Ankara Üniversitesi Veteriner Fakültesi Dergisi/Ankara Univ Vet Fak Derg; 2026:73(1): 33-39
DOI: 10.33988/auvfd.1703476
Research Article

Morphological confirmation and preliminary molecular data on *Tetraserialis tscherbakovi* from *Microtus mystacinus* in Türkiye

Öykü BARILI[a,✉], Şinasi UMUR[b]

Ondokuz Mayıs University, Faculty of Veterinary Medicine, Department of Parasitology, Samsun, Türkiye

[a]ORCID: 0000-0001-7692-5171; [b]ORCID: 0000-0001-9766-2817

ABSTRACT

Tetraserialis tscherbakovi (Petrov and Chertkova, 1960) is a rare monostomic trematode belonging to the family Notocotylidae. This study aimed to provide detailed information on *Tetraserialis tscherbakovi.* In this study, the digestive systems of 25 rodents captured in the Sarıkamış district of Kars Province were examined, and 19 trematodes morphologically consistent with *Tetraserialis tscherbakovi* were detected in a single *Microtus mystacinus* individual. Light microscopy images of the parasites were obtained, along with scanning electron microscopy (SEM) images, which are presented for the first time worldwide. SEM examination revealed, in detail, a previously undescribed cap-like helical structure of the eggs. The sequencing of the ITS1, 5.8S rRNA, and ITS2 gene regions was conducted; the obtained isolate was deposited in GenBank (PP812223). BLAST analysis showed the highest similarity to *Notocotylus malhamensis* (97.54%) and *Notocotylus* sp. (96.89%). Since these values are below the generally accepted threshold for definitive species-level molecular identification, the molecular data were considered preliminary and supported by morphological findings. Since the analysis was based only on the ITS1–5.8S–ITS2 region and showed similarity values slightly below the accepted species-level threshold, the molecular results should be interpreted with caution until additional markers (e.g., COI, 28S) are studied. This study reports the first morphologically identified case of *Tetraserialis tscherbakovi* from *M. mystacinus* in Türkiye and provides preliminary data on the phylogenetic position of the species.

Keywords: *Microtus mystacinus*, Notocotylidae, *Tetraserialis tscherbakovi*, Trematoda, Türkiye

✉**Corresponding author:** oykudoyran5@gmail.com

Received: 21.05.2025, **Accepted:** 07.10.2025, **Publication Date:** 01.01.2026

How to cite this article: Barılı Ö, Umur Ş (2026): Morphological confirmation and preliminary molecular data on *Tetraserialis tscherbakovi* from *Microtus mystacinus* in Türkiye. Ankara Univ Vet Fak Derg, 73 (1), 33-39. DOI: 10.33988/auvfd.1703476.

Introduction

The genus *Notocotylus*, the largest member of this family, includes 50 species that parasitize mainly waterfowl, to a lesser extent mammal, and primarily rodents of the family *Microtidae*. These species are common in wetland habitats and use freshwater gastropods (water slugs) as intermediate hosts (7,15,23). Some species of the family Notocotylidae, their hosts and distributions are shown in Table 1.

The adults of Notocotylidae trematodes inhabit the caecum of their final hosts. In their life cycle, eggs excreted with feces from the last host develop in water, and miracidia are formed. Cercariae develop from the miracidia that enter the water slugs, the first intermediate hosts. After leaving the first intermediate host, these cercariae develop in the second intermediate host, which includes freshwater crustaceans or fish, Metacercariae develop, marking the infective period for the final host. When the final hosts eat the crustaceans or fish the metacercariae are activated, migrate to the intestine, mature, and complete development (10).

Tetraserialis tscherbakovi is a rarely seen trematode in the family Notocotylidae, characterized by the presence of only an oral appendage. Although cosmopolitan Notocotylid trematodes usually parasitize birds, they are also found in various vertebrates, especially rodents (14). The genus *Microtus*, one of the parasite's final hosts, is distributed over a wide region, including Europe, Asia, and

Table 1. Some species of the family Notocotylidae, their final hosts and distribution

Parasite	Hosts	Location	References
Notocotylus attenuatus	*Lymnaea stagnalis* (sporocyst to cercariae in thesuccession)	Czech Republic	(22)
	Aythya ferina	Kherson,Ukrania	(24)
N. fosteri	*Oryzomys palustris*	Florida, USA	(15)
N. imbricatus	*Hydromys chyrsogaster*	Australia	(6)
N. johnstoni	*Hydromys chyrsogaster*	Australia	(6)
N. loeiensis	*Rattus losea*	Thailand	(4)
N. malhamensis	*Myodes glareolus,Microtus agrestis*	United Kingdom	(3)
N. neyrai	*Arvicola sapidus*	Europe	(8)
	Arvicola amphibius	Iran	(16)
N. primulus	*Lophonetta specularioides*	Argentina, Patagonia	(7)
N. ratti	*Rattus rattus alexandrinus*	China	(26)

North Africa, and is divided into numerous species and subspecies (5). To date, 62 species of *Microtus* have been reported worldwide (17,18).

This study aimed to provide detailed information on *Tetraserialis tscherbakovi*, a species that is poorly known and scarcely represented in the literature. The morphological characteristics of the parasite were documented in detail, and scanning electron microscope images were obtained and presented for the first time worldwide. Additionally, the ITS1, 5.8S rRNA, and ITS2 gene regions were sequenced, and the molecular data were deposited in GenBank, providing the first publicly available genetic record for this species.

Materials and Methods

The research material consisted of the digestive system of a total of 25 rodents, including 16 *Microtus mystacinus*, seven *M. daghestanicus*, and two *Apodemus mystacinus*, caught in the Sarıkamış district in the Kars province as part of the TÜBİTAK project numbered 115O281. For parasitological diagnosis, three of the collected trematodes were stained with Semichon's acetocarmine (11), morphological characteristics were recorded, and measurements were made and photographed.

Two of the parasites collected for electron microscopic examination were fixed in 2.5% glutaraldehyde solution, washed with phosphate buffer solution (PBS) according to the procedure, dehydrated with serial alcohol dilutions, and stored in 96% alcohol. Due to the small and delicate structure of the parasites, drying was carried out using a Quorum k850 critical point drying device since deterioration would occur under the pressure generated in the electron microscope. After this process, the samples were coated with gold- palladium (Au/Pd) and detailed photographs of various regions of the parasite were taken using different magnifications in an electron microscope (JEOL, JSM-7001F).

For molecular analyses, two adult parasites were collected, preserved in 70% ethyl alcohol, and a 20 mg piece was cut, and total DNA was extracted. A commercial DNA extraction kit (PureLink, Invitrogen) was used for DNA extraction.

Since no previous molecular studies have been conducted on this parasite, no sequence records were found in GenBank searches. Therefore, primers BR5 and Dig11 were used to amplify by PCR amplify the approximately 1200 bp ITS gene region, which is used in most similar studies (25). The COX gene region, which would allow for better comparison of intraspecific specificity, could not be examined because there is no previous record of the parasite.

BR:(5'-GTAGGTGAACCTGCGGA-3') dig11:(5'-GTGATATGCTTAAGTTCAGC-3') (25) was used as a primer, and a 1218 bp fragment of the ITS-1/5.8S/ITS-2/28S gene region was amplified by PCR. PCR was performed in a 50 µL reaction mixture containing 4 µL template DNA, 0.5 µM of each primer, 10 mM Tris-HCl, 50 mM KCl, 1.5 mM MgCl2, 0.2 mM dNTP mix, and 3 U of Taq polymerase. The reaction mixture was amplified in a thermocycler (Applied Biosystems, SimpliAmp) under the following conditions: initial denaturation at 94 °C for 3 min, followed by 40 cycles of denaturation at 94 °C for 40 s, annealing at 52 °C for 45 s, elongation at 72 °C for 70 s and a final extension at 72 °C for 10 min. The PCR products were analyzed by electrophoresis on 1.5% agarose gel (stained with ethidium bromide) at 100 V for 1 h. Gels were visualized and photographed on a transilluminator.

Purification of the PCR product and duplex DNA sequence analysis with the same primer pairs were performed by a commercial company (BM Labosis). The isolate obtained was deposited in GenBank under accession number PP812223.

Bidirectional sequence analysis of the purified PCR products was performed on an ABI PRISM 3130xl

automated sequencer (Applied Biosystems). Sequence-analysed samples were merged with Contig Express in the Vector NTI Advance 11.5 (Invitrogen) sequence analysis program. BLASTn (https://blast.ncbi.nlm.nih.gov/Blast.cgi) analysis (1) of the obtained sequences in the GenBank database was performed to determine the similarity percentages of the isolates with each other and with other recorded isolates. Then, multiple alignments of the nucleotide sequences of the haplotypes were performed with the Clustal W algorithm using BioEdit (13) The phylogenetic tree was constructed with the Maximum Likelihood (ML) method using PhyML version 3.1 (12). The jModelTest program (9,12,20) was run using the Akaike (AIC) criterion to determine the appropriate model, which was found to be HKY+G for partial ITS1, all 5.8S and partial ITS2 gene regions. This model was used in ML and Bayesian inference analyses. The phylogenetic tree was constructed using FigTree v1.4.2 (http://tree.bio.ed.ac.uk/software/figtree/) and Inkscape 0.92 (http://inkscape.org/en/).

Results

Among the 25 rodent specimens examined, 19 *Tetraserialis tcherbakovi* were detected in the digestive tract of a single adult male rodent belonging to the species *Microtus mystacinus.*

Morphologic characteristics of the parasite were as follows ventrally curved, oval in shape with lateral margins, and measured 2.02-3.85 mm in length and 1.65-2.90 mm in width (Figure 1a). The tegument is thornless, and the ventral surface of the body is characteristically covered by four longitudinal rows of tegument glands. Each row consisted of 13-14 skin glands (usually 14) in the lateral rows and 11-12 glands in each of the two lower middle adjacent rows (Figure 2a-c). Occasionally, the glands of the lower middle rows were close together. In addition to the 11-12 glands in each lower row, one (rarely two) unpaired median tegument gland was observed at the anterior and posterior ends of the body.

The oral sucker appeared to have a transverse oval shape, measuring 0.16-0.28 mm in length and 0.19-0.23 mm in width (Figure 1b,2b). The pharynx was absent, and the oesophagus was short and measured 0.05 to 0.09 mm. The intestinal branches ran irregularly on both sides of the body, in the anterior and middle third of the body length, passing between the testes and ovary and terminating at the posterior end of the body (Figure 1c).

The testes had 6-12 lobes and were unequal in size. They were located at the back of thebody, lateral to the branches of the intestine, and were 0.51-0.89 mm long and 0.4-0.6 mm wide.

The vitellogenous glands, which are oval or round in shape, begin at the anterior level of the uterus, in front of the mid-level of the body. The rings of the uterus showed a wide curved distribution; crossing the intestinal branches to reach the vitellogenous glands. The length was measured as 0.68-1.13 mm and the width as 0.18-0.28 mm. The eggs were characterized by the presence of filaments on both poles. Excluding the filaments, the size of the eggs was 0.021 x 0.013 mm. The length of the threads varied from 0.09 to 0.18 mm. Light microscopic photographs of the parasite are shown in Figure 1.

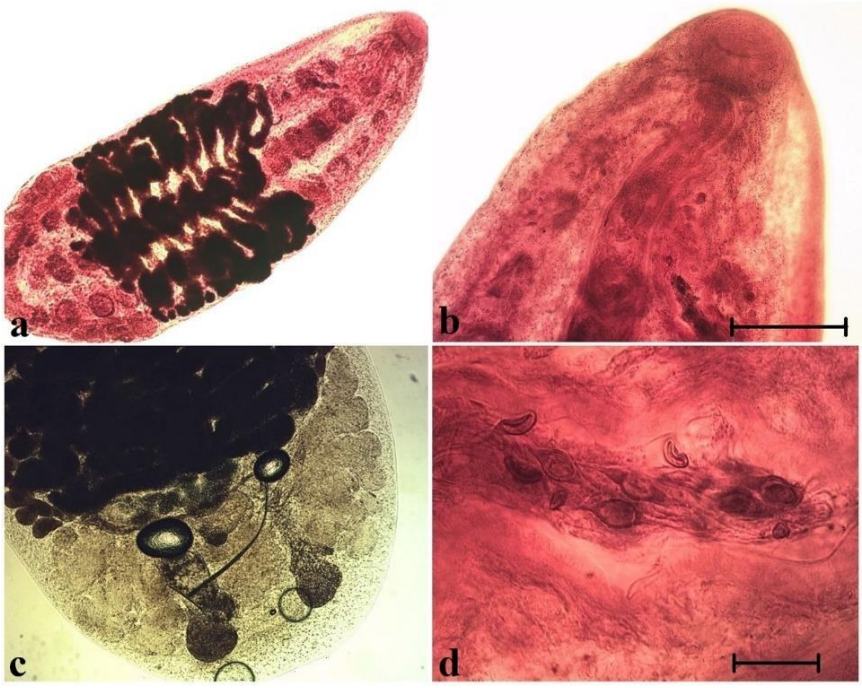

Figure 1. *Tetraserialis tscherbakovi;* a) Semichon acetocarmin stained preparation, b) Oral sucker and cirrus structure of the stained preparation, Scale: 200 µm, c) Testis, ovary and intestine of the original unstained image of the parasite, d) Eggs in the uterus, Scale: 50 µm

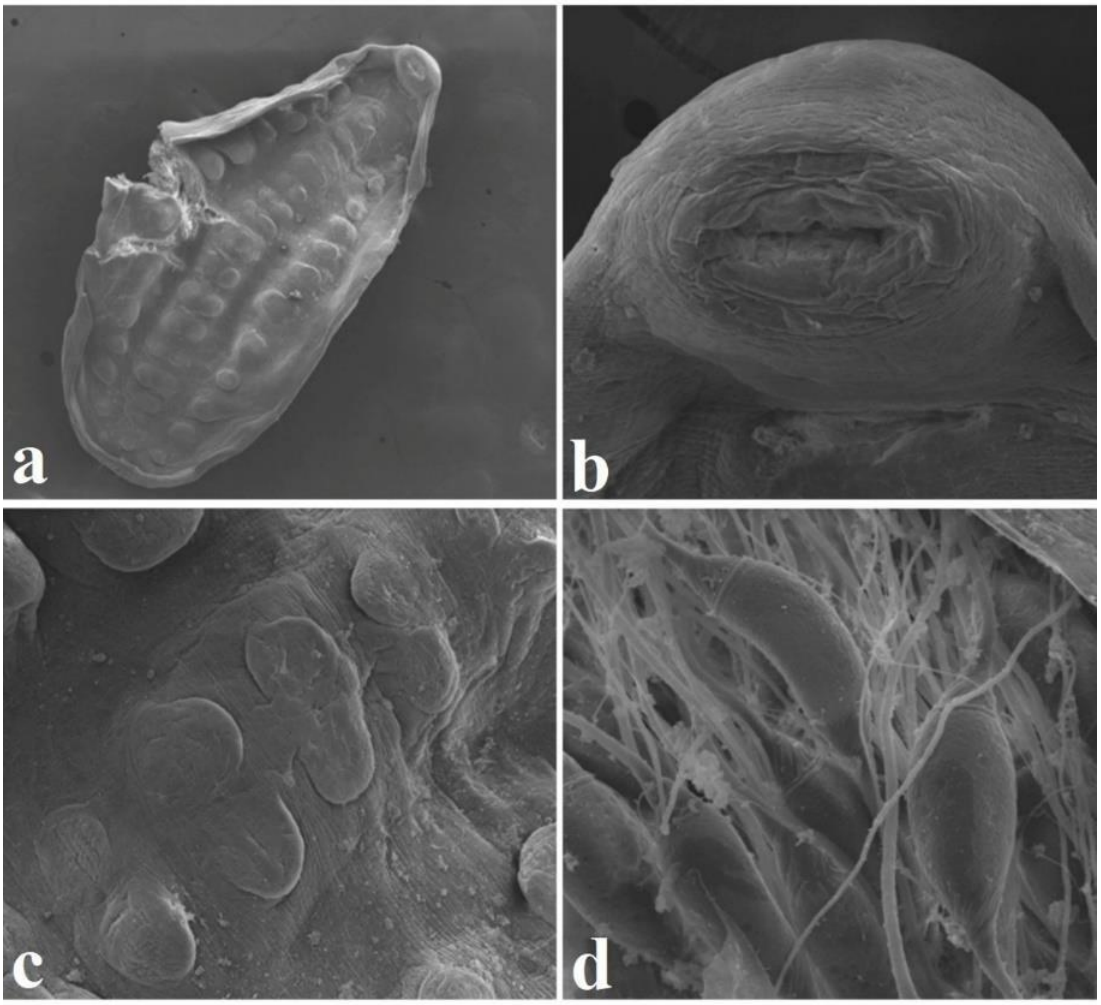

Figure 2. Electron microscopic views of *Tetraserialis tscherbakovi*; a) General structure of the parasite, x40, b) Oral sucker, x350, c) Characteristic gland structures on the upper surface, x250, d) Eggs of the parasite and cap-like structure on the eggs. x1,600 magnification

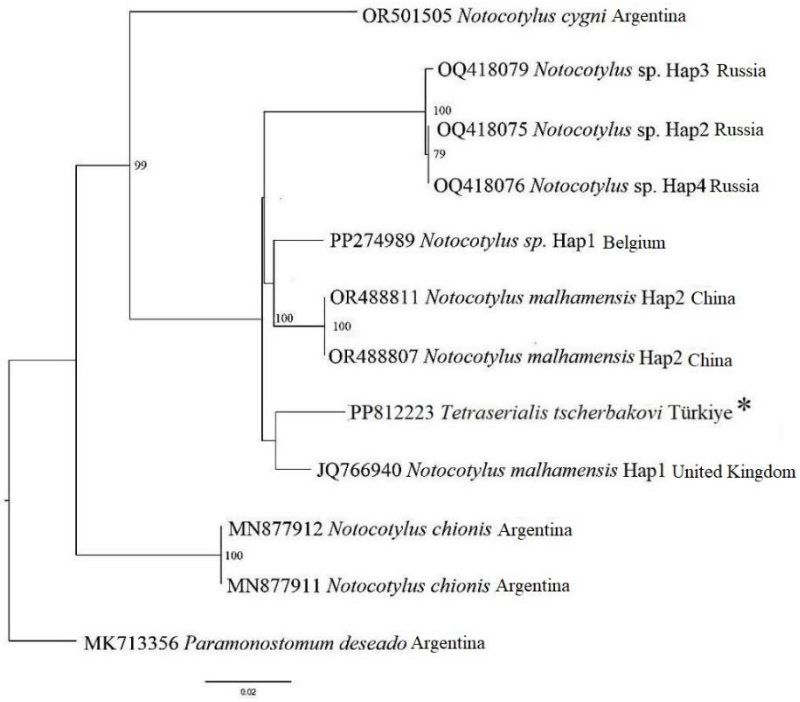

Figure 3. ML tree prepared according to ribosomal DNA ITS1, 5.8S rRNA gene region and ITS2 gene region partial sequence results of *Notocotylidae* species

Table 2. Partial sequences, accession numbers and locations of Notocotylidae species constituting the data set of the study

Species and haplotypes	GenBank Accession No	Location	Mansion
Tetraserialis tcherbakovi	PP812223	Kars, Türkiye	*Microtus mystacinus*
Notocotylus malhamensis Haplotype 1	JQ766940	United Kingdom	*Myodes glareolus Microtus agrestis*
Notocotylus sp. Haplotype 1	PP274989	Belgium	*
Notocotylus malhamensis Haplotype 2	OR488811 OR488807	Beijing, China	*Anatidae*
Notocotylus sp. Haplotype 2	OQ418075	Russia	*Planorbarius corneus*
Notocotylus sp. Haplotype 3	OQ418079	Russia	*Planorbarius corneus*
Notocotylus sp. Haplotype 4	OQ418076	Russia	*Planorbarius corneus*
Paramonostomum deseado	MK713356	Argentina	*Haematopus ater*
Notocotylus chionis	MN877912 MN877911	Argentina	*Charadrius falklandicus Calidris fuscicollis*
Notocotylus cygni	OR501505	Argentina	*Cygnus melancoryphus*

* : Not specified.

The parasite, which was placed in the imaging field whole, was deformed due topressure. When the deformed area was examined in more detail, the eggs of the parasite were clearly visible and particular attention was given to this area. A spiral cap-like structure and filamentous appendages were observed in the eggs (Figures 1d and 2d).

When the characteristic gland structures of the parasite were examined, it was determined that the glands located in the midline had the appearance of two round glands joined in the shape of eight “8” and were larger than the other glands. It was also observed that the size of the glands decreased as they moved towards the anterior and posterior ends. Electron microscopic images are shown in Figure 2.

When the sequence results were compared with other results in GenBank using the BLASTn program, it was observed that the *Tetraserialis tscherbakovi* isolate obtained in this study showed 96-97% similarity with *Notocotylus malhamensis* and *Notocotylus* sp. isolates reported from various countries.

The parasite species, haplotypes, GenBank accession numbers and locations in the data set used in the phylogenetic analysis of *Tetraserialis tscherbakovi* are given in Table 2. The ML tree showing the phylogenetic relationships of *Tetraserialis tscherbakovi* species according to the partial sequence results of ITS1, 5.8S rRNA gene region and ITS2 partial gene region is shown in Figure 3.

Discussion and Conclusion

There are very few studies on *Tetraserialis tscherbakovi*, which was reported for the first time in Türkiye. Tscherbakova (1942) identified the trematodes found in the caecum of *Arvicola terrestris* and *Microtus arvalis* in Armenia as *Notocotylus noyeri*. Later, in 1960, Petrov and Chertkova reported that this parasite was a new species (19). In addition, various morphological characteristics, and measurements of the parasite were recorded (19). It is observed that there are no significant differences between the morphological measurements of the parasite specimens found in our study and the parasites in Petrov 's (19) article, and their organ structures are similar.

Aslanova (2) reported *Tetraserialis tscherbakovi* in *Arvicola terrestris* in Azerbaijan. In this study, the research area in the Caucasus includes temperate-humid subtropical regions (2). It was also mentioned that these regions are dense in terms of parasites and that *Tetraserialis tscherbakovi* may be common in Türkiye. The fact that this parasite has been previously reported in Armenia and Azerbaijan (2,19) suggests that it may be a trematode species in the Caucasian ecosystem. In this study, the province of Kars, where the parasites were collected, is located in the north-east of Türkiye and is close to Armenia and Azerbaijan. From this point of view, the parasite may be considered as being distributed in a wide region extending from eastern Türkiye to the Caucasus.

Aslanova (2) reported that 10-30% of *Arvicola terrestris* were infected in Azerbaijan. In this study, the prevalence of the parasite was lower and was found to be lower at 4%, and the high number of parasites in infected rodents (n= 19) suggests that the infection in the region has the potential to spread (2). These data suggest that *Tetraserialis tscherbakovi* maybe widespread throughout

the Caucasus and may affect rodent populations in Türkiye.

Our findings show that Notocotylidae species are limited to birds and rodents, constituting an important parasite group. Since rodent populations, in particular, play a critical role in ecosystems, the effects of these parasites on biodiversity and ecological balance should be further investigated.

Members of the Notocotylidae family, which are generally associated with freshwater ecosystems, use freshwater slugs and crustaceans as intermediate hosts (10). Since the Kars-Sarıkamış region, where the study was conducted, is particularly rich in wetlands and river systems, these habitats provide suitable environments for *Tetraserialis tscherbakovi* to continue its life cycle. The host *Microtus* species and the geography of the parasite are consistent with the information in the literature (2,19)

Regarding the morphological characteristics of the parasite, the main distinguishing features of *Tetraserialis tscherbakovi* specimens, such as the number of ventral gland rows (Figure 2a), the structure of the testicular lobes, and the cap-like structure of the eggs (Figure 2d), were confirmed by comparison with Petrov and Chertkova's 1960 paper. However, the valve-like helical structure of the eggs, which had not been previously described in the literature, was visualized in detail for the first time by electron microscopy.

Since there was no previous isolate entry for *Tetraserialis tscherbakovi* in GenBank, theisolates with the closest similarity in BLAST analysis belonged to *Notocotylus* species. In our study, the isolate of *Tetraserialis tscherbakovi* was 97.54% similar to *N. malhamensis* JQ766940 (3) from *Myodes glareolus* in the United Kingdom. It was also 96.89% similar to *Notocotylus* sp. OK143568.1 (21) from Belgium, which was detected in the cercariae of the water slug *Ampullaceana balthica*. The molecular similarity with *Notocotylus* species suggests that these species may have common evolutionary origins. The molecular analysis in this study was restricted to the ITS1–5.8S–ITS2 region. This region is commonly used for identifying trematodes, but a single region may not be sufficient for complete identification at the species level. The obtained similarity ratios (96–97%) were slightly below the generally accepted threshold for species identification. According to this ratio, is suggested that *Tetraserialis tscherbakovi* is closely related to *Notocotylus* species and may share a common evolutionary origin. However, these values are insufficient to confirm conspecificity, and the molecular data should therefore be regarded as preliminary. Further analyses of other gene regions, such as COI and 28S, are required to confirm the species' identity and clarify its phylogenetic position.

In addition, it is thought that the genetic differences between the isolates may be due to the species differences of the parasite, as well as the host and geographical location differences.

In this study, detailed information on the morphological structure of *T. tcherbakovi* was provided, electron microscopic images of the parasite were presented for the first time in the world and we performed molecular identification and deposited it in GenBank. The morphological characteristics and measurements of the parasites in our study were found to be similar to those in the literature. These findings contribute to the helminth fauna of Türkiye. However, the molecular results presented here should be regarded as preliminary, and large-scale field studies including additional genetic markers (e.g., COI, 28S rDNA) are required to confirm the identity and better to understand the life cycle and ecological importance of *Tetraserialis tscherbakovi*.

Financial Support

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Ethical Statement

This study was conducted using the gastrointestinal systems of mice investigated within the scope of the TUBITAK project numbered 115O281. The ethics committee number of the relevant project is B.30.2.ODM.0.20.09.00-050.04-15, and the decision number is 2015-01.

Conflict of Interest

The authors declared that there is no conflict of interest.

Author Contributions

ÖB and ŞU conceived the idea and planned the article. ÖB provided the laboratory analysis of the samples. SU provided important scientific support and also contributed to the interpretation of the results. All authors made important contributions by providing feedback and helping to shape the manuscript.

Data Availability Statement

The data supporting this study's findings are available from the corresponding author upon reasonable request.

Animal Welfare

The authors confirm that they have adhered to ARRIVE Guidelines to protect animals used for scientific purposes.

References

1. **Altschul SF, Madden TL, Schäffer AA, et al** (1997): *Gapped BLAST and PSI-BLAST: a new generation of protein database search programs.* Nucleic Acids Res, **25,** 3389-3402.
2. **Aslanova EK, Fataliev GG** (2017): *Trematode fauna of the water vole (Arvicola terrestris L.) in plain zone of the Lenkoran region of Azerbaijan*. Russian J Parasitol, **42,** 316-319.
3. **Boyce K, Hide G, Craig PS, et al** (2012): *Identification of a new species of digenean Notocotylus malhamensis n. sp. (Digenea: Notocotylidae) from the bank vole (Myodes glareolus) and the field vole (Microtus agrestis).* Parasitol, **139**, 1630-1639.
4. **Chaisiri K, Morand S, Ribas A** (2011): *Notocotylus loeiensis n. sp. (Trematoda: Notocotylidae) from Rattus losea (Rodentia: Muridae) in Thailand*. Parasite, **18**, 35.
5. **Corbet GB** (1978): The mammals of the Palaearctic region: a taxonomic review. London: Cornell University Press, London.
6. **Cribb TH** (1991): *Notocotylidae (Digenea) from the Australian water rat Hydromys chrysogaster Geoffroy, 1804 (Muridae).* Syst. Parasitol. **18**, 227-237.
7. **Diaz JI, Gilardoni C, Lorenti E, et al** (2020): *Notocotylus primulus n. sp. (Trematoda: Notocotylidae) from the crested duck Lophonetta specularioides (Aves, Anatidae) from Patagonian coast, southwestern Atlantic Ocean*. Parasitol Int, **74,** 101976.
8. **Feliu C, Molina MT, Gisbert J** (1986): *Consideraciones acerca del hallazgo de Notocotylus neyrai González Castro, 1945 (Trematoda: Notocotylidae) en nuevos hospedadores Arvicólidos de la Península Ibérica.* Rev Iber Parasitol, **46**, 393-394.
9. **Felsenstein J** (2004): PHYLIP (Phylogeny Inference Package) version 3.6.
10. **Galaktionov KV, Dobrovolskij A** (2013): Types of Trematode Life Cycles. The biology and evolution of trematodes: an essay on the biology, morphology, life cycles, transmissions, and evolution of digenetic trematodes. Springer Science & Business Media.
11. **Georgiev B, Biserkov V, Genov T** (1986): *In toto staining method for cestodes with iron acetocarmine.* Helminthologia, **23**, 279–81.
12. **Guindon S, Gascuel O** (2003): *A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood.* Syst Biol, **52**, 696-704.
13. **Hall TA** (1999): *BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT*. 95-98 In: Proceedings Nucleic Acids Symposium Series.
14. **Izrailskaia AV, Besprozvannykh VV, Tatonova YV,** et al (2019): *Developmental stages of Notocotylus magniovatus Yamaguti, 1934, Catatropis vietnamensis n. sp., Pseudocatatatropis dvoryadkini n. sp., and phylogenetic relationships of Notocotylidae Lühe, 1909*. Parasitol Res, **118**, 469-481.
15. **Kinsella JM, Tkach VV** (2005): *Notocotylus fosteri sp. nov. (Trematoda, Notocotylidae) from the rice rat, Oryzomys palustris in Florida.* Acta Parasitol, **50,** 194-198.
16. **Moradpour N, Borji H, Darvish J, et al** (2018): *Rodents helminth parasites in different region of Iran.* Iranian J Parasitol, **13,** 275.
17. **Nowak RM** (1999): Walker's Mammals of the World. Volume 1. The Johns Hopking University Press. Baltimore and London.
18. **Ognev SI** (1966): Mammals of the USSR and Adjacent Countries Mammals of Eastern Europeand Northern Asia: Volume IV: Rodents. Israel Program for Scientific Translations. Jerusalem.
19. **Petrov A, Chertkova A** (1960): *Tetraserialis tscherbakovi n.g., n.sp. (Trematoda: Notocotylinae Kossack, 1911*. Helminthologia. **2**, 307-311.
20. **Posada D** (2008): *jModelTest: phylogenetic model averaging.* Mol Biol Evol, **25,** 1253-1256.
21. **Schols R, Smitz N, Vanderheyden A, et al** (2024): *Expanding the swimmer's itch pool of the Benelux: a first record of the neurotropic Trichobilharzia regenti and potential link to human infection.* Parasit Vectors, **17**, 126.
22. **Skála V, Bulantová J, Walker AJ, et al** (2014): *Insights into the development of Notocotylus attenuatus (Digenea: Notocotylidae) in Lymnaea stagnalis: from mother sporocyst to cercariae.* Parasitol Int, **63**, 94-99.
23. **Thi Le N**. (1986): *Some trematodes of the freshwater intermediate hosts in the Phungthuong area (Phuctho-Hanoi).* Vietnam J Biotechnol, **8**, 18-19.
24. **Tkach VV, Pawlowski J, Mariaux J, et al** (2001): Molecular phylogeny of the suborder Plagiorchiata and its position in the system of Digenea. (186-193). In Interrelationships of the Platyhelminthes. CRC Press.
25. **Tkach VV, Pawlowski J, Sharpilo VP** (2000): *Molecular and morphological differentiation between species of the Plagiorchis vespertilionis group (Digenea, Plagiorchiidae) occurring in European bats, with a re-description of P. vespertilionis (Müller, 1780).* Syst Parasitol, **47,** 9-22.
26. **Yie Y, Qiu M, Wen T, et al (**1956): *Morphological description of Notocotylus ratti sp. n. (Trematoda: Notocotylidae), a new trematode species parasitic in rats from Shanghai.* Acta Microbiol Sin, **4**, 211-218 (in Chinese).