Prevalence and genetic characterization of Cryptosporidium in pre-weaned cattle in Urmia (Northwestern Iran)

Mahmoud Mahmoudi¹, Khosrow Hazrati Tapeh¹, Esmaeil Abasi¹, Hojjat Sayyadi², Arash Aminpour¹

¹ Department of Parasitology and Mycology, Faculty of Medicine, Urmia University of Medical Sciences, Urmia, Iran
² Cellular and Molecular Research Center, Urmia University of Medical Sciences, Urmia, Iran

Abstract
Introduction: Cryptosporidiosis is a zoonotic disease causing digestive problems in pre-weaned calves. Considering the zoonosis of the parasite and its importance in veterinary medicine, we evaluated the prevalence and genotyping of Cryptosporidium spp. in diarrheic pre-weaned calves in the northwest of Iran.

Methodology: A total of 100 stool samples of the infant calves with diarrhea were collected from industrial and conventional livestock farms in Urmia City. All the samples were tested with acid-fast staining, ELISA, and PCR. Positive samples of the PCR method were sequenced to determine the Cryptosporidium species. The obtained results were compared for the mentioned methods based on statistical factors, sensitivity, specificity, positive and negative predictive values, as well as duration of the experiment and the costs of testing.

Results: The results of this study showed that the prevalence of Cryptosporidium spp. in diarrheic infant calves in Urmia city was 5%, and C. parvum species of Cryptosporidium was detected in all the sequenced samples. According to the findings of the current study, the most appropriate method for the detection of the parasite is the ELISA that has a higher sensitivity and predictive value than acid-fast staining method and should be used in veterinary laboratories.

Conclusions: In the current investigation, C. parvum was identified as the only infectious agent in the region and could be the main cause of human infection. More studies are needed to find the source of infection for establishing the control measures.

Key words: Cryptosporidium; prevalence; genetic characterization; sensitivity; specificity.

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Introduction
Cryptosporidium is a zoonotic protozoan parasite infecting the gastrointestinal tract of a wide range of vertebrates, including humans, livestock, wild animals, and birds [1]. The presence of Cryptosporidium-infected animals, especially domestic ones, poses as a serious risk factor to human health. The infection of this parasite is mainly transmitted from animals to humans by resistant oocytes.

Currently, Cryptosporidium infection in cattle have been associated with four main species, i.e. C. parvum, C. bovis, C. andersoni, and C. ryanae; however, species such as C. suis, C. hominis, C. serpentis, C. xiaoi, C. ubiquitum, C. meleagridis, C. muris, and C. felis have been identified. C. andersoni gives rise to mucosal destruction of the abomasums in cattle, but C. parvum, C. bovis, and C. ryanae often cause atrophy of villus, shortening of microvillus, and destruction of the intestine, which leads to diarrhea [2-4]. C. parvum generally infects human and cattle, whereas C. andersoni and C. bovis have infrequently been detected in humans [5,6]. Hence, infected cattle are regarded potentially significant reservoirs of Cryptosporidium for human infections. C. parvum is chiefly detected in pre-weaned [7], while C. ryanae and C. bovis are found in post-weaned [8]. Meanwhile, C. andersoni have been reported to primarily infect adult calves [9]. Other species such as C. felis [10], C. scrofarum [11], C. suis-like genotype [12], C. suis [12], C. hominis [12,13], C. ubiquitum [14], and C. meleagridis [15] have also been isolated from cattle; therefore, pre-weaned cattle are the most leading factor of infection for humans. Contamination with this protozoan in calves is highly important in terms of economic damages; in Iran, calf casualties are virtually 16%, of which 75% is related to diarrhea [16,17].

Diverse approaches have already been suggested for the detection of Cryptosporidium. The majority of the approaches encompass direct examination of stained fecal smears under microscope [18]. The modified acid-fast staining is broadly applied for clinical diagnosis owing to its simplicity and cost
effectiveness. However, it displays relatively low sensitivity with feces [19,20]. Although several immunological techniques using antibodies or antigens have hitherto been developed, all of them are more expensive than conventional staining methods. Nonetheless, their sensitivity and specificity appear to be the same [21]. PCR-based methods are additional valuable techniques for detecting Cryptosporidium spp. in clinical samples. The PCR technique has high sensitivity and specificity and can detect organisms such as Cryptosporidium, just with a single cell. Nucleotide amplification methods that target genes encoding the oocyst wall protein, the small-subunit of rRNA, β-tubulin, TRAP-C1, TRAP-C2, ITS1, polythreonine repeat, unknown DNA sequences, mRNA of heat shock proteins, and dihydrofolate reductase are successful for detecting and differentiating Cryptosporidium parasites [22]. Partial sequencing of Cryptosporidium small subunit (SSU) rRNA gene has routinely been applied (in 86% of publications) to genotype Cryptosporidium in the environment (i.e. water and invertebrate sources), wild and domestic animals, and human samples. Multiple copies of the SSU rRNA gene throughout the genome render this marker significantly more sensitive than single-copy genes. PCR amplification and sequence analyses of the amplicon allow genetic characterization and differentiation between Cryptosporidium spp. that assists in finding the possible and actual risk sources to human or animal health. The prevalence of cryptosporidiosis has been reported to be high among renal transplant recipients in Urmia (11.5%) [23], suggesting that the area is highly contaminated with the oocysts of the parasite. The present study aimed to investigate the rate of infection with Cryptosporidium spp. in pre-weaned calves in Urmia city, West Azerbaijan province, Iran. Additionally, the diagnostic methods viz the acid-fast staining, molecular method, and ELISA were compared in terms of statistical factors, duration of the laboratory experiment, and the cost-effectiveness of testing, to determine the superior method for the detection of Cryptosporidium in the infected calves.

**Methodology**

**Sample collection**

For this study, 100 stool samples were collected from diarrheic pre-weaned calves in 10 conventional and industrial livestock farms from October 2017 to March 2018. The samples in a plastic container were transferred to the Parasitology Laboratory at Urmia Medical School on the same day of collection.

**Laboratory evaluation**

Due to the impossibility of performing the methods simultaneously, each diarrheal stool sample was divided into three parts: one part for the diagnosis of Cryptosporidium oocysts by the acid-fast staining method of Ziehl-Neelsen, one part for PCR method (kept in 70% alcohol test tube), and one part for the ELISA method (kept in saline at -20ºC).

**Ziehl-Neelsen staining method**

The sedimentation method of formalin-ethyl acetate was first carried out for all the samples. To perform the method, 7 mL of formalin was poured into each test tube, 2-3 ml of the diarrheal stool was removed by Pasteur's pipette and added to the tubes, and three milliliters of ethyl acetate was added. The tubes were then shaken vigorously to mix formalin, stool, and ethyl acetate. After five minutes of centrifugation of the mixture at 450 ×g, four layers were formed. The layer from top to bottom contained ethyl acetate, fat and stool wastes, formalin, and the sediments containing oocytes. The first three layers were discarded, and a smear was prepared on a glass slide and dried at room temperature. The air-dried, methanol-fixed slides were then stained with Ziehl-Neelsen method. Briefly, the slides were stained with carbol fuchsin for 15 minutes, decolorized with 50% alcohol for 3 - 5 seconds, and finally washed with water. The samples were decolorized with 1% sulfuric acid until the disappearance of red color and then rinsed with water. After the slides were dried, the samples were stained with methylene blue for one minute and then washed with water. The slides were evaluated under a microscope with the magnification of 1,000, and Cryptosporidium oocysts were identified (4 - 6 microns, red cells with black granules in the blue background). The duration of acid-fast staining method to detect Cryptosporidium was 30 minutes [24].

**PCR method**

The DNA was extracted using a commercial kit (Yekta Tajhiz Azema, Iran) according to the manufacture's instruction. Forward and reverse primers designed for the multiplication of SSU rRNA gene of Cryptosporidium spp. were as follows: Forward primer: 5'GACATATCATTCAAGT TTCTGACC3' and Reverse primer: 5'CTGAAGGAGTAAGGAACAACC3'. To perform the experiment, 1 μL of each forward and reverse primer, 3 μL of extracted DNA, 12.5 μL of Master Mix, and 7.5 μL of sterile distilled water were added to the micro-tubes, and the experiment was performed with a thermocycler device with the following program: 2 min
incubation at 94°C to denature double-stranded DNA, 35 cycles of 60 s at 58°C (annealing step), 120 s at 68°C (extension step), and 45 s at 94°C (denaturing step). PCR was finally accomplished with the additional extension step for 7 minutes at 68°C.

The PCR product was loaded on 1% agarose gel and electrophoresed using 1% solution of TBE for 20 minutes. Finally, digital images were taken using a gel imaging system. Cryptosporidium spp. bands with the length of 830 bp were identified. Positive PCR products were sequenced, and the sequences were visualized using the Chromas software version 2.6 and compared to those registered in the GenBank using Basic Local Alignment Search Tool (BLAST) software. Duration of DNA extraction of Cryptosporidium and PCR method for the detection of this parasite was eight hours.

ELISA method

The experiment was performed using a commercial ELISA kit (Cryptosporidium 2nd Generation [Fecal], USA). Six samples were randomly removed due to the limitation of ELISA plate wells. To conduct the experiment, positive and negative controls were poured into wells 1 and 2, respectively, and buffer solution was added to all the wells. Afterward, samples were added to each well individually, except for negative and positive control wells, and incubated at room temperature for one hour. The plates were rinsed with washing solution, and then the conjugated enzyme was added to all the wells. The plates were eventually incubated at room temperature for 30 minutes. The wells were washed with washing solution, and 100 μL of chromogenic solution was added to each well, and the plate was incubated at room temperature for 10 minutes. In the end, 100 μL of stop solution was added to each well, and the optical densities were read by an ELISA reader device. The optical density above 0.08 was considered as positive for Cryptosporidium antigens. The duration of the ELISA method took 2.5 hours to detect Cryptosporidium antigens.

Statistical analysis

In the current study, acid-fast staining, PCR, and ELISA methods were compared in terms of sensitivity and specificity, as well as negative and positive predictive values [25]. PCR method was considered as the gold standard.

\[
\text{Specificity} = \frac{\text{FalseNegative}}{\text{FalsePositive} + \text{TrueNegative}} \times 100
\]

\[
\text{Sensitivity} = \frac{\text{TrueNegative}}{\text{FalseNegative} + \text{TruePositive}} \times 100
\]

\[
\text{Negative predictive value} = \frac{\text{TrueNegative}}{\text{FalseNegative} + \text{TrueNegative}} \times 100
\]

\[
\text{Positive predictive value} = \frac{\text{TruePositive}}{\text{FalsePositive} + \text{TruePositive}} \times 100
\]

Results

Stool samples under study were collected from 10 (four industrial and six conventional) livestock farms, where the health status of animals varied from inappropriate to good. Five samples were positive for Cryptosporidium: two from Band, one from each of Karim Abad, Rahim Abad, and Shorkandy farms. Based on the data from Table 1, the percentage of Cryptosporidium infection prevalence in pre-weaned calves suffering from diarrhea in Urmia city was 5%.

Among 100 stool samples, Ziehl-Neelsen staining method detected five positive cases, while three cases were confirmed by PCR; two cases were false-positive

| Location of the livestock farm | Type of the livestock farm | Health status  | PCR method | Staining method | ELISA method |
|-------------------------------|---------------------------|----------------|------------|-----------------|--------------|
| Khangah Sorkh                 | conventional              | Good           | -          | -               | -            |
| Karim Abad                    | conventional              | Inappropriate  | +          | +               | +            |
| Rahim Abad                    | conventional              | Proper         | +          | +               | -            |
| Saatluo                       | conventional              | Proper         | -          | +               | -            |
| Shorkandy                     | industrial                | Inappropriate  | +          | -               | +            |
| Arnesa                        | industrial                | Good           | -          | -               | -            |
| Dastgerd                      | industrial                | Good           | -          | -               | -            |
| Band                          | conventional              | Inappropriate  | + +        | + -             | + +          |
| Gara-aghaj                    | conventional              | Inappropriate  | -          | +               | -            |
| Par                           | industrial                | Good           | -          | -               | -            |
and two cases were false-negative. ELISA method identified four positive cases, which all were affirmed by PCR. Therefore, one case was false-negative, but there was no false-positive cases. The results are summarized in Table 1.

In this work, Ziehl-Neelsen staining and ELISA were compared with PCR method regarding the statistical parameters. Sensitivity, specificity, positive predictive value, and negative predictive value for the staining method and ELISA were 60%, 97.89%, 60%, and 97.89%, as well as 80%, 100%, 100%, and 98.8%, respectively.

Five Cryptosporidium-positive isolates in PCR method were sequenced by Kawsar Biotech Company (Iran) based on the Sanger method. Sequence results showed that all the five isolates were C. parvum and registered in the GenBank under the accession numbers MK426792, MK426793, MK426794, MK426795, and MK426796.

**Discussion**

*Cryptosporidium* infection has been reported by numerous countries so that the prevalence rates of the infection in the cattle in India, Japan, France, China, Argentina, and Turkey were 26.15%, 33%, 39%, 2.55%, 8%, and 7.5%, respectively [26-31]. In the present study, the prevalence rate of the infection in pre-weaned calves suffering from diarrhea in Urmia city was 5%. The results of the present study in terms of *Cryptosporidium* infection prevalence was relatively close to those obtained from Isfahan and Ilam cities, which were 6.25% and 3.68%, respectively [32,33]. Previous studies, however, showed a higher prevalence which were 6.25% and 3.68%, respectively [32,33].

Comparing the staining method and ELISA with PCR technique, as the gold standard, displayed the sensitivity of 45% and specificity of 100% for staining method and 57% and 96% for ELISA, respectively [38]. Our results were in line with those reported by Yilmaz et al. [37] and Gawad et al. [38].

In this study, three diagnostic methods of *Cryptosporidium* were compared in stool samples by considering some factors, such as cost of the methods, time of performing the experiments, sensitivity, specificity, and positive and negative predictive values of the methods, to determine the superior method for detecting the parasite. Most comparisons of *Cryptosporidium* diagnostic methods have performed in human specimens, but we compared the diagnostic methods in calves to obtain a standard and cost-effective method. Our results showed that PCR and ELISA methods were more accurate than the microscopic method. Yilmaz et al. [37] made a comparison between two methods, ELISA and acid-fast staining, using the stool samples of 2,000 children in Turkey, in order to detect *Cryptosporidium* parasite. The ELISA results identified *Cryptosporidium* antigens in 97 children, while acid-fast staining method found 31 positive cases, suggesting the higher sensitivity of the ELISA compared to the staining method [37]. In a study performed in 2015, Gawad et al. [38] collected fecal specimens from 200 diarrhea patients in Egypt for the detection of *Cryptosporidium*. All the specimens were tested with acid-fast staining, sandwich ELISA, and PCR methods; their results showed 19 (9.5%), 25 (12%), and 42 (21%) positive cases, respectively. Comparing the staining method and ELISA with PCR technique, as the gold standard, displayed the sensitivity of 45% and specificity of 100% for staining method and 57% and 96% for ELISA, respectively [38].

In this study, regarding the costs and the time spent for conducting the experiments, the acid-fast staining method required less time to perform, and it was more cost-effective than ELISA and PCR, but low sensitivity and predictive value were the downsides of the method. These disadvantages increase the false-negative cases, and, therefore, the true-positive cases may be ignored. ELISA method did not need a long time to perform and had high sensitivity, which is comparable with the molecular methods, and its cost was affordable to the breeders and livestock farmers. PCR method is a time-consuming and costly experiment and is not a cost-effective test for livestock farmers, but it is more suitable for researches. According to the results of the present study, it is recommended to apply ELISA method for the detection of *Cryptosporidium* in diarrheic calves in veterinary laboratories. Using the ELISA method, as a cost-effective and sensitive method
for detecting Cryptosporidium in diarrheic calves, which are the potential carriers of the parasite and a possible contaminator of the environment, could prevent the destruction of community’s valuable protein sources and provide significant contribution to the livestock farmers, thereby promoting the economy of the livestock farming sectors and public health.

The current work is the first research on the prevalence and molecular characterization of Cryptosporidium in pre-weaned cattle in West Azerbaijan province in the northwest of Iran. In this study, all the species isolates from pre-weaned cattle were identified as a C. parvum using PCR. Santin and the colleagues [39] found 19.2% positive cases in cattle of all ages in Meryland (USA), but in pre-weaned calves, the prevalence was 45.8%. Besides, 97% of the samples were C. parvum. Similar to our finding, various investigations conducted in Iran have found C. parvum as the dominant species of Cryptosporidium. Using nested PCR-RFLP of SSU rRNA (SSU 18s rRNA) gene, Saki and Asadpour [40] showed that all the positive Cryptosporidium spp. cases from cattle in the southwest of Iran were C. parvum. Oskouei et al. [33] reported that all 217 fecal samples (3.68% - 8/217) from cattle in Western Iran were C. parvum-positive. The same result was also obtained by Asadpour et al. [41] in the northeast of Iran. In cattle in Qazvin province, 72.6% of positive cases belonged to C. parvum, followed by C. andersoni (17.7%), C. bovis (7.8%), and a new subgenotype of C. parvum (1.9%) [42]. Mirzai et al. [35] have also identified C. parvum and C. andersoni in cattle in the northwest of Iran. A number of studies in Northwestern and Northeastern China, Brazil, and Sir Lanka have demonstrated that the common incidence of C. bovis, C. ryanae, and C. andersoni is due to the lack or low prevalence of C. parvum in pre-weaned cattle, which is not in agreement with our results [15,43-45].

Conclusions
In the current investigation, we utilized microscopy, immunological and molecular methods to determine the prevalence and discernment of Cryptosporidium spp. in pre-weaned cattle of Urmia city, in the northwest of Iran. C. parvum was identified as the only infectious agent in the region and could be the main cause of human infection. More studies are needed to find the source of infection for establishing the control measures.

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References
1. Fayer R, Morgan U, Upton SJ (2000) Epidemiology of Cryptosporidium: transmission, detection and identification. Int J Parasitol 30: 1305–1322.
2. De Graaf DC, Vanopdenbosch E, Ortega-Mora LM, Abbassi H, Peeters JE (1999) A review of the importance of cryptosporidiosis in farm animals. Int J Parasitol 29: 1269–1287.
3. Guselle NJ, Appelbee AJ, Olson ME (2003) Biology of Cryptosporidium parvum in pigs: from weaning to market. Vet Parasitol 113: 7–18.
4. Olson ME, Guselle NJ, O’Handley RM, Swift ML, McAllister TA, Jelinski MD, and Morck DW (1997) Giardia and Cryptosporidium in dairy calves in British Columbia. The Canadian Vet J 38: 703.
5. Ryan UNA, Fayer R, Xiao L (2014) Cryptosporidium species in humans and animals: current understanding and research needs. Parasitology 141: 1667–1685.
6. Ryan U, Hijiawi N (2015) New developments in Cryptosporidium research. Int J Parasitol 45: 367–373.
7. Santin M, Trout JM, Xiao L, Zhou L, Greiner L, Fayer R (2004) Prevalence and age-related variation of Cryptosporidium species and genotypes in dairy calves. Vet Parasitol 122: 103–117.
8. Fayer R, Santin M, Trout JM, Greiner E (2006) Prevalence of species and genotypes of Cryptosporidium found in 1–2-year-old dairy cattle in the eastern United States. Vet Parasitol 135: 105–112.
9. Fayer R, Santin M, Trout JM (2007) Prevalence of Cryptosporidium species and genotypes in mature dairy cattle on farms in eastern United States compared with younger cattle from the same locations. Vet Parasitol 145: 260–266.
10. Bornay-Llinares FJ, Da Silva AJ, Moura LN, Myjak P, Pietkiewicz H, Krumins-Lozowska W, Graczyk TK, Pieniazek NJ (1999) Identification of Cryptosporidium felisinf a Cow by Morphologic and Molecular Methods. Appl Environ Microbiol 65: 1455–1458.
11. Langkjær RB, Vigers H, Enemark HL, Maddox-Hyttel C (2007) Molecular and phylogenetic characterization of Cryptosporidium and Giardia from pigs and cattle in Denmark. Parasitology 134: 339–350.
12. Mi R, Wang X, Li C, Huang Y, Zhou P, Li Z, Lei M, Cai J, Chen Z (2013) Prevalence and genetic characterization of Cryptosporidium in yaks in Qinghai Province of China. PLoS One 8: e74985.
13. Smith HV, Nichols RAB, Mallon M, Macleod A, Tait A, Reilly WJ, Browning LM, Gray D, Reid SWJ, Sastling JM (2005) Natural Cryptosporidium hominis infections in Scottish cattle. Vet Record 56: 710–711.
14. Follet J, Guyot K, Leruste H, Follet-Dumoulin A, Hammouma-Ghelboun O, Certad G, Dei-Cas E, Halama P (2011) Cryptosporidium infection in a veal calf herd in France: molecular characterization of species in a longitudinal study. Vet Res 42: 116.
15. Zhang W, Wang R, Yang F, Zhang L, Cao J, Zhang X, Ling H, Liu A, Shen Y (2013) Distribution and genetic characterizations of Cryptosporidium spp. in pre-weaned dairy
calves in Northeastern China’s Heilongjiang Province. PLoS One 8: e54857.
16. Brook E, Hart CA, French N, Christley R (2008) Prevalence and risk factors for Cryptosporidium spp. infection in young calves. Vet Parasitol 152: 46-52.
17. Nourmohammadzadeh F, Davoodi Y, Jamali R, Nowrouzian I (2010) Epidemiological study on cryptosporidiosis in newborn calves in Eastern Azarbaijan Province. J Vet Res. 65: 247-270.
18. Garcia LS, Bruckner DA, Brewer TC, Shimizu RY (1983) Techniques for the recovery and identification of Cryptosporidium oocysts from stool specimens. J Clin Microbial 18: 185-190.
19. Weber R, Bryan RT, Bishop HS, Sullivan JJ, Juranek DD (1991) Threshold of detection of Cryptosporidium. J Infect Dis 163: 775-779.
20. Jafari R, Maghsood AH, Safari M, Latifi F, Farnia S, Bai rami A, Rezaeian M (2012) Cryptosporidium spp. infection in human and domestic animals. Iran J Parasitol 7: 53-58.
21. Garcia LS, Shimizu RY (1997) Evaluation of nine immunoassay kits (enzyme immunoassay and direct fluorescence) for detection of Giardia lamblia and Cryptosporidium parvum in human fecal specimens. J Clin Microbiol 35: 1526-1529.
22. Sulaiman IM, Xiao L, Lal AA (1999) Evaluation of Cryptosporidium parvum Genotyping Techniques. Appl Environ Microb 65: 4431-4435.
23. Tappeh KH, Gharavi M, Makhdoumi K, Rahbar M, Taghizadeh A (2006) Prevalence of Cryptosporidium spp. infection in renal transplant and hemodialysis patients. Iran J Public Health 35: 54-57.
24. Garcia LS (2006) Diagnostic medical parasitology, 5th edition. Washington, DC: American Society for Microbiology Press. 1202 p.
25. Celentano D, szklo M (2018) Goshard Epidemiology, 6th edition. Elsevier press. 433p.
26. Joute J, Gill J, Singh B (2016) Prevalence and molecular epidemiology of Cryptosporidium parvum in dairy calves in Punjab (India). J Parasit Dis 40: 745-749.
27. Uga S, Matsuo J, Kono E, Kimura K, Inoue M, Rai S, Ono K (2008) First longitudinal study of Cryptosporidium parvum in dairy cattle from birth to 2 years of age. Vet Parasitol 155: 15-23.
28. Qi M, Fang Y, Wang X, Zhang L, Wang R, Du S, Gua Y, Jia Y, Yao Q, Liu Q, Zhao G (2015) Molecular characterization of Cryptosporidium spp. in pre-weaned calves in Shananxi Province, north-western China. J Med Microbiol 64: 111-116.
29. Gharavi M, Makhdoumi K, Rahbar M (2006) Prevalence of Cryptosporidium parvum infection and pattern of oocyst shedding in calves in Japan. Vet Parasitol 94: 27-32.
30. Delafosse A, Chartier C, Dupuy MC, Demoulin M, Pors I, Paraud C (2015) Cryptosporidium parvum infection and associated risk factors in dairy calves in western France. Prev Vet Med 118: 406-412.
31. Huang I, Yue D, Qi M, Wang R, Zhao J, Li j, Shi K, Wang M, Zhang L (2014) Prevalence and molecular characterization of Cryptosporidium spp. and Giardia duodenalis in dairy calf in Ningxia, northwestern China. BMC Vet Res 10: 292.
32. Garro CJ, Morici GE, Ugtés ME, Tomazic ML, Schnittiger L (2016) Prevalence and risk factors for shedding of Cryptosporidium spp. oocysts in dairy calves of Buenos Aires Province, Argentina. Parasite Epidemiol Control 1: 36-41.
33. Oskouei MM, Fallah E, Ahmadi M, Safa’iyen A, Bakhtiyari S, Naseri fr A, Dousti M (2014) Molecular and parasitological study of Cryptosporidium isolates from cattle in Ilam, west of Iran. Iran J Parasitol 9: 435-440.
34. Jafari R, Maghsood AH, Fallah M (2012) Prevalence of Cryptosporidium infection among livestock and humans in contact with livestock in Hamadan district, Iran. J Res Health Sci 13: 86-90.
35. Mirzai Y, Yakhchali M, Mardani K (2014) Cryptosporidium parvum and Cryptosporidium andersoni infection in naturally infected cattle of northwest Iran. Vet Res Forum 5: 55-60.
36. Heidarnegadi S, Mohebali M, Maraghi S, Baba Z, Farnia S, Bairami A, Rezaeian M (2012) Cryptosporidium spp. Infection in human and domestic animals. Iran J Parasitol 7: 53-58.
37. Yilmaz H, Tas-Cengiz Z, Cicek M (2008) Investigation of cryptosporidiosis by enzyme-linked immunosorbent assay and microscopy in children with diarrhea. Saudi Med J 29: 526-529.
38. Gawad SSA, Isma il MA, Imam NF, Eassa AH (2018) Detection of Cryptosporidium spp. in Diarrheic Immunocompetent Patients in Beni-Suef, Egypt: Insight into Epidemiology and Diagnosis. Korean J Parasitol 56: 113-119.
39. Santin M, Trout JM, Fayer R (2008) A longitudinal study of cryptosporidiosis in dairy cattle from birth to 2 years of age. Vet Parasitol 155: 15-23.