v3i3.97.
 43. Bairami Kuzehkhanan A, Rezaeian M, Zeraati H, Mohebbali M, Meamar AR, Babaei Z, et al. A sensitive and specific PCR based method for identification of *Cryptosporidium* sp. using new primers from 18S ribosomal RNA. Iran J Parasitol. 2011;6(4):1-7.
 44. Taghipour N, Nazemalhosseini-Mojarad E, Haghghi A, Rostami-Nejad M, Romani S, Keshavarz A, et al. Molecular epidemiology of cryptosporidiosis in Iranian children, Tehran, Iran. Iran J Parasitol. 2011;6(4):41-5.
 45. Nazemalhosseini-Mojarad E, Haghghi A, Taghipour N, Keshavarz A, Mohebi SR, Zali MR, et al. Subtype analysis of *Cryptosporidium parvum* and *Cryptosporidium hominis* isolates from humans and cattle in Iran. Vet Parasitol. 2011;179(1-3):250-2. doi: 10.1016/j.vetpar.2011.01.051.
 46. Hassanpour A, Mashayekhi M, Safarmashaei S. Prevalence of cryptosporidiosis in foals and humans to be in contact them in Tabriz area in Iran. Adv Environ Biol. 2011;5(6):1070-2.
 47. Heidarnegadi S, Mohebbali M, Maraghi S, Babaei Z, Farnia S, Bairami A, et al. *Cryptosporidium* spp. infection in human and domestic animals. Iran J Parasitol. 2012;7(1):53-8.
 48. Jafari R, Maghsood AH, Fallah M. Prevalence of *Cryptosporidium* infection among livestock and humans in contact with livestock in Hamadan district, Iran, 2012. J Res Health Sci. 2012;13(1):86-9.
 49. Tahvildar-Biderouni F, Salehi N. Detection of *Cryptosporidium* infection by modified Ziehl-Neelsen and PCR methods in children with diarrheal samples in pediatric hospitals in Tehran. Gastroenterol Hepatol Bed Bench. 2014;7(2):125-30.
 50. Gholami S, Khanmohammadi M, Ahmadvanpour E, Pagheh AS, Khadem Nakhjiri S, Ramazannipour H, et al. *Cryptosporidium* infection in patients with gastroenteritis in Sari, Iran. Iran J Parasitol. 2014;9(2):226-32.
 51. Rafiei A, Rashno Z, Samarbafzadeh A, Khademvatan S. Molecular characterization of *Cryptosporidium* spp. isolated from immunocompromised patients and children. Jundishapur J Microbiol. 2014;7(4):e9183. doi: 10.5812/jjm.9183.
 52. Sharbatkhori M, Nazemalhosseini Mojarad E, Taghipour N, Pagheh AS, Mesgarian F. Prevalence and genetic characterization of *Cryptosporidium* Spp. in diarrheic children from Gonbad Kavoos city, Iran. Iran J Parasitol.

- 2015;10(3):441-7.
53. Mahdavi Poor B, Rashedi J, Asgharzadeh M, Fallah E, Hatam-Nahavandi K, Dalimi A. Molecular characterization of *Cryptosporidium* species in children with diarrhea in north west of Iran. *Int J Mol Cell Med*. 2015;4(4):235-9.
 54. Aghamolaie S, Rostami A, Fallahi S, Tahvildar Biderouni F, Haghghi A, Salehi N. Evaluation of modified Ziehl-Neelsen, direct fluorescent-antibody and PCR assay for detection of *Cryptosporidium* spp. in children faecal specimens. *J Parasit Dis*. 2016;40(3):958-63. doi: 10.1007/s12639-014-0614-4.
 55. Dabirzadeh M, Khoshsima Shahraki M, Rostami D, Bagheri S. Prevalence of *Cryptosporidium* species in children referred to central and hospital laboratories of Zabol city, south east of Iran. *Int J Pediatr*. 2017;5(12):6359-64. doi: 10.22038/ijp.2017.22358.1871.
 56. Berahmat R, Mahami-Oskouei M, Rezamand A, Spotin A, Aminisani N, Ghoyounchi R, et al. *Cryptosporidium* infection in children with cancer undergoing chemotherapy: how important is the prevention of opportunistic parasitic infections in patients with malignancies? *Parasitol Res*. 2017;116(9):2507-15. doi: 10.1007/s00436-017-5560-5.
 57. Fallahi S, Moosavi SF, Karimi A, Sharafi Chegeni A, Saki M, Namdari P, et al. An advanced uracil DNA glycosylase-supplemented loop-mediated isothermal amplification (UDG-LAMP) technique used in the sensitive and specific detection of *Cryptosporidium parvum*, *Cryptosporidium hominis*, and *Cryptosporidium meleagridis* in AIDS patients. *Diagn Microbiol Infect Dis*. 2018;91(1):6-12. doi: 10.1016/j.diagmicrobio.2017.12.017.
 58. Ghafari R, Rafiei A, Tavalla M, Moradi Choghakabodi P, Nashibi R, Rafiei R. Prevalence of *Cryptosporidium* species isolated from HIV/AIDS patients in southwest of Iran. *Comp Immunol Microbiol Infect Dis*. 2018;56:39-44. doi: 10.1016/j.cimid.2017.12.002.
 59. Mirshekari F, Hatam-Nahavandi K, Abdolahi Khabisi S, Salimi-Khorashad A. *Cryptosporidium parvum* in children with diarrhea in Zahedan, Iran. *Jundishapur J Microbiol*. 2019;12(8):e95109. doi: 10.5812/jjm.95109.
 60. Mahmoudi MR. Molecular detection and characterization of *Cryptosporidium* spp. in the sewage-contaminated rivers entering Bandar-e Anzali Lagoon in Guilan province, Iran. *J Adv Environ Health Res*. 2020;8(2):102-6.
 61. Borad AJ, Allison GM, Wang D, Ahmed S, Karim MM, Kane AV, et al. Systemic antibody responses to the immunodominant p23 antigen and p23 polymorphisms in children with cryptosporidiosis in Bangladesh. *Am J Trop Med Hyg*. 2012;86(2):214-22. doi: 10.4269/ajtmh.2012.11-0273.
 62. Guyot K, Follet-Dumoulin A, Lelièvre E, Sarfati C, Rabodonirina M, Nevez G, et al. Molecular characterization of *Cryptosporidium* isolates obtained from humans in France. *J Clin Microbiol*. 2001;39(10):3472-80. doi: 10.1128/jcm.39.10.3472-3480.2001.
 63. Xiao L. Molecular epidemiology of cryptosporidiosis: an update. *Exp Parasitol*. 2010;124(1):80-9. doi: 10.1016/j.exppara.2009.03.018.
 64. Wang RJ, Li JQ, Chen YC, Zhang LX, Xiao LH. Widespread occurrence of *Cryptosporidium* infections in patients with HIV/AIDS: epidemiology, clinical feature, diagnosis, and therapy. *Acta Trop*. 2018;187:257-63. doi: 10.1016/j.actatropica.2018.08.018.
 65. Feng Y, Ryan UM, Xiao L. Genetic diversity and population structure of *Cryptosporidium*. *Trends Parasitol*. 2018;34(11):997-1011. doi: 10.1016/j.pt.2018.07.009.
 66. Fayer R. *Cryptosporidium*: a water-borne zoonotic parasite. *Vet Parasitol*. 2004;126(1-2):37-56. doi: 10.1016/j.vetpar.2004.09.004.
 67. Hijjawi N, Zahedi A, Kazaleh M, Ryan U. Prevalence of *Cryptosporidium* species and subtypes in paediatric oncology and non-oncology patients with diarrhoea in Jordan. *Infect Genet Evol*. 2017;55:127-30. doi: 10.1016/j.meegid.2017.08.033.
 68. Xiao L, Bern C, Sulaiman IM, Lal AA. Molecular epidemiology of human cryptosporidiosis. In: Thompson RCA, Armson A, Ryan UM, eds. *Cryptosporidium*. Amsterdam: Elsevier; 2003. p. 121-46. doi: 10.1016/b978-044451351-9/50018-5.
 69. Feng Y, Zhao X, Chen J, Jin W, Zhou X, Li N, et al. Occurrence, source, and human infection potential of *Cryptosporidium* and *Giardia* spp. in source and tap water in Shanghai, China. *Appl Environ Microbiol*. 2011;77(11):3609-16. doi: 10.1128/aem.00146-11.