Pakistan Veterinary Journal

ISSN: 0253-8318 (PRINT), 2074-7764 (ONLINE)
DOI: 10.29261/pakvetj/2023.049

RESEARCH ARTICLE

Molecular Characterization of *Hydatigera taeniaeformis* Recovered from Rats: An Update from Pakistan

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ARTICLE HISTORY (23-138)

Received:	April 20, 2023
Revised:	June 9, 2023
Accepted:	June 15, 2023
Published online:	July 09, 2023

Key words:
Hydatigera taeniaeformis
NADH dehydrogenase subunit 1
Phylogeny
Genetic variation
Pakistan

ABSTRACT

Rodents are one of the most abundant and successful mammals on the planet. The rats harbor the metacestode stage of *Hydatigera taeniaeformis* serving as the intermediate hosts, whereas cats act as definitive hosts of the parasite. The incidence of the larval stage in rats has been documented in various regions of the world. To best of our knowledge, the mainstream studies on the genetic diversity of *H. taeniaeformis* are based on the *cox*1 gene which precludes an in-depth analysis of genetic variation in the parasite. To provide insights about *nad*1 gene-based genetic variation, in continuation of our previous work, we thereby in this study report *H. taeniaeformis* infection in the urban murine population from the Faisalabad district of Pakistan and presented genetic polymorphism using the *nad*1 gene. Out of 38 isolates investigated in the study, a total of 13 haplotypes were found with high haplotype diversity (Hd = 0.909), while the nucleotide diversity was found to be 0.02340 in the study population. The neutrality study found a significant level of nucleotide polymorphism, indicating a rise in low-frequency polymorphism, which might be attributed to global population growth of the parasite. Construction of phylogenetic comprising isolates from Kazakhstan, Finland, Turkiye, Canada, Germany, France, and China revealed that Pakistani isolates of *H. taeniaeformis* are distinct and formed a separate cluster. Further research utilising full-length multiple mitochondrial genes is required to understand the molecular epidemiology of *H. taeniaeformis* on the global scale.

To Cite This Article: Alvi MA, Alshammari A, Ali RMA, Rashid I, Saqib M, Qamar W, Shafeeq M, Askar H, Abdelsater N, Li L, Ashfaq K, Butt AA, Fu BQ, Yan HB, Jia WZ, 2023. Molecular characterization of *Hydatigera taeniaeformis* recovered from rats: An update from Pakistan. Pak Vet J, 43(3): 601-605. http://dx.doi.org/10.29261/pakvetj/2023.049

INTRODUCTION

The Taeniidae family (Order Cyclophyllidea) possesses four genera, namely *Hydatigera*, *Taenia*, *Echinococcus*, and *Versteria*, according to a recent revision. The genus *Hydatigera* contains four species: *Hydatigera taeniaeformis*, *Hydatigera parva*, *Hydatigera kamiyai*, and *Hydatigera krepkogorski* (Catalano *et al*., 2019). Members of the genus *Taenia* and *Echinococcus* primarily cause production losses in animals.

Hydatigera taeniaeformis inhabits the intestinal tracts of felids (definitive host), and become infected with the larvae of *H. taeniaeformis* by consuming the liver of mice and rats (intermediate host) (Moudgil *et al*., 2016). The definitive hosts spread eggs of *H. taeniaeformis* into the environment through feces that are taken up by the intermediate host, resulting in the development of cysts in the liver. The feeding habits between felines and rodents are responsible for the parasite life cycle to be completed (Jia *et al*., 2012).

Infections caused by helminths, especially cestodes, pose a huge threat to animals as the majority of these infections remain latent. Mature *H. taeniaeformis* in the gut of cats and dogs seldom causes the onset of clinical symptoms, but if present, clinical signs vary depending on the severity of the infection, and the host's age, health, and breed (Kahn and Line, 2010). In rats, subclinical infection results in the creation of tumor-like growths on the liver (Kumar *et al*., 2006) whereas chronic infections lead to gastric disorders like gastric hyperplasia and gastric enteropathy (Konno *et al*., 1999). Praziquantel is considered to be the drug of choice for this parasite. However, the irrational use of anthelmintics leads to the development of resistance in helminths.

Rodents infected with *H. taeniaeformis* have been reported from different continents, namely Asia (India, Korea, China, Malaysia, and Pakistan), Europe (Serbia and Switzerland), Africa (Nigeria and West Indies), North America (Mexico), South America (Colombia) and Oceania (Australia) (Seong *et al*., 1995; Chikweto *et al*., 2009; Kataranovski *et al*., 2010; Malsawmtluangi *et al*., 2011; Burlet *et al*., 2011; Duque *et al*., 2012; McInnes *et al*., 2014; Premaalatha *et al*., 2016; Onoja *et al*., 2017; Medina-Pinto *et al*., 2019; Guo, 2020; Alvi *et al*., 2021). Human cases of *H. taeniaeformis* infection have been reported in a number of countries, including Japan, Sri Lanka and Argentina (Ekanayake *et al*., 1999; Hoberg, 2002).

Although many measures were devised to prevent and control cestode infection, strategies to reduce and overcome the infection are continuously influenced by the diversity of tapeworm species and variation among species. There is a significant gap in the molecular characterization of several members of the Taeniid family in underdeveloped countries. To best of our knowledge, the mainstream studies on the genetic diversity of *H. taeniaeformis* are based on the *cox*1 gene which precludes an in-depth analysis of genetic variation in the parasite. To provide insights about *nad*1 gene-based genetic variation, in continuation of our previous work, we thereby in this study report *H. taeniaeformis* infection in the urban murine population from the Faisalabad district of Pakistan and presented genetic polymorphism using the *nad*1 gene.

MATERIALS AND METHODS

Study locale: District Faisalabad is one of the most famous agricultural and industrial cities in Pakistan. It has an extensive canal system and rivers that make this land highly fertile, seeking the attention of people towards husbandry practices and agriculture farming. As markets are the main source of food for rodents in the central part of the city, their population has significantly increased in this region. In continuation of research collaboration between the CMS Department of University of Agriculture, Faisalabad, Pakistan, and Lanzhou Veterinary Research Institute, Lanzhou, China, *H. taeniaeformis* isolates recovered from urban rats in a previous study performed by Alvi *et al*. (2021) were used in the current investigations and all samples were collected from district Faisalabad.

DNA extraction and amplification of the nad1 gene: Already extracted DNA was used as a template to amplify the *nad*1 gene portion using a pair of primers as reported by Bowles *et al*. (1992). Briefly, the twenty-five microliter reaction volume consisted of 12.5 µl Premix, 10 pmol of each of reverse and forward primers, 0.5 µl genomic DNA, and RNAse free water up to final volume. Agarose gel was prepared and stained with GelRed^{TM}. 5 µl of amplicon in each well of agarose gel were visualized under an ultraviolet light transilluminator. A DNA ladder (2000bp length) was run to estimate the sizes of each amplicon. Then PCR products were sent to the Chinese collaborators for sequencing.

Molecular analyses: DNA sequences were examined for any misread nucleotide with the aid of UGENE software. After alignment, the confirmation of each isolate was achieved through the BLASTn tool. The population diversity and neutrality indices were calculated using DnaSP. Phylogenetic analysis was carried out using a dataset of *nad*1 (220 bp) gene sequences (representative haplotype) and other *Taenia* species. MrBayes software was used to construct the phylogenetic tree based on Bayesian method.

RESULTS AND DISCUSSION

Infectious diseases including parasitic infestations are important health problems in both animals and humans, which cause economic losses and severe illness (Pinilla *et al*., 2022; Nawaz *et al*., 2022; Dahab *et al*., 2022). Parasites are responsible for causing diseases that lead to heavy economical losses in terms of decreased productivity and illness (Mo'awad *et al*., 2022; Mahmoud *et al*., 2022). *Hydatigera taeniaeformis* has two transmission cycles: a sylvatic cycle comprising wild rodents and felines, and a synanthropic or urban cycle involving domestic felids and rats (Tull *et al*., 2021). The study area is the main industrial zone of the country, and its agricultural land is very productive due to the vast canal system and the presence of rivers on the periphery. In this study, urban cycle transmission was found as the major source of the parasite dissemination to urban rats, with food and water contaminated with cat excrement regarded as the main sources of spread that is according to the research conducted by Medina-Pinto *et al*. (2019) and declared that no transmission cycle was associated with wild rodents. Maintenance of the *H. taeniaeformis* life cycle may be seriously influenced by the continuously changing habitat of wild rodents, their density, and relative population dispersion (Sosa-Escalante *et al*., 1997; Tovar and Villanueva, 2009). In the future, investigations concentrating on non-industrialized parts of Pakistan with different wildlife populations are recommended to gain a better understanding of involvement of wild animals in the life cycles, as their existence in India has already been verified (Malsawmtluangi *et al*., 2011). As the record of *H. taeniaeformis* distribution in rodents was restricted to a single zone, the high prevalence identified in rats cannot be extrapolated to other parts of the country to explain why the prevalence rate is so high (Alvi *et al*., 2021).

Following successive alignment of the 38 sequences, a total of 12 parsimony informative sites were discovered, yielding 13 haplotypes. Tajima's D (-1.85891) and Fu's Fs (-3.022) values were found non-significant and the diversity indices are mentioned in Table 1.

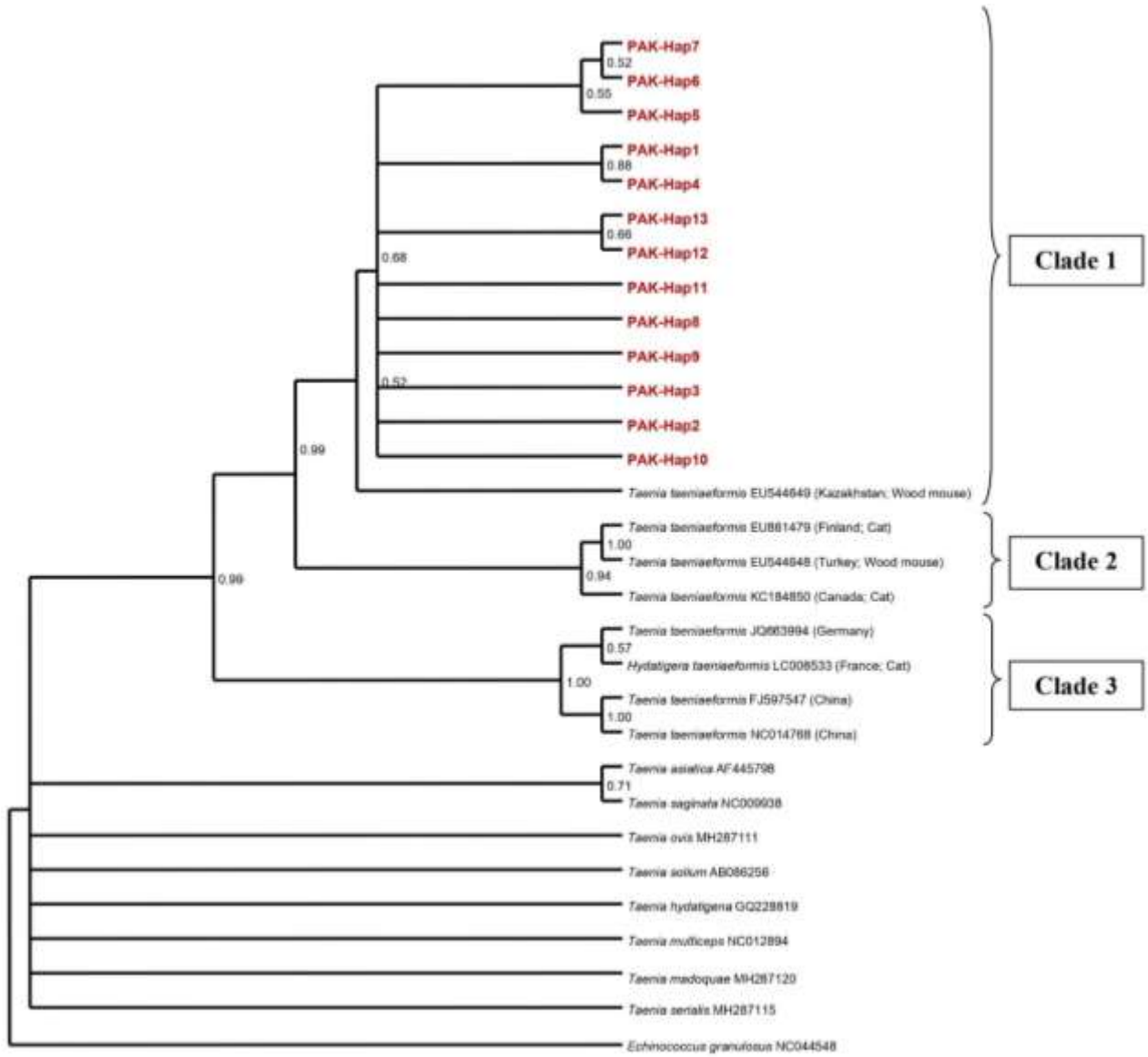

Fig. 1: Bayesian phylogeny of Pakistani isolates of *Hydatigera taeniaeformis* inferred from *nad1* gene.

Table 1: Population indices for *H. taeniaeformis* based on *nad*1 gene sequences

Indices	*nad*1 (220 bp)
Number of isolates	38
Number of mutations	36
Total parsimony informative sites	12
Number of haplotypes	13
Overall haplotype diversity (Hd)	0.909
Overall nucleotide diversity (π)	0.02340
Tajima's *D*	-1.85891
Fu's Fs	-3.022

Mitochondrial genomic DNA (mtDNA) is commonly used to research intraspecific variations in metazoans due to its lack of recombination, conserved structure, and rapid evolutionary rate (Wei *et al*., 2010; Shen *et al*., 2010; Gasser, 2006; Liu *et al*., 2011). As a result of some of the detected nucleotide modifications indicated in Table 2a, a few substitutions in amino acids were identified (Table 2b). The neutrality investigation discovered considerable nucleotide polymorphism, indicating an increase in low-frequency polymorphism that could be attributable to world population expansion. The genetic population structure of H. taeniaeformis is likewise comparable to that of other parasitic species previously studied (Carmena and Cardona, 2014; Alvi *et al*., 2020). The availability of information on *H. taeniaeformis* neutrality and polymorphism indices is limited internationally, which has hampered a comprehensive investigation of these measurements.

As the observed amino acid alterations did not display a clear trend, the cause might be the examination of partial gene sequences. However, a new nucleotide and amino acid arrangement might imply that *H. taeniaeformis* has been genetically classified by geographic area. The importance of these variations at molecular levels is yet unknown. However, research on *Echinococcus granulosus sensu lato* has revealed the impact of genetic diversity on epidemiology, host infectivity and control techniques (Carmena and Cardona, 2014). Mitochondrial genome analysis of *T. saginata* and *T. solium* has also depicted intraspecific variations that might influence the pathogenicity of disease in various host species (Rostami *et al*., 2015).

Phylogenetic analysis implies that *H. taeniaeformis* might be divided into regionally different species. Pakistani isolates were grouped at an acceptable distance near the

isolates of Asian, European, and North American countries namely Kazakhstan, Finland, Turkey, and Canada while isolates from Asian and European countries (Germany, France, and China) formed an independent cluster (Fig. 1). As shown by the Bayesian phylogeny and previously documented by Lavikainen *et al*. (2016), Asian strains have significant haplotype diversity, whereas non-Asian isolates have modest diversities (Lavikainen *et al*., 2016). Interestingly, Pakistani haplotypes (cluster 1) were found closer to European and American haplotypes (cluster 2) instead of the Chinese haplotypes (cluster 3).

The representative sequences of this study have been submitted in the NCBI GenBank database under accession numbers MZ868741-MZ868753. *Echinococcus granulosus* (accession number NC044548) was used as an outgroup that validated the authenticity of the constructed tree.

The isolates obtained in this study were supposed to fall under the *H. taeniaeformis* sensu stricto (s. s.) lineage rather than *H. kamiyai which was further confirmed through sequencing analysis and by the fact that H. kamiyai* lineage was found to occur predominantly in northern Eurasia infecting arvicoline rodents (voles) and mice of the genus *Apodemus* whereas *H. taeniaeformis* was identified in members of subfamily Murinae (rats and mice) having Asian origin and now it has a worldwide distribution (Lavikainen *et al*., 2016).

In this study, the diversity of the partial *nad*1 gene marker among isolates of *H. taeniaeformis* was investigated. As far as we know, the majority of information on the genetic diversity of *H. taeniaformis* is based on incomplete cox1 gene sequences, which prohibits a full investigation of the genotypic diversity situation. Investigations into genetic variants have been reported to be influenced by the length of the gene under investigation (Yanagida *et al*., 2012; Romig *et al*., 2015). It is recommended that longer DNA fragments, rather than full-length genes, should be sequenced to improve the resolution of genetic analyses. As a result, more research is needed to understand the molecular epidemiology of *H. taeniaeformis* on global scale.

Table 2: Mitochondrial *nad*1 gene based nucleotide sequence polymorphism

Table 2a: *nad*1 mutation sites

Haplotype	*nad*1 DNA mutation sites																	
	14	15	34	45	47	50	54	73	87	91	98	108	111	112	113	117	118	121
PAK-HAP1	A	T	C	C	C	C	C	C	T	T	C	C	C	C	C	C	C	C
PAK-HAP2	.	.	G	A	T	T	A	T	.	.	.	T	T	T	T	T	A	T
PAK-HAP3	.	.	G	A	T	T	A	T	.	.	T	T	T	T	T	T	A	T
PAK-HAP4	.	.	.	A	T	T	A	T	.	.	.	C	C	T	T	T	A	T
PAK-HAP5	.	.	.	A	T	T	A	T	.	C	.	T	T	T	T	T	A	T
PAK-HAP6	.	.	G	A	T	T	A	T	.	.	.	T	T	T	T	T	A	T
PAK-HAP7	.	.	G	A	T	T	A	T	.	.	.	T	T	T	T	T	A	T
PAK-HAP8	.	.	G	A	T	T	A	T	.	.	T	T	T	T	T	T	A	T
PAK-HAP9	.		G	A	T	T	A	T	.	.	.	T	T	T	T	T	A	T
PAK-HAP10	.	C	G	A	T	T	A	T	.	.	.	T	T	T	T	T	A	T
PAK-HAP11	.		G	A	T	T	A	T	C	.	.	T	T	T	T	T	A	T
PAK-HAP12	.		G	A	T	T	A	T	.	C		T	T	T	T	T	A	T
PAK-HAP13	C		G	A	T	T	A	T	.	C	.	T	T	T	T	T	A	T

Haplotype	*nad*1 DNA mutation sites																	
	127	136	156	164	173	177	178	180	186	187	193	197	203	204	205	211	212	217
PAK-HAP1	T	T	C	C	C	T	C	C	T	C	A	T	G	T	T	T	C	C
PAK-HAP2	.	.	G	G	.	.	T	T	.	T	.	.	.	.	.	.	A	G
PAK-HAP3	.	.	G	G	.	C	T	T	.	T	.	.	.	.	.	.	A	G
PAK-HAP4	.	.	.	G	.	C	.	.	.	T	.	.	C	.	C	.	A	.
PAK-HAP5	.	C	G	G	.	C	T	T	C	T	G	.	.	C	.	C	A	G
PAK-HAP6	.	.	G	G	T	C	T	T	.	T	G	.	.	.	.	.	A	.
PAK-HAP7	.	.	G	G	.	C	T	T	.	T	G	.	.	.	.	.	A	G
PAK-HAP8	.	.	G	G	.	.	T	T	.	T	.	.	.	.	.	.	A	G
PAK-HAP9	C	.	G	G	.	.	T	T	.	T	.	C	.	.	.	.	A	.
PAK-HAP10	.	.	G	G	.	.	T	T	.	T	.	.	.	.	.	.	A	G
PAK-HAP11	.	.	G	G	.	.	T	T	.	T	.	.	.	.	.	.	A	.
PAK-HAP12	.	C	G	G	.	.	T	T	.	T	.	.	.	.	.	.	A	G
PAK-HAP13	.	.	G	G	.	.	T	T	.	T	.	.	.	.	.	.	A	G

Table 2b: *nad*1 amino acid substitution

Haplotype	*nad*1 amino acid substitution											
	5	12	16	17	36	38	40	41	46	66	68	71
PAK-HAP1	D	R	T	P	D	P	H	H	C	F	G	S
PAK-HAP2	.	G	M	L	G	F	N	Y	.	.	.	Y
PAK-HAP3	.	G	M	L	G	F	N	Y	.	.	.	Y
PAK-HAP4	.	.	M	L	G	F	N	Y	.	.	A	Y
PAK-HAP5	.	.	M	L	G	F	N	Y	R	.	.	H
PAK-HAP6	.	G	M	L	G	F	N	Y	.	.	.	Y
PAK-HAP7	.	G	M	L	G	F	N	Y	.	.	.	Y
PAK-HAP8	.	G	M	L	G	F	N	Y	.	.	.	Y
PAK-HAP9	.	G	M	L	G	F	N	Y	.	S	.	Y
PAK-HAP10	.	G	M	L	G	F	N	Y	.	.	.	Y
PAK-HAP11	.	G	M	L	G	F	N	Y	.	.	.	Y
PAK-HAP12	.	G	M	L	G	F	N	Y	R	.	.	Y
PAK-HAP13	A	G	M	L	G	F	N	Y	.	.	.	Y

Conclusions: The results of the *nad*1 gene sequence analysis revealed a considerable genetic polymorphism, which is further supported by population studies of isolates from Asia, Europe, and North America. Further studies are highly recommended for better conceptualization regarding the distribution and prevalence of *H. taeniaeformis* in both final and all possible intermediate hosts as well as intraspecies diversity and relationships with other populations. In this study, we amplified only a segment of the *nad*1 gene. It is recommended that longer DNA fragments, rather than full-length genes, should be sequenced to improve the resolution of genetic analyses. Therefore, further investigations are needed to comprehend the global molecular epidemiology of *H. taeniaeformis*.

Authors contributions: MAA, HBY, AA, IR, and MS conceptualized the study. The methodology was designed by MAA, AAB, MS, and RMAA while MAA, RMAA, MSh, KA, LL, and WQ carried out validation. Writing—original draft preparation was done by MAA and RMAA while review and editing and performed by HA, HBY, NA, BQF, and WZJ. Funds were acquired by HBY and WZJ. All authors have read and agreed to the published version of the manuscript.

Funding: We acknowledge the funding received from the National Key Research and Development Program (2022YFC2304000; 2022YFD1302101), NBCITS (CARS-37) and Central Public-Interest Scientific Institution Basal Research Fund (Y2022GH13; 1610312020016).

REFERENCES

Alvi MA, Li L, Ohiolei JA, *et al*., 2021. *Hydatigera taeniaeformis* in urban rats (*Rattus rattus*) in Faisalabad, Pakistan. Infect Genet Evol 92:104873.

Alvi MA, Ohiolei JA, Saqib M, *et al*., 2020. First report on molecular characterization of *Taenia multiceps* isolates from sheep and goats in Faisalabad, Pakistan. Front Vet Sci 7.

Bowles J, Blair D and McManus DP, 1992. Genetic variants within the genus *Echinococcus* identified by mitochondrial DNA sequencing. Mol Biochem Parasitol 54:165-73.

Burlet P, Deplazes P and Hegglin D, 2011. Age, season, and spatio-temporal factors affecting the prevalence of *Echinococcus multilocularis* and *Taenia taeniaeformis* in *Arvicola terrestris.* Parasit Vectors 4:1-9.

Carmena D and Cardona GA, 2014. Echinococcosis in wild carnivorous species:epidemiology, genotypic diversity, and implications for veterinary public health. Vet Parasitol 202:69-94.

Catalano S, Bâ K, Diouf ND, *et al*., 2019. Rodents of Senegal and their role as intermediate hosts of *Hydatigera* spp.(Cestoda:Taeniidae). Parasitology 146:299-304.

Chikweto A, Bhaiyat MI, Macpherson CNL, *et al*., 2009. Existence of *Angiostrongylus cantonensis* in rats (*Rattus norvegicus*) in Grenada, West Indies. Vet Parasitol 162:160-2.

Dahab MAE, Sayed A and Mahana N, 2022. Curcumin impact on ex vivo *Toxocara vitulorum* adult worms and eggs. Int J Vet Sci 11:280-8.

Duque BA, Aranzazu D, Agudelo-Flórez P, *et al*., 2012. *Rattus norvegicus* as an indicator of circulation of *Capillaria hepatica* and *Taenia taeniaeformis* on a groceries trade center of Medellín, Colombia. Biomedica 32:510-8.

Ekanayake S, Warnasuriya ND, Samarakoon PS, *et al*., 1999. An unusual infection of a child in Sri Lanka, with *Taenia taeniaeformis* of the cat. Ann Trop Med Parasitol 93:869-73.

Gasser RB, 2006. Molecular tools-advances, opportunities and prospects. Vet Parasitol 136:69-89.

Guo X, 2020. Proteomics analysis of *Hydatigera taeniaeformis* Metacestode stage. Front Vet Sci 7:474.

Hoberg EP, 2002. *Taenia* tapeworms:their biology, evolution and socioeconomic significance. Microbes Infect 4:859-66.

Jia W, Yan H, Lou Z, *et al*., 2012. Mitochondrial genes and genomes support a cryptic species of tapeworm within *Taenia taeniaeformis*. Acta Tropica 123:154-63.

Kahn CM and Line S, 2010. eds. The Merck veterinary manual. Kenilworth, NJ:Merck. Vol 2825.

Kataranovski M, Zolotarevski L, Belii S, *et al*., 2010. First record of *Calodium hepaticum* and *Taenia taeniaeformis* liver infection in wild Norway rats (*Rattus norvegicus*) in Serbia. Arch Biol Sci 62:431-40.

Konno K, Abella IA, Oku Y, *et al*., 1999. Histopathology and physiopathology of gastric mucous hyperplasia in rats heavily infected with *Taenia taeniaeformis*. J Vet Med Sci 61:317-24.

Kumar JM, Reddy PL, Aparna V, *et al*., 2006. *Strobilocercus fasciolaris* infection with hepatic sarcoma and gastroenteropathy in a Wistar colony. Vet Parasitol 141:362-7.

Lavikainen A, Iwaki T, Haukisalmi V, *et al*., 2016. Reappraisal of *Hydatigera taeniaeformis* (Batsch, 1786) (Cestoda:Taeniidae) sensu lato with description of *Hydatigera kamiyai* n. sp. Int J Parasitol 46:361-74.

Liu GH, Lin RQ, Li MW, *et al*., 2011. The complete mitochondrial genomes of three cestode species of *Taenia* infecting animals and humans. Mol Biol Rep 38:2249-56.

Malsawmtluangi C, Prasad PK, Biswal DK, *et al*., 2011. Morphological and molecular identification of the metacestode parasitizing the liver of rodent hosts in bamboo growing areas of mizoram, northeast India. Bioinformation 7:393.

Mahmoud HYAH, Ali AAA, Khalil AM, *et al.,* 2022. The infection rate of *Fasciola* and *Anaplasma* in cattle and buffaloes in Qena, Egypt. Int J Vet Sci 11:308-14.

Mo'awad HFM, Sobhy MM, Ismail TF, *et al.,* 2022. Seroprevalence of *Coxiella burnetti* (Q fever) in cows and buffaloes in Egypt. Int J Vet Sci 11:16-22.

McInnes E, Kohn H, Carmichael I, *et al*., 2014. Larvae of *Taenia taeniaformis* in the liver of a laboratory rat (*Rattus norvegicus*). Ann Clin Pathol 2:2-5.

Medina-Pinto RA, Torres-Castro MA, Medina-Pinto RA, *et al*., 2019. Natural *Cysticercus fasciolaris* infection in rodents from a rural area in Yucatan, Mexico. Vet Méx 6:1-10.

Moudgil AD, Singla LD, Gupta K, *et al*., 2016. Histopathological and morphological studies on natural *Cysticercus fasciolaris* infection in liver of Wistar rats. J Parasit Dis 40:255-8.

Nawaz M, Zhou J, Khalid I, *et al.,* 2022. Antiparasitic activity of plants extract against gastrointestinal nematodes and *Rhipicephalus microplus*. Int J Vet Sci 11:474-8.

Onoja RI, Idika IK, Ezeh IO, *et al*., 2017. Histopathological detection of the larval stage of *Taenia taeniaeformis* (strobilocerci) and its associated lesions in liver of laboratory rats:case report. Explor Anim Medical Res 7:97-9.

Pinilla JC, Gutierrez A and Florez AA, 2022. Canine visceral leishmaniasisin Colombia resistant to treatment of choice (Meglumine antimoniate plus allopurinol). Int J Vet Sci 11:117-20.

Premaalatha B, Chandrawathani P, Tan PS, *et al*., 2016. *Taenia taeniaeformis* in wild rats. Malaysian J Vet Res 7:21-3.

Romig T, Ebi D and Wassermann M, 2015. Taxonomy and molecular epidemiology of *Echinococcus granulosus* sensu lato. Vet Parasitol 213:76-84.

Rostami S, Salavati R, Beech RN, *et al*., 2015. Genetic variability of *Taenia saginata* inferred from mitochondrial DNA sequences. Parasitol Res 114:1365-76.

Seong IK, Huh S, Lee IS, *et al*., 1995. Helminths in *Rattus norvegicus* captured in Chunchon, Korea. Korean J Parasitol 33:235-8.

Shen X, Wang H, Ren J, *et al*., 2010. The mitochondrial genome of *Euphausia superba* (Prydz Bay) (Crustacea: Malacostraca: Euphausiacea) reveals a novel gene arrangement and potential molecular markers. Mol Biol Rep 37:771-84.

Sosa-Escalante J, Hernández S, Segovia A, *et al*., 1997. First record of the coyote, *Canis latrans* (Carnivora:Canidae), in the Yucatan Peninsula, Mexico. Southwest Nat 42:494-5.

Tovar CC and Villanueva HZ, 2009. Distribución potencial del hábitat del jaguar y áreas de conflicto humano–jaguar en la Península de Yucatán. Revista Mexicana de Mastozoología (Nueva Época) 13:46-62.

Tull A, Moks E and Saarma U, 2021. Endoparasite prevalence and infection risk factors among cats in an animal shelter in Estonia. Folia Parasitol 68:010.

Wei SJ, Tang P, Zheng LH, *et al*., 2010. The complete mitochondrial genome of *Evania appendigaster* (Hymenoptera:Evaniidae) has low A+ T content and a long intergenic spacer between atp8 and atp6. Mol Biol Rep 37:1931-42.

Yanagida T, Mohammadzadeh T, Kamhawi S, *et al*., 2012. Genetic polymorphisms of *Echinococcus granulosus* sensu stricto in the Middle East. Parasitol Int 61:599-603.