



Phylogenetic analysis of *Isospora* spp from cats in Mosul city

A.M. Abdulhammed¹, W.A. Alobaidii²

Department of Microbiology, College of Veterinary Medicine, University of Mosul, Mosul, Iraq

Article information

Article history:

Received May 7, 2025

Accepted December 3, 2025

Published July 5, 2026

Keywords:

Isospora

Cats

Diarrhea

Polymerase chain reaction

Correspondence:

W.A. Alobaidii

wasenamkad@uomosul.edu.iq

Abstract

Through this study two hundred samples were previously examined using conventional microscopic methods to investigate the *Isospora* parasite. Through the conventional tests, 45 positive samples were found, which were subjected to molecular tests in this study, DNA extraction from fecal samples, to complete molecular identification of *Isospora*, with specific target genes using specific primers, all samples were screened using ITS-1 gene for *Isospora* as described by previous reports PCR reaction mixture the amplification program. The results of the polymerase chain reaction showed positive results, Through the molecular detection of 45 traditional positive test samples, the molecular detection of ITS-1 gene of *Isospora* showed 39 (86.7%) positive samples out of 45 samples. The results of polymerase chain reaction showed stray cats recorded high infection rate, female showed high rate of infection, according to age the infection rate decreases when age of animals increase, the native cats recorded high infection, the clinical presentations showed lowest infective rates in healthy appearance cats when compared with cats that suffer from diarrhea. The results of the genetic sequencing of the ITS1 gene of the *Isospora* spp showed the presence of a genetic sequence for the samples, It was found that there were only five isolates out of the total samples sent for genetic sequencing, and they were registered in GenBank with the serial number (LC856630.1, LC856631.1, LC856632.1, LC856633.1 and LC856634.1), this study concludes that *Isospora* is widespread in Mosul city, Iraq. This first study highlights the phylogenetic analysis in Mosul city, Iraq.

DOI: [10.33899/ijvs.2025.159952.4291](https://doi.org/10.33899/ijvs.2025.159952.4291), ©Authors, 2026, College of Veterinary Medicine, University of Mosul.

This is an open access article under the CC BY 4.0 license (<http://creativecommons.org/licenses/by/4.0/>).

Introduction

Protozoan parasites belonging to the coccidian group, *Isospora* spp. (Cystoisospora), have long been known to pose a threat to cats. Cats' gastrointestinal tracts are where the sexual phase of reproduction takes place, and it ends with the passing of unsporulated oocysts in feces (1).

For *I. felis* and *I. rivolta*, cats are the definitive hosts. *Isospora* species are host-specific, widely distributed, and frequently cause infections, especially in young animals. Prevalence rates for *Isospora* spp. infection in cats range from 3% to over 30% in the United States, according to the Companion Animal Parasite Council (2). The presence of

Isospora felis oocysts was found in 3% of 1,355 cats in a UK study. Although young animals are typically more likely to be shedding oocysts than adults, gender and breed typically have little effect on the shedding rates of *Isospora* spp. *I. felis* was discovered in the feces of 9% of cats younger than six months in the UK study (3).

Cats can become infected with *Isospora* species by consuming tissues from other infected vertebrate intermediate hosts or by consuming sporulated oocysts found in the environment. Ingestion by the cat of sporulated oocysts carried by paratenic hosts such as flies, cockroaches, or dung beetles can also result in infection (4). Infected animals' small intestines go through an enteroepithelial

phase, which ends with the passage of unsporulated oocysts in feces. As little as 12 hours may pass before sporulation takes place, depending on the surrounding circumstances. Animals that are young, weak, and immunocompromised are more likely to have clinical illness (5). The areas of the small intestine where *Isospora* species multiply differ according to the species. Some infected animals exhibit microscopic lesions such as hyperplasia of lymph nodes in Peyer's patches, dilatation of lacteals, and villous atrophy (6).

Infections with *Isospora* spp. are often only linked to illness in kittens, who may have vomiting, inappetence, abdominal pain, and watery diarrhea that occasionally contains blood. Death and severe dehydration may result, depending on the animal's age and parasite burden. During stressful times, kittens with subclinical infections may exhibit recurrent shedding and clinical symptoms (7).

When oocysts are found in fecal samples from afflicted animals, coccidiosis is conclusively diagnosed. Due to their size and frequent occurrence in large quantities, *Isospora* spp. oocysts are typically simple to identify through microscopic analysis of feces following fecal flotation. Positive test findings may not always indicate a link to a disease, either, because healthy animals can sometimes transfer *Isospora* spp. oocysts. Although clinically infected animals seldom have false-negative fecal float results, in certain situations a second fecal flotation may be required to confirm infection since clinical indications can sometimes occur before oocyst shedding (8).

The majority of normally healthy kittens will get diarrhea that goes away on its own without treatment since coccidiosis is typically self-limiting. Nonetheless, treatment can hasten the remission of clinical illness and may reduce environmental pollution and the risk of infection among animals in touch (9).

Oocysts of *Isospora* species exhibit high resistance to both environmental factors and disinfectants. Providing proper sanitation, which includes removing feces as soon as possible before oocyst sporulation, is essential for control. Surface-contaminating oocysts can be eliminated by steam washing. The incidence of coccidiosis in young animals can be reduced by treating queens with anticoccidial medicines before parturition. All in-contact animals, especially kittens, may need to be treated in circumstances with high infection rates. Ponazuril may help control coccidiosis if it is given to all at-risk kittens when they are brought into shelters (10).

Humans are not infected by canine or feline *Isospora* species. However, some afflicted animals have co-infections with other parasites, such as *Giardia* spp. and *Cryptosporidium* spp., that can spread zoonotically to humans. Therefore, when an animal has diarrhea, a thorough diagnostic workup should be performed (11).

Materials and methods

Ethical approval

The scientific board of the College of Veterinary Medicine at Mosul University in Mosul, Iraq, approved this study; the approval number for this study is UM.VET.2023.037.

Animals

Two hundred samples were previously examined using conventional microscopic methods to investigate the parasite. Through these tests, 45 positive samples were found, which were subjected to molecular tests in this study.

Sample collection

Gathering of samples fecal samples were taken from companions, stray animals, of all ages, and with various health conditions in the Mosul provinces between August 2024 and March 2025. Application documents were used to document the place, sex, and date of sample collection. Until a subsequent attempt at molecular research, all fecal samples were kept at -20°C (12).

DNA extraction

DNA extraction was performed according to a fecal sample-based adaptation of the Maxwell®RSCPure Food GMOKit (REF AS1600; PromegaCo., Madison, WI, USA)

Molecular identification and PCR amplification *Isospora* molecular identification is accomplished by utilizing a thermocycler to extract DNA containing particular target genes from fecal samples. The ITS-1 gene was used to screen for *Isospora* in all samples (13).

Polymerase chain reaction

Molecular identification of *Isospora*, was carried out by removing DNA containing particular target genes from fecal samples employing specific primer F1: CCGTTGCTCCTACCGATTGAGTG and R1: GCATTTCGCTGCGTCCTTCATCG (14). All samples were screened using the *Isospora* ITS-1 gene as reported in earlier studies. In order to verify contamination with the PCR reaction mixture and the amplification protocol, a negative template control sample (RNase-free water) was added to each PCR. which used is initial denaturation 94°C for 60 sec ,1 cycle then 40 cycle (denaturation 98 °C for 10 sec, elongation 62°C for 60 sec, extension 68°C for 60 sec) and final extension 68°C for 5 min, by employing 1.5% agarose gel in TAE solution for gel electrophoresis, the amplified products were found. In the presence of UV light, 0.5% ethidium bromide was used to observe DNA bands.

Phylogenetic analysis

Using the greatest likelihood approach, phylogenetic analysis was carried out utilizing MEGA X (www.megasoftware.net). A bootstrap value of 1,000 repeats was used to evaluate the stability of the phylogenetic tree, and the reference sequences were chosen based on earlier research (15).

Results

The results of the polymerase chain reaction showed positive results, which showed as bands in electrophoresis at 700 bp (Figure 1).

Through the molecular detection of 45 traditional positive test samples, the molecular detection of ITS-1 gene of *Isospora* showed 39 (86.7%) positive samples out of 45 samples.

According to animal management the stray cats recorded high infection rate when compare with companion cats, female showed high rate of infection while male showed lowest infection rate, according to age the infection rate decreases when age of animals increases, the native cats recorded high infective rates, while imported showed lowest infective rates, the clinical presentations showed lowest infective rates in healthy appearance when compare with cats which suffer from diarrhea (Table 1).

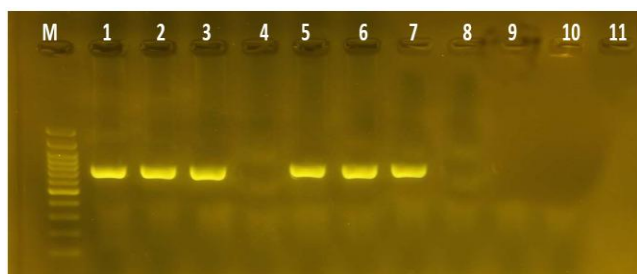


Figure 1: Gel electrophoresis image showing: Lane (M) DNA ladder; Lanes 1-3, 5-7) positive samples *Isospora* spp DNA; Lanes (4,8-11) negative samples to *Isospora* spp DNA in approximately band size 700 bp.

DNA sequencing and submission to GeneBank

The Sanger sequencing method was used to sequence the PCR product of the positive samples, which were delivered to Macrogen in Korea. In short, the matching primer was sent with 25 µl of the target gene's PCR product. Sequencing results were saved as text files in the FASTA format. A particular accession number was obtained by registering the chosen strains with GenBank, NCBI.

The findings of the genetic sequencing of the *Isospora* spp. ITS1 gene revealed that the samples sent in cats in the city of Mosul had a genetic sequence. Out of all the samples sent for genetic sequencing, only five isolates were

discovered to exist. These isolates were registered in GenBank with the serial numbers LC856630.1, LC856631.1, LC856632.1, LC856633.1, and LC856634.1 (Table 2).

Table 1: showed the infection rates of *Isospora* spp.

Factors	No. tested cases	No. of Positive	(%)
Animals management			
Stray	26	24	92.3
Companion	19	15	78.9
Gender			
Males	20	16	80
Females	25	23	92
Age			
Less than 2 months	26	25	96.1
More than 2months-6 months	14	12	85.7
More than 6 months	5	2	40
Source			
Native	26	24	92.3
Imported	19	15	78.9
Clinical presentation			
Healthy appearance	11	9	81.8
Diarrhea	34	30	88.2

Results of the molecular nucleotide sequence of the ITS1 gene of the *Isospora* in the database. The results showed the presence of gene sequences that have a percentage of similarity to the nucleotide sequence of the ITS1 gene for each of the *Isospora* strains that were diagnosed in the study when BLAST was performed in the database compared to the nucleotide sequences of the international strains, which were identified during this study and which were used for the purpose of constructing the genetic phylogenetic tree. The results showed that there was a similarity rate between the local isolates bearing the registration number in GenBank (LC856630.1, LC856631.1, LC856632.1, LC856633.1 and LC856634.1) where the highest similarity rate was reached. 100 % with the strain registered in the World GenBank under the name PP097750.1 and PP097754.1 in China, OM870395.1 in Australia and isolated OQ473178.1 OQ473172.1, in South Korea, followed in terms of similarity by the strain under the genetic name PP844939.1 in Iraq, reaching 99.5% and also KP411388.1 in USA (Table 3).

The results of the study showed that the phylogenetic tree that was constructed showed that the ITS1 gene for the five genotypes that were isolated during the study possessed phylogenetic and evolutionary characteristics with the recorded genotypes, as the percentage of evolutionary relationship ranged from 45.12-100%, knowing that the strains that have characteristics similar to the local strains declined among Australia, China and the Korea (Table 4) (Figure 2).

Table 2: Local genetic sequences of the ITS-1 gene of *Isospora* spp. diagnosed in different samples of the cat with their serial numbers in GenBank

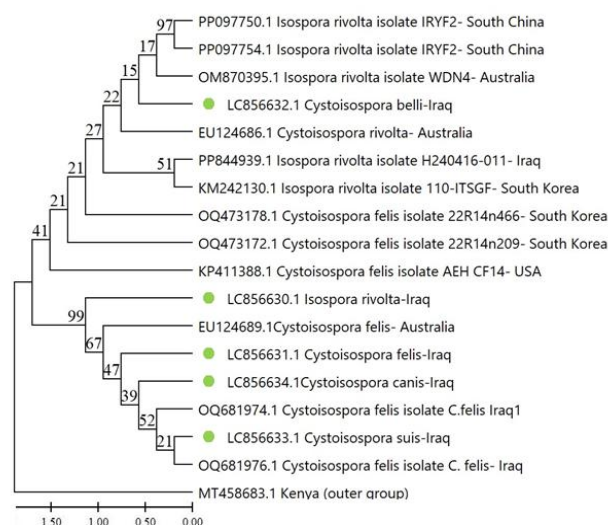
Local isolate	Gene	Isolation source	Sequences 5'-----3'	Accession No.
Isospora spp.	ITS-1		TGCCCCANATGGAAAGTTTTGTGAACCTTAACACTTAGAGGAAGGAGAAGTCGTAAC AAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACACAGTGGCCCCCGAAACGTC TAAAACCTTCTTGCTACTGAATCCCATAATCAGGACTCACGAGTCATGTTGTTACAGCA CGGGAAAGTGTTTTGTGTTTTCCGTTGCGGCAACTACCTCGGGTGACCTCTGTAAGGGC ATTCGCTGTTGCCCGTGCTACTTCCTCCACATGGAGCACTTTCCACCGGACCTACCC AAAAAGGGCTGGAGCATAATGGATGTGGATTTCATCCGTTTCTCCTATCTCCTTGAG ATTTTGCCCGGTGAGGACTCGGTTGTCCATGAGGGCGGGATAGCGTAAGGGCGGAA GCTAATGGTGCTCTGGTACACATTCTTATTCTATACAATGTGGTGACACGAGCTGTCT ACTTCCATTTCTGCGACGACCCAACGTGGGCGAGTCGAACTCTGGGTCTGGACGCCT TCTCTGCGGATTTGGTAGAAAGAGAATGTGTATCTCTGATGCGCCCCCCCCACAAT GGGTGCGACGGCTGCCATGAAAAGAAAAAGATGTG	LC856630.1
			TGCCCCGAGATGGAAAGTTTTGTGAACCTTAACACTTAGAGGAAGGAGAAGTCGTAAC AAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACACAGTGGCCCCCGAAACGTC TAAAACCTTCTTGCTACTGAATCCCATAATCAGGACTCACGAGTCATGTTGTTACAGCA CGGGAAAGTGTTTTGTGTTTTCCGTTGCGGCAACTACCTCGGGTGACCTCTGTAAGGGC ATTCGCTGTTGCCCGTGCTACTTCCTCCACATGGAGCACTTTCCACCGGACCTACCC AAAAAGGGCTGGAGCATAATGGATGTGGATTTCATCCGTTTCTCCTATCTCCTTGAG ATTTTGCCCGGTGAGGACTCGGTTGTCCATGAGGGCGGGATAGCGTAAGGGCGGAA GCTAATGGTGCTCTGGTACACATTCTTATTCTATACAATGTGGTGACAGGAGCTGTCT ACTTCCATTTCTGCGTCGTCCCAGCGTGGGCGAGTCAGACTCTGGGTCTGGACGCATT CTCTTGCCACCGTTGGTAGAGAAGGAATGTGTATCGTTATTTCTCCTCCACATTGTCT GGTGTCTCTTCTCTGATGAA	LC856631.1
			ATGCCCGAAATGGAAAGTTTTGTGAACACTTAACACTTAGAGGAAGGAGAAGTCGT AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACACAGTGGCCCTCGAAAC ATCTTCAAAACCTTAGCGACTGAATCCCCATATTTATGGCCATCTTCTGGAACAAGCT GGTGAGCAGCAGGAGAGGAAGCCCTATTCCACGGTGCCCCCAGATGTTCCAAATGG CCGCTTTAAGAGCATTAGTCGTTGTCGCTGGTGCCCTTCGCTGCAGCGGACGGTGCA ATTCTCTCCGATCTGCTCAAAGGGTTGAAACAGAATAGAGGTCGTTCCACTCTTTTCT TGCCCTTTGAACTATGGAAGGTGAGGAAGTGGTTGTCTATGTATGCGTGGGGGAGTC CGGACTGCAGCGGCAGCCTCAGGTGCTCTGCTACACACATTCGTTCTCTGCCACTTG GTGGTACGGCCAGTCTGTCTCCATTGGAGTCGCCGCTTGCCCGTGAGGGATGTGCTCT ATGGATTTA	LC856632.1
			TGCCCCGACATGGAAAGTTTTGTGAACCTTAACACTTATCGGAAGGAGAAGTCGTAACA AGGTTTCCGTATGTGAACCTGCGGAAGGATCATTACACAGTGGCCCCCGAAACGTC AATAACTTCTTGCTACTGAATCCCATAATCAGGACTCAGATGTCATGTTGTTACGAC GGGAAAGTGTGTTTTGTTTTCCGTTGCGGCAACTACCTCGGGTGACCTCTGTAAGGGCA TTCGCTGTGTTGCCCGTGCTACTTCCTCCACATGGAGCACTTTCCACCGGACCTACCCA AAAAGGGCTGGAGCATAATGGATGTGGATTTCATCCGTTTCTCCTATCTCCTTGAGAT TTTGCCCGGTGAGGACTCGGTTGTCCATGAGGGCGGGATAGCGTAAGGGCGGAAGC TAATGGTGCTCTGGTACACATTCTTATTCTATACAATGTGGTGACAGGAGCTGTCTAC TTCTATTTCTGCGTCGTCCCAGCGTGGGCGAGTCAGACTCTGGGTCTGGAGCTCATTCT CTTGCCACCGTTGGTAGAGAAGGAATGTGTATCGTTATTTCTCCTCCACATTGTCTGG TTGCTCTTCTCTGATGAAGGTGAACGGGTATATACATACCTGTTGTCCGCCCTCTTTG AGAAAATAAAC	LC856633.1
			GATCCCCGAGATGGAAAGTTTTGTGAACCTTAACACTTAGAGGAAGGAGAAGTCGT AACAAGGTTTCCGTAGGTGAACCTGCGGAAGGATCATTACACAGTGGCCCCCGAAAC GTCTAAAACCTTCTTGCTACTGAATCCCATAATCAGGACTCACGAGTCATGTTGTTCA GCACGGGAAAGTGTTTTGTGTTTTCCGTTGCGGCAACTACCTCGGGTGACCTCTGTAAG GGCATTTCGTGTTGCCCGTGCTACTTCCTCCACATGGAGCACTTTCCACCGGACCTA CCCAAAAAGGGCTGGAGCATAATGGATGTGGATTTCATCCGTTTCTCCTATCTCCTTG AGATTTTGCCCGGTGAGGACTCGGTTGTCCATGAGGCGGGATAGCGTAAGGGCGG AAGCTAATGGTGCTCTGGTACACATTCTTATTCTATACAATGTGGTGACAGGAGCTGT CTACTTCCATTTCTGCGTCGTCCCAGCGTGGGCGAGTCAGACTCTGGGTCTGGACGCA TTCTCTTGCCACCGTTGGTAGAGAAGGAATGTGTATCGTTATTTCTCCTCCACATTGT CTGGTTGCTCTTCTCTGATGAAAGTGAACGGGTATATACATACCTGTTGTCCGCCCTC TTTGAGAAAA	LC856634.1

Table 3: Using NCBI BLASTn, compare the local *Isospora* spp. sequences to other sequences of the same pathogen in GenBank

Local sequences Accession No.	Pathogen Identified	Name of gene	Identic Number %	GenBank Accession Number	Country Identification
LC856630.1	<i>Isospora spp.</i>	ITS-1	100	PP097750.1	South China
			100	PP097754.1	South China
LC856631.1			98.72	EU124689.1	Australia
			99.75	EU124686.1	Australia
			100	OM870395.1	Australia
LC856632.1			98.06	KM242130.1	South Korea
			100	OQ473178.1	South Korea
			100	OQ473172.1	South Korea
LC856633.1			98.44	OQ681974.1	Iraq
			99.50	PP844939.1	Iraq
			98.45	OQ681976.1	Iraq
LC856634.1			99.50	KP411388.1	USA

Table 4: Alignment score within and between obtained local sequences of *Isospora* spp. using multiple sequence alignment- CLUSTALW

Sequences Accession No.	Alignment score
LC856630.1	45.12 – 100
LC856631.1	
LC856632.1	
LC856633.1	
LC856634.1	

Figure 2: *Isospora* spp. phylogenetic tree from cats in Iraq's Mosul province Using bootstrap analysis with 1000 resamplings and the Maximum Likelihood technique based on the Tamura-Nei model in MEGA11 software, the phylogenetic tree was built. Concatenated partial ITS1 gene partial DNA sequences were utilized as input data. The outgroup was MT458683.1-Kenya.

Discussion

Around the world, communities place a high value on animals, particularly dogs and cats. Due to their ability to provide biological and nutritional circumstances, cats are the reservoir hosts of parasites, including helminthes and protozoa.

In this study the total infection rates with *Isospora* protozoa were 86.7%, when compared these results with other study this percentage was too high, 5.8% infection rates were recorded by (16) in Iran, 12% infection rates reported by (17) in Babylon Province, Iraq, Erbil had an infection rate of 16%, greater than the 5.2% seen in another study carried out in Duhok Province (18). Nonetheless, the infection rate found in this investigation was lower than the 75.55% rate seen in Basrah (19), 77.3% infection rates recorded by (20) in Malaysia. The discrepancy in infection rates between our study and other similar studies is due to many reasons, some of which may be due to the host (cats) and some of which may be due to the nature of the surrounding environment and the nature of upbringing. However, the most important reasons are the specificity of each study and the nature of the samples in it (21). Since the nature of the samples in our study, as well as the aim of the study, was to study a specific goal, which is to diagnose the parasite, the samples that were examined were previously examined using routine methods. Therefore, the molecular study was for the purpose of confirming the infection, in addition to studying the genetic patterns of the parasite. Another reason for the variation in infection rates is also due to the nature of the tests used for diagnosis, as our study confirmed the routine diagnosis of cat fecal samples that were previously examined, in addition to the fact that molecular tests have a high accuracy and very high specificity, which led to a high infection rate in the examined samples, as our study is selective of samples and far from randomness in examining samples (22).

The results showed variations in several factors which study the relationship between cat related with factors and infection rates with *Isospora* protozoa, the age-related factors with *Isospora* infection showed high infection rates in younger animals (less than 2 months) while high infection rates recorded in aged animals (more than 2 years old), very few studies have addressed this disparity in infection rates and age groups of cats. One of these few studies confirmed the results obtained, as this study recorded a high infection rate in young cats compared to older ones (23), *I. felis* (67.1%) and *I. rivolta* (48.6%) were the most common protozoa infections in 100 farm-raised kittens in southern Germany (24). Another study showed opposite results, indicating that young cats are less likely to be infected than older ones (25). Cats of all ages are susceptible to infection, as evidenced by the prevalence of gastrointestinal protozoa in both young and adult cats.

It was found that 414 domestic cats in various counties in Transylvania, Romania, had *I. rivolta* (8.9%), *I. felis* (5.3%), *T. gondii*/*Hammondia hammondi* (1.2%), *Sarcocystis* spp. (1%), and *G. duodenalis* (0.7%) (26). In line with earlier research, our study's findings revealed that 103 cats were gathered and that *Isospora* spp. 6/103 (5.8%) were present (26).

Only four isolates were identified from the total number of samples sent for genetic sequencing, according to the results of the ITS1 gene of the *Isospora* genetic sequencing. This variation in the similarity rate points to the parasite's genetic diversity, which is caused by various genetic alterations and mutations (27). The various sequence alignment results also revealed that the gene included missing sections in addition to constant, common, and variable regions. These findings align with the findings published by (28), who stated that the distinction between global strains and isolated strains. However, it can be because of the different isolation site and the different environmental circumstances. (29) said that the nucleotide sequence of the parasite is highly susceptible to producing genetic mutations, which helps the parasite adapt throughout infection to evade the immune response and the creation of new strains. In several nations around the world, there have been outbreaks of novel diseases or emergency infections of varying severity. The study's genetic strains' ITS1 gene phylogenetic tree revealed that the five strains found belong to the same subgroup and are among certain species that are listed worldwide in (30). This association provides unmistakable proof that these animals are highly genetically related. In addition, the study's isolated strains' positions in the phylogenetic tree, which show genetic divergence between them (31,32). Geographical location may play a part in the divergence and convergence of local and global strains, which suggests that the strains share a shared evolutionary origin from a genetic perspective (33). Thus, the existence of the *Isospora* and its threat to cat mating are made evident to

us by this study. In Iraq, cats are imported at random, without rigorous quarantine regulations, and regardless of whether the animal is examined (34,35). Furthermore, our research has demonstrated the existence of recombinant genetic strain patterns of the virus, which arise from the coexistence of multiple parasite strains. Additionally, the frequent exacerbation of parasite presence in cats may be caused by veterinary clinics' failure to use anti-protozoal medications (36-38).

Conclusion

Cats are afflicted with intestinal protozoa, and Nineveh province has a higher prevalence of parasites.

Acknowledgment

The authors acknowledge the invaluable assistance provided by the veterinary teaching hospital and the financial support offered by the College of Veterinary Medicine at the University of Mosul for this work.

Conflict of interest

The authors affirm that the paper has no conflicts of interest.

References

1. Alobaidii WA. The serological diagnosis of canine Leishmaniasis by using ELISA in Nineveh province. *Iraqi J Vet Sci.* 2019;33(2):111-114. DOI: [10.33899/ijvs.2019.163194](https://doi.org/10.33899/ijvs.2019.163194)
2. Jarad NI, Al-Difaie RS, Mohammed NQ. Molecular recognition and phylogenetic tree analysis of *Cystoisospora canis* in stray dogs in Diwaniyah city, Iraq. *Iraqi J Vet Sci.* 2025;39(2):307-312. DOI: [10.33899/ijvs.2025.156053.4058](https://doi.org/10.33899/ijvs.2025.156053.4058)
3. Tzannes S, Batchelor DJ, Graham PA, Pinchbeck GL, Wastling J, German AJ. Prevalence of *Cryptosporidium*, *Giardia* and *Isospora* species infections in pet cats with clinical signs of gastrointestinal disease. *J Feline Med Surg.* 2008;10(1):1-8. DOI: [10.1016/j.jfms.2007.05.006](https://doi.org/10.1016/j.jfms.2007.05.006)
4. Dubey JP. A review of *Cystoisospora felis* and *Cystoisospora rivolta* induced coocidiosis in cats. *Vet Parasitol.* 2018;263:34-48. DOI: [10.1016/j.vetpar.2018.09.016](https://doi.org/10.1016/j.vetpar.2018.09.016)
5. Najm ND, Khalaf WK, Mekhael YR. Detection of Intestinal Parasites in Domestic Cats in Mosul City, Iraq. *Environ Pollut.* 2023;10:11. DOI: [10.5455/OVJ.2022.v12.i5.13](https://doi.org/10.5455/OVJ.2022.v12.i5.13)
6. Mitchell SM, Zajac AM, Charles S, Duncan RB, Lindsay DS. *Cystoisospora canis* Nemeséri, 1959 (syn. *Isospora canis*), infections in dogs: Clinical signs, pathogenesis, and reproducible clinical disease in beagle dogs fed oocysts. *J Parasitol.* 2007;93(2):345-52. DOI: [10.1645/GE-1024R.1](https://doi.org/10.1645/GE-1024R.1)
7. Jassim E, Al-Emarah GH, Mustafa J. Microscopic and Molecular Diagnosis of *Isospora* spp Parasites in Cats and Dogs. *Assiut Vet Med J.* 2024;70(183):413-20. [\[available at\]](#)
8. Cama VA, Mathison BA. Infections by intestinal coccidia and *Giardia duodenalis*. *Clin Lab Med.* 2015;35(2):423. DOI: [10.1016/j.cll.2015.02.010](https://doi.org/10.1016/j.cll.2015.02.010)
9. Tropical Council for Companion Animal Parasites (TroCCAP). Guidelines for the diagnosis, treatment and control of feline

- endoparasites in the tropics. 2nd ed. Australia: Tropical Council for Companion Animal Parasites Ltd.; 2019. [\[available at\]](#)
10. Lindsay DS, Dubey JP, Blagburn BL. Biology of *Isospora* spp. from humans, nonhuman primates, and domestic animals. Clin Microbiol Rev. 1997;10(1):19-34. DOI: [10.1128/cmr.10.1.19](#)
11. Shukla R, Giraldo P, Kraliz A, Finnigan M, Sanchez AL. *Cryptosporidium* spp. and other zoonotic enteric parasites in a sample of domestic dogs and cats in the Niagara region of Ontario. Can Vet J. 2006;47(12):1179. [\[available at\]](#)
12. Alobaidii WA. Molecular detection of *Hammondia heydorni* in dogs in Mosul city. Iraqi J Vet Sci. 2020;34(2):329-332. DOI: [10.33899/ijvs.2019.126052.1219](#)
13. Yun CS, Moon BY, Lee K, Kang SM, Ku BK, Hwang MH. The detection and phylogenetic characterization of *Cryptosporidium*, *Cystoisospora*, and *Giardia duodenalis* of cats in South Korea. Front Cell Infect Microbiol. 2023;13:1296118. DOI: [10.3389/fcimb.2023.1296118](#)
14. Shafiei R, Najjari M, Kheirabad AK, Hatam G. Severe diarrhea due to *Cystoisospora belli* infection in an HTLV-1 woman. Iran J Parasitol. 2016;11:121-125. [\[available at\]](#)
15. Zaki ZD, Alobaidii WA. Molecular investigation of *Hepatozoon canis* in dogs in Mosul city. Iraqi J Vet Sci. 2025;39(1):129-134. DOI: [10.33899/ijvs.2024.151603.3768](#)
16. Mahdi NK, Ali NH. Intestinal parasites, including *Cryptosporidium* species, in Iraqi patients with sickle-cell anaemia. East Mediterr Health J. 2002;8(2-3):345-349. [\[available at\]](#)
17. Idan SR, Al-Hasnawy MH. Microscopic and molecular diagnoses of *Giardia duodenalis* in pet animals in Babylon Province, Iraq. Vet World. 2023;16(11):2263-2270. DOI: [10.14202/vetworld.2023.2263-2270](#)
18. Muhamed TA, Al-Barwary LO. Prevalence of Intestinal Parasites in the Intestine of Dogs (Sheep-Keeper, Owned, Pet and Stray) in Duhok Province, Kurdistan Region. J Vet Sci Technol. 2016;7(6):379. [\[available at\]](#)
19. Thamer NK, Al-Idreesi SR, Farhood NN. Detection Of Gastrointestinal Parasites of Cats and Dogs in Basrah Province. Basrah J Vet Res. 2022;21(S1):67-74. DOI: [10.23975/bjvetr.2022.177426](#)
20. Abdulwahab MH, Al-Talib HA. Estimation of protozoal diversity among stray cats in Malaysia. Biodiver J Biol Diver. 2024;25(5). DOI: [10.13057/biodiv/d250529](#)
21. Adhikari RB, Dhakal MA, Ale PB, Regmi GR, Ghimire TR. Survey on the prevalence of intestinal parasites in domestic cats (*Felis catus* Linnaeus, 1758) in central Nepal. Vet Med Sci. 2023;9(2):559-571. DOI: [10.1002/vms3.999](#)
22. Cossío TI, Luna AM, Mejia MR, Ortega AF, Cárdenas RH, Núñez CR. Risk factors associated with cat parasites in a feline medical center. JFMS Open Rep. 2021;7(2):20551169211033183. DOI: [10.1177/20551169211033183](#)
23. Yang Y, Liang H. Prevalence and risk factors of intestinal parasites in cats from China. Biomed Res Int. 2015;2015(1):967238. DOI: [10.1155/2015/96723](#)
24. Beelitz P, Göbel E, Gothe R. Fauna and incidence of endoparasites in kittens and their mothers from different husbandry situations in south Germany. 1992;20(3):297-300. [\[available at\]](#)
25. Lee SH, Ock Y, Choi D, Kwak D. Gastrointestinal parasite infection in cats in Daegu, Republic of Korea, and efficacy of treatment using topical emodepside/praziquantel formulation. Korean J Parasitol. 2019;57(3):243. DOI: [10.3347/kjp.2019.57.3.243](#)
26. Dărăbuș G, Lupu MA, Mederle N, Dărăbuș RG, Imre K, Mederle O, Imre M, Paduraru AA, Morariu S, Olariu TR. Epidemiology of *Cryptosporidium* infection in Romania: a review. Microorganisms. 2023;11(7):1793. DOI: [10.3390/microorganisms11071793](#)
27. Megía-Palma R, Martínez J, Nasri I, Cuervo JJ, Martín J, Acevedo I, Belliure J, Ortega J, García-Roa R, Selmi S, Merino S. Phylogenetic relationships of *Isospora*, *Lankesterella*, and *Caryospora* species (Apicomplexa: Eimeriidae) infecting lizards. Org Diver Evol. 2016;16:275-88. DOI: [10.1007/s13127-015-0253-3](#)
28. Carreno RA, Schnitzler BE, Jeffries AC, Tenter AM, Johnson AM, Barta JR. Phylogenetic analysis of coccidia based on 18S rDNA sequence comparison indicates that *Isospora* is most closely related to *Toxoplasma* and *Neospora*. J Eukaryot Microbiol. 1998;45(2):184-8. DOI: [10.1111/j.1550-7408.1998.tb04523.x](#)
29. Keckeisen C, Šujanová A, Himmel T, Matt J, Nedorost N, Chagas CF, Weissenböck H, Harl J. *Isospora* and *Lankesterella* Parasites (Eimeriidae, Apicomplexa) of Passeriform Birds in Europe: Infection Rates, Phylogeny, and Pathogenicity. Pathogens. 2024;13:337. DOI: [10.3390/pathogens13040337](#)
30. Zhijun H, Mingwei X, Hongliang C, Yuping H. Phylogenetic Position Analysis of an *Isospora* Isolated From Siberian Tiger in Eimeriid Coccidian Based on 18S rDNA Sequence. Pak J Zool. 2011;43(3):505-510. [\[available at\]](#)
31. Megía-Palma R, Martínez J, Nasri I, Cuervo JJ, Martín J, Acevedo I, Belliure J, Ortega J, García-Roa R, Selmi S, Merino S. Phylogenetic relationships of *Isospora*, *Lankesterella*, and *Caryospora* species (Apicomplexa: Eimeriidae) infecting lizards. Org Diver Evol. 2016;16:275-88. DOI: [10.1007/s13127-015-0253-3](#)
32. Matsubara R, Fukuda Y, Murakoshi F, Nomura O, Suzuki T, Tada C, Nakai Y. Detection and molecular status of *Isospora* sp. from the domestic pigeon (*Columba livia domestica*). Parasitol Int. 2017;66(5):588-92. DOI: [10.1016/j.parint.2017.05.004](#)
33. Alobaidii WA, Almashhadany DA. Molecular detection of *Leishmania* in cutaneous scrapping and blood samples of dogs in Mosul city. Iraqi J Vet Sci. 2023;37(I):15-19. DOI: [10.33899/ijvs.2023.138603.2815](#)
34. Alobaidii WA, Albaroodi SY, Almashhadany DA. Molecular and phylogenetic analysis of *Babesia gibsoni* in dogs and its infested ticks in Nineveh province, Iraq. Iraqi J Vet Sci. 2024;38(II):27-33. DOI: [10.33899/ijvs.2024.149751.3663](#)
35. Hamdan AK, Al-Baroodi SY. Molecular investigation of feline calicivirus in cats in Mosul city, Iraq. Iraqi J Vet Sci. 2022;36(3):731-735. DOI: [10.33899/ijvs.2022.131706.1993](#)
36. Al-Baroodi SY, Al-Attar MY. Isolation and identification of Circovirus in pigeon. Iraqi J Vet Sci. 2021;35(1):207-210. DOI: [10.33899/ijvs.2020.126706.1364](#)
37. Khudhur WI, Albaroodi SY, Sadiqnomi B. Molecular detection of Feline herpesvirus 1 in cats in Mosul city. Indian Vet J. 2024;101(8):20-7. DOI: [10.62757/iva.2024.101.8.20-27](#)
38. Alobaidii, W.A., Abdullah, D.A., Alkatab, Y.N.M., ... Ola-Fadunsin, S.D., Gimba, F.I. The first molecular investigation of *Besnoitia besnoiti* infections among cattle in Mosul, Iraq. Molecular Biology Reports, 2024, 51(1), 585. doi.org/10.1007/s11033-024-09377-w

التحليل التطوري لطفيلى متماثلة الابواغ فى القطط فى مدينة الموصل

افراح مسعود عبد الحميد , وسن امجد العبيدي

فرع الاحياء المجهرية، كلية الطب البيطري، جامعة الموصل، الموصل، العراق

الخلاصة

تم خلال هذه الدراسة، فحص مائتي عينة مفحوصة مسبقا باستخدام الطرق المجهرية التقليدية للتحقق من طفيلى متماثلة الابواغ. حيث تم الكشف عن ٤٥ عينة ايجابية، والتي من ثم خضعت للاختبارات الجزيئية من خلال استخلاص الحمض النووي من عينات البراز، ولغرض اتمام الكشف الجزيئي على الجينات للطفيلى باستخدام بادئ محدد، تم فحص جميع العينات باستخدام جين كما هو موضح فى التقارير السابقة لبرنامج

تضخيم تفاعل البلمرة المتسلسل. أظهرت نتائج تفاعل البلمرة المتسلسل نتائج ايجابية، للعينات ٤٥ عينة وإيجابية بالاختبارات تقليدية، اذ أظهر الكشف الجزيئي وجود ٣٩ عينة ايجابية (٨٦,٧%) من مجموع ٤٥ عينة. أظهرت نتائج تفاعل البلمرة المتسلسل أن القطط الضالة سجلت أعلى معدل إصابة، وأظهرت الإناث معدل إصابة مرتفع، ووفقاً للعمر ينخفض معدل الإصابة بزيادة عمر الحيوانات، وسجلت القطط المحلية معدل إصابة مرتفع، فى حين أظهرت القطط السليمة ظاهرياً أدنى معدلات إصابة عند مقارنتها بالقطط التي تعاني من الإسهال. أظهرت نتائج التسلسل الجيني لجين الطفيلى الذي تم الكشف عنه وجود تسلسل جيني للعينات، حيث وجد أنه من إجمالي العينات المرسله للتسلسل الجيني خمس عزلات فقط، وقد تم تسجيلها بالرقم التسلسلي فى بنك الجينات العالمي وكالاتي LC856630.1, LC856631.1, LC856632.1, LC856633.1 and LC856634.1. خلصت هذه الدراسة إلى أن هذا طفيلى متماثلة الابواغ منتشر على نطاق واسع فى مدينة الموصل بالعراق. وتعد هذه الدراسة الأولى تتناول التحليل التطوري فى مدينة الموصل بالعراق.