Research Article

Morphological and Molecular-Genetic Characterization of *Trichuris discolor* (Linstow, 1906) (Nematoda: Trichuridae)

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Abstract | In this research, for the first time in the fauna of our republic, morphological and molecular-genetic analyses were conducted on the species Trichuris discolor, belonging to the genus Trichuris. Samples were collected from the digestive systems of Bukhara deer (*Cervus elaphus bactrianus*) and sheep (*Ovis aries*). According to the results of morphological and morphometric analysis, the Tr. The discolor sample obtained from the Bukhara deer was found to be larger in body length and width compared to the sample from the sheep, and the host species was found to explain these morphometric differences. Molecular-genetic analysis (ribosomal DNA, ITS2 region) revealed a two-nucleotide variation between the Tr. discolor samples from the Bukhara deer and sheep. The host species and ecological environment can explain these differences. Phylogenetic analysis showed that all Trichuris isolates formed a monophyletic group with high bootstrap support (≥85). The Tr. discolor samples from the Bukhara deer and sheep clustered together, forming a close branch with T. muris, which reflects host-specific adaptation and phylogenetic relationships among the species.

Keywords | Family, Genus, Species, *Trichuris discolor*, Ribosomal DNA, ITS, Nucleotide, Phylogeny

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INTRODUCTION

The genus *Trichuris* Roederer, 1761 includes numerous species that parasitize humans and animals, and have a cosmopolitan distribution (Doležalová *et al.*, 2015). Species identification has generally been based on morphological characters and morphometrical measurements, including host species as a guide (García-Sánchez *et al.*, 2019). Molecular phylogenetics is also providing evidence of species complexes within *Trichuris*, where it is highly possible that *Trichuris* can harbour cryptic species due to their wide geographic distribution and capability to parasitize a variety of host species (Callejón *et al.*, 2012; Ravasi *et al.*, 2012; Robles *et al.*, 2014; Rivero *et al.*, 2021). In ruminants, more than 23 species of *Trichuris* have been described, including *T. globulosa* (Linstow, 1901), *T. ovis* (Abildgaard, 1795), *T. skrjabini* Baskakov, 1924, and *T. discolor* (Linstow, 1906) (Knight, 1971; Cutillas *et al.*, 1995). In camels, specifically, nine species of Trichuris have been identified. They are *T. barbetonensis* Ortlepp, 1937, *T. globulosa*, *Trichuris infundibulus* (Linstow, 1906), *T. lani* (Artjuch, 1948), *T. skrjabini*, *T. tenuis* Chandler, 1930, *T. vulpis* (Froelich, 1798), *T. raoi* (Alwar and Achutan, 1960), and *T. cameli* (Sazmand and Joachim, 2017). Aside from

parasitizing camels, some species have also been found in other hosts, for example, *T. globulosa* has also been found in sheep and goats. At the same time, *T. skrjabini* has been reported in other large and small ruminants (sheep, deer, goats, elk) (Knight, 1971). Similarly, *T. ovis* and *T. discolor*, which are parasites of sheep and cattle, respectively, were also found in many hosts globally (Oliveros *et al*., 2000; Wang *et al*., 2012).

Trichurid worms are known as whip-worms because they have a broad, short posterior end and a very long, narrow, whip-like anterior end (with a stichosome pharynx) which is embedded in the mucosa of the lower intestines of humans and domestic animals. Heavy infections may cause dysentery, anaemia, malnutrition, and occasionally rectal prolapse. They have simple, direct life-cycles involving the fecal-oral transmission of eggs containing infective larvae. Eggs excreted with host faeces contaminate soil, food, and water supplies and have a characteristic barrel-shape with mucoid polar plugs at each end.

Nematodes of the genus *Trichuris* are widespread internal parasites of both domestic and wild ruminants. Different *Trichuris* species are primarily distinguished from each other based on host specificity, body length, the length of the anterior oesophageal portion, and body width. However, the main differences between them are observed in the shape and size of their reproductive structures.

In male *Trichuris*, the length of the spicule is considered the main diagnostic feature for species identification. In contrast, identifying females is relatively more difficult (Tenora *et al*., 1993), mainly due to the variability of their reproductive organs. The classification of female individuals is based mainly on the external features of the vulva (Cutillas *et al*., 2009), the structure and lining of the vagina, and also on the distance from the vulva to the uterine sphincter (Callejón *et al*., 2012, 2015). However, the size and shape of these structures can be highly variable, which means they are not always reliable as consistent diagnostic criteria (Tenora *et al*., 1993).

Another species that possesses an uneverted vagina is *Trichuris discolor* (Callejón *et al*., 2012). *T. discolor* has been described from cattle (Callejón *et al*., 2012). These nematodes have also been obtained from zebu (*Bos indicus*), Japanese serow (*Capricornis crispus*), mountain sheep (*Ovis canadensis mexicana*), and okapi (*Okapia johnstoni*) (Baer, 1950; Allen, 1955). Most recently, this nematode has been found in wild yak (*Bos grunniens*) and roe deer (*Capreolus capreolus*) (Salaba *et al*., 2013). Morphological descriptions of *T. discolor* females are provided in several studies (Callejón *et al*., 2012).

Species belonging to the genus Trichuris have been identified in small-hoofed animals (*T. dazellae, T. ovis, T. schumakovitschi, T. skrjabini*) and large-hoofed animals (*T. baskakowi, T. dzeirani, T. erschovi, T. globulosa, T. indicus, T. lani, T. media, T. ovis, T. skrjabini*) in the Republic of Uzbekistan. The species *T. discolor* was recorded for the first time (Ivashkin *et al*., 1989).

Numerous researchers have investigated the phylogenetic relationships within the Trichuris genus through the application of molecular tools. Among the earliest of these studies, Cutillas *et al*. (1995) explored the genetic variation between *T. ovis* and *T. globulosa* using isoenzyme analysis. Based on both biochemical and morphological data, they proposed that these two taxa could, in fact, belong to the same biological species.

Whipworms are widespread soil-transmitted helminthes (=geohelminths) that can be found in a broad range of hosts, including humans (*Trichuris trichiura*), pigs (*Trichuris suis*), sheep, goats, and bovines (*Trichuris ovis* and *Trichuris discolor*), dogs (*Trichuris vulpis*), and non-human primates (*Trichuris* spp.) (Khalafalla *et al*., 2011; Hotez *et al*., 2012).

At present, numerous molecular-genetic studies are being carried out on vertebrate and invertebrate animals within the fauna of our republic, including insects (Kimyonazarov *et al*., 2024; Kadirov *et al*., 2024), nematodes (Aliyev, 2024; Mirzaev, 2024), and fish (Quvatov *et al*., 2023; Ubaydullayev *et al*., 2025), which have all been studied at the molecular level.

Subsequently, Oliveros *et al*. (2000) assessed the internal transcribed spacer 2 (ITS2) region among several Trichuris species - including *T. ovis, T. globulosa, T. suis*, and *T. leporis* - and found that the ITS2 sequences of *T. ovis* and *T. globulosa* were identical. Expanding on this, Cutillas *et al*. (2004) examined sequence differences across the ITS1-5.8S rRNA-ITS2 region in *T. skrjabini, T. ovis, T. globulosa, T. leporis, T. muris,* and *T. arvicolae*, also analyzing the lengths and G+C content of ITS1 and ITS2. Among all examined species, only *T. ovis* and *T. globulosa* lacked variation in the length of these regions.

In a later study, Liu *et al*. (2012) were the first to characterize the complete mitochondrial genomes of *T. ovis* and *T. discolor*. Meanwhile, Callejón *et al*. (2012) employed partial sequences of the mitochondrial *16S rRNA* gene, as well as the ITS1 and ITS2 regions of ribosomal DNA, to differentiate between *T. ovis* and *T. discolor*. Their work included samples collected from Bos taurus in Iran and Spain. Phylogenetic analyses revealed that T. discolor individuals from Iran formed a distinct group, separate from those in Spain.

Callejón *et al*. (2015) further examined the taxonomy and

evolutionary history of *Trichuris* species from Camelus dromedarius, along with T. globulosa samples obtained from sheep in Iran and South Africa. Their findings indicated that ITS2 polymorphisms alone were insufficient to reliably distinguish *T. globulosa* from *T. discolor*. As a result, they sequenced partial regions of the cytochrome c oxidase and cytochrome b genes, which allowed them to identify distinct genetic lineages within both *T. globulosa* and *T. discolor*.

This research work aims to provide a morphological, morphometric, and molecular-genetic description of the species Trichuris discolor (Linstow, 1906), belonging to the genus Trichuris Roederer, 1761, which has been identified for the first time in the fauna of Uzbekistan.

MATERIALS AND METHODS

Helminthological methods

To carry out this research, helminthological samples were collected from sheep (Ovis aries) belonging to agricultural and farm households in Samarkand Region (Zarafshan National Nature Park) and Naryn Region (Kusonsay and Yangiqurghon districts) of Uzbekistan during 2024–2025. Additionally, samples were taken from small ruminants slaughtered at a slaughterhouse. Helminthological examination was performed on the complete and partial stomachs and intestines of one Bukhara deer (*Cervus elaphus bactrianus*) and 17 sheep using the helminthological method (Skrjabin, 1928). From the Bukhara deer, 68 samples were collected (27 from males and 41 from females), and from sheep, 173 samples were collected (81 from males and 92 from females). These samples were fixed in 70% ethanol solution. Furthermore, fecal samples from 8 Bukhara deer and over 470 sheep were analyzed using the Berman-Orlov method.

Throughout the study, helminthological, comparative morphological, morphometric, and ecological research methods were employed (Demidov, 1987; Ivashkin, 1971, 1981, 1989; Kuznetsov, 2004), along with computer programs Biostat 2007 and Microsoft Office Excel 2003.

Molecular-genetic methods

For the molecular-genetic part of the research, ITS fragments of ribosomal DNA were isolated from the nematodes mentioned above. Specifically, three male specimens of *Trichuris discolor* nematodes from the digestive tracts of Bukhara deer and sheep kept in a private farm in the Yangikurgon district (Namangan region) were collected and analyzed.

Genomic DNA was extracted from nematode tissue using the DNeasy Blood and Tissue Kit (Qiagen, https://www.qiagen.com). The ITS fragments of the ribosomal DNA (rDNA) were amplified using primers AV28 forward (ATA TGC TTA AGT TCA GCG GGT) and TW81 reverse (GTT TCC GTA GGT GAA CCT GC), which are commonly used in molecular taxonomy (Curran *et al*., 1994; Amirov *et al*., 2021).

Polymerase Chain Reaction (PCR) was conducted as follows: Initial denaturation at 94°C for 5 minutes, denaturation at 95°C for 45 seconds, primer annealing at 55°C for 45 seconds, extension at 72°C for 1 minute and 40 seconds, final extension at 72°C for 5 minutes. Steps 2–4 were repeated in a 35-cycle loop.

The presence of DNA in PCR products was verified by electrophoresis in a 1.0% agarose gel at 120 V. DNA amplification and extraction from the gel were performed using reagents from Silex M (Moscow, Russia), following the manufacturer's instructions.

Sequencing of the DNA was carried out using the ABI PRISM® BigDye™ Terminator v3.1 Cycle Sequencing Kit, and sequencing products were analyzed on an ABI PRISM 3100-Avant automatic sequencer (Moscow, Russia).

The obtained nucleotide sequences were analyzed using specialized software such as BioEdit, Clustal W, DNASTAR™, and PAUP4.

Phylogenetic tree construction. To determine the molecular phylogenetic relationships of *Trichuris discolor*, the ITS2 rDNA gene sequences were analyzed alongside those of other *Trichuris* species retrieved from the GenBank database. A representative sequence from a different genus was included as an outgroup. Sequence alignments were conducted using the MAFFT algorithm (Katoh et al., 2008) and manually refined with BioEdit version 7.0.5.2 to ensure alignment quality. Phylogenetic trees were constructed using the Maximum Likelihood (ML) method implemented in the IQ-TREE 2 software package (Minh et al., 2020). The best-fitting nucleotide substitution model was automatically selected using the ModelFinder module. Node support was assessed via 1,000 ultrafast bootstrap replicates (Felsenstein, 1985). The final phylogenetic tree was visualized using the Interactive Tree of Life (iTOL) online tool (Letunic and Bork, 2021), which enabled an interactive and customizable representation of phylogenetic relationships.

RESULTS AND DISCUSSION

Morphological studies. Based on the conducted morphological investigations, male and female individuals

of Trichuris discolor a species belonging to the genus Trichuris and parasitizing both Bukhara deer and sheep in Uzbekistan - were comparatively studied.

Table 1: Morphometric measurements of *Trichuris discolor*, belonging to the genus *Trichuris*, in mm (Lim, M±m).

Main characteristics	Bukhara cattle	Sheep
(Male), n = 10		
Body length	51.9±0.95 (48.1-54.3)	50.7±0.71 (47.1-52.7)
Anterior part length	35.7±0.47 (33.4-37.6)	34.8±0.39 (33.1-35.8)
Posterior part length	14.6±0.14 (12.7-16.3)	13.9±0.17 (11.9-15.8)
Anterior body width	0.26±0.2 (0.19-0.29)	0.21±0.09 (0.17-0.26)
Posterior body width	0.52±0.23 (0.48-0.58)	0.49±0.21 (0.45-0.54)
Spicule length	1.91±0.08 (1.89-2.10)	1.79±0.14 (1.62-1.95)
(Female), n = 10		
Body length	53.4±0.62 (47.4-58.7)	51.5±0.48 (45.7-59.6)
Anterior part length	36.3±0.31 (31.6-39.3)	35.9±0.42 (32.7-37.6)
Posterior part length	14.6±0.09 (11.7-17.3)	14.1±0.8 (11.3-16.4)
Anterior body width	0.15±0.02 (0.08-0.17)	0.14±0.02 (0.08-0.16)
Posterior body width	0.59±0.11 (0.49-0.67)	0.56±0.13 (0.44-0.62)
Egg length	75±0.2 (65-85)	74±0.2 (63-82)
Egg width	39±0.2 (30-48)	37±0.2 (25-45)

Note: Lim, M±m. Lim–range, M- mean, m-standard error of the mean.

For each specimen belonging to the genus Trichuris, the following morphometric parameters were measured: total body length, length of the anterior part, length of the posterior part, width at the mid-region of the anterior part, maximum width of the posterior part, vulva opening length (in females), and spicule length (in males) (Table 1).

Male: According to the results of morphometric analysis, the body length of Trichuris discolor males was found to be 50,7–51,9 mm, the length of the anterior part of the body was 34,8–35,7 mm, the length of the posterior part was 13,9–14,6 mm, the anterior body width was 0,21–0,26 mm, the posterior body width was 0,49–0,52 mm, and the spicule length was 1,79–1,91 mm.

Female: The body length of the females was found to be 51,5–53,4 mm, the anterior part length was 35,9–36,3 mm, the posterior part length was 14,1–14,6 mm, the anterior body width was 0,14–0,15 mm, the posterior body width was 0,56–0,59 mm, while the egg length was 74-75 µm and the width was 37–39 µm (Figure 1).

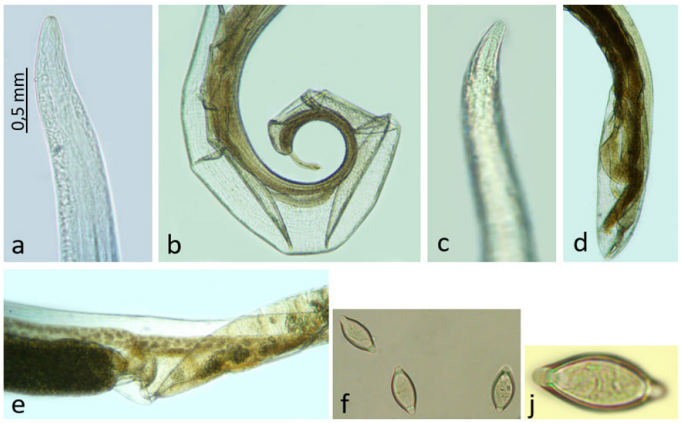

Figure 1: Morphological appearance of *Trichuris discolor* (genus *Trichuris*).
Note: Male: a: anterior part of the body, b: posterior (tail) part. Female: c: anterior part of the body, d: posterior (tail) part, e: vulva area, f, j: general appearance of the eggs.

When comparing the morphometric measurements of *Trichuris discolor* found in the digestive system of Bukhara cattle with those found in sheep, it was determined that the *Trichuris discolor* specimens from the digestive system of Bukhara cattle were relatively larger in body length and width, as well as in other morphological characteristics, compared to the specimens found in sheep.

Differences between the two sexes (male and female) in overall body length, length and width of the anterior and posterior parts of the body, as well as in sex-specific structures (spicule and eggs), confirm this observation.

Molecular-genetic study results

Based on the results of the molecular-genetic study conducted (sequence chromatography), the rDNA of *Trichuris discolor* belonging to the genus *Trichuris* was isolated from the ITS2 region, with a length of 282 base pairs. For comparative analysis, international bioinformatics data from the database (https://blast.ncbi.nlm.nih.gov) were used, including sequences of *Trichuris discolor* (accession number: OP824836) and *Trichuris ovis* (accession number: JF680987) species (Figure 2).

According to the molecular-genetic studies and bioinformatic analysis conducted, two nucleotide differences were found between the *Trichuris discolor_Cb* sample obtained from the Bukhara bull and the *Trichuris discolor_Oa* sample obtained from the sheep. These differences were recorded at the 43rd nucleotide, where *Trichuris discolor_Cb* had thymine (T) and *Trichuris*

discolor_Oa had cytosine (C), and at the 128th nucleotide, where *Trichuris discolor_Cb* had cytosine (C) and *Trichuris discolor_Oa* had thymine (T).

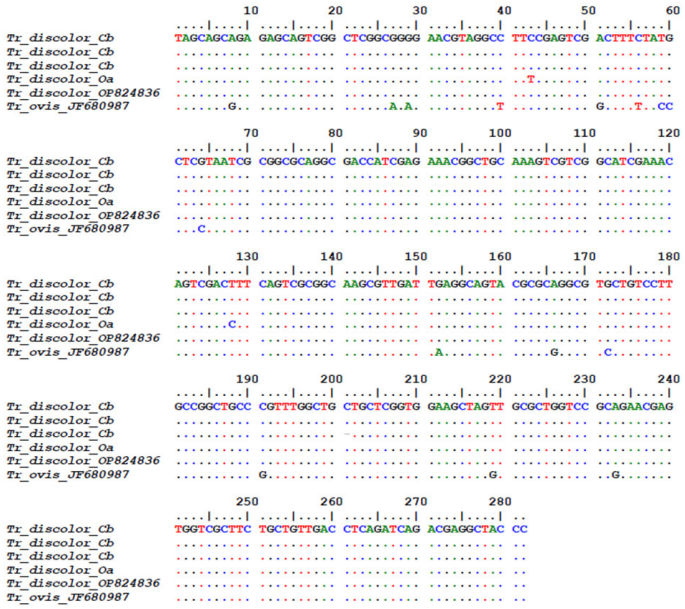

Figure 2: Comparison of nucleotide sequences of the ribosomal DNA ITS2 region of *Trichuris discolor*, belonging to the genus *Trichuris*.
Note: *Trichuris discolor_Cb*-Бухоро буғиси, *Trichuris discolor_Oa*- қўйнинг ҳазм тизимидан олинган *Trichuris discolor* туринг намуналари.

No nucleotide differences were observed between the *Trichuris discolor_Cb* sample and the *Trichuris discolor* sample (accession number: OP824836) obtained from the international bioinformatics database (https://blast.ncbi.nlm.nih.gov). However, 15 nucleotide differences were identified between the *Trichuris discolor_Cb* sample and *Trichuris ovis* (accession number: JF680987) from the database. These differences were noted at the following nucleotide positions: at 7, 51, 166, and 233, *Trichuris discolor_Cb* had adenine (A) while *Trichuris ovis* had guanine (G); at 27, 29, and 151, *Trichuris discolor_Cb* had guanine (G) and *Trichuris ovis* had adenine (A); at 40 and 56, *Trichuris discolor_Cb* had cytosine (C) and *Trichuris ovis* had thymine (T); at 59, *Trichuris discolor_Cb* had cytosine (C) and *Trichuris ovis* had thymine (T); at 60, 64, and 172, *Trichuris discolor_Cb* had guanine (G) and *Trichuris ovis* had cytosine (C); at 191, *Trichuris discolor_Cb* had cytosine (C) and *Trichuris ovis* had guanine (G); and at 219, *Trichuris discolor_Cb* had thymine (T) while *Trichuris ovis* had guanine (G).

Between the *Trichuris discolor_Oa* sample and the *Trichuris discolor* sample (accession number: OP824836) from the international bioinformatics database, two nucleotide differences were found: at the 43rd nucleotide, *Trichuris discolor_Oa* had thymine (T) while the database sample had cytosine (C); and at the 128th nucleotide, *Trichuris discolor_Oa* had cytosine (C) and the database sample had thymine (T). Additionally, 17 nucleotide differences were observed between *Trichuris discolor_Oa* and *Trichuris ovis* (accession number: JF680987). These were at positions 7, 51, 166, and 233 where *Trichuris discolor_Oa* had adenine (A) and *Trichuris ovis* had guanine (G); at 27, 29, and 151, *Trichuris discolor_Oa* had guanine (G) and *Trichuris ovis* had adenine (A); at 40, 43, and 56, *Trichuris discolor_Oa* had cytosine (C) and *Trichuris ovis* had thymine (T); at 59 and 128, *Trichuris discolor_Oa* had cytosine (C) and *Trichuris ovis* had thymine (T); at 60, 64, and 172, *Trichuris discolor_Oa* had guanine (G) and *Trichuris ovis* had cytosine (C); at 191, *Trichuris discolor_Oa* had cytosine (C) and *Trichuris ovis* had guanine (G); and at 219, *Trichuris discolor_Oa* had thymine (T) and *Trichuris ovis* had guanine (G).

The two nucleotide differences found between the *Trichuris discolor* samples from the digestive systems of Bukhara bulls and sheep indicate that *Trichuris discolor_Cb* and *Trichuris discolor_Oa* are individuals of the same species (*Trichuris discolor*) adapted to different hosts. Both samples show a high degree of similarity to the *Trichuris discolor* sequence (accession number: OP824836) in the international bioinformatics database. Samples of *Trichuris discolor* belonging to the genus *Trichuris*, which were analyzed in molecular-genetic studies, were deposited in the GenBank database, and accession numbers were obtained as follows: *Trichuris discolor_Cb*-PX241247, *Trichuris discolor_Cb* -PX240973, *Trichuris discolor_Cb*-PX240910, and *Trichuris discolor_Oa*-PX241226.

Phylogenetic tree

The phylogenetic analysis of 14 operational taxonomic units (OTUs) within the genus Trichuris indicated that all samples formed a well-supported monophyletic group (bootstrap= 98), with Amphibiocapillaria tritonispunctati (LC605543) positioned as the basal outgroup. This result confirms that the genus Trichuris constitutes an independent phylogenetic clade (Figure 3).

- Subclade A (bootstrap 92–100) comprised only *Trichuris* sp. (LC512872, LC512871) samples.
- Subclade B (bootstrap= 97) included several internal clusters:

A cluster containing *T. discolor* samples (FR870273, HE608854) exhibited very high genetic similarity (bootstrap= 92–100), indicating minimal intraspecific divergence. Within this subclade, a group composed of *T. discolor Ov* and *T. discolor Cb* samples (bootstrap = 93–94) was also observed, with the two *T. discolor Cb* samples showing particularly high similarity (bootstrap= 88). The inclusion of *T. muris* (AW288460) in this clade may reflect phylogenetic proximity or potential host-switching events

between rodents and other hosts.

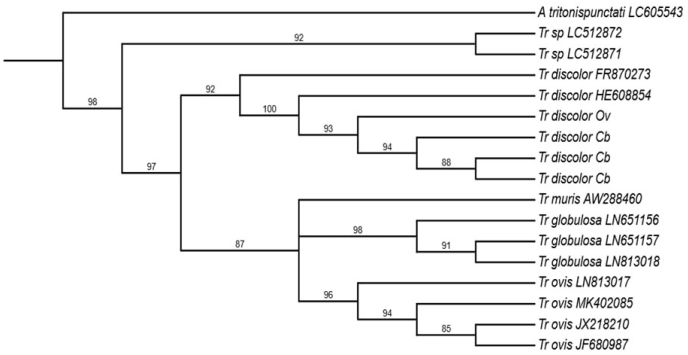

Figure 3: Phylogenetic Tree of Species Belonging to the Genus *Trichuris*. Within the internal branching, two main subclades were identified.

Three *T. globulosa* samples (LN651156, LN651157, LN813018) formed a well-supported cluster (bootstrap 91–96), reflecting intraspecific genetic variation.

An independent clade composed of *T. ovis* samples (LN813017, MK402085, JX218210, JF680987) was also identified (bootstrap = 85). Within this clade, the pair MK402085 and JX218210 was strongly supported (bootstrap = 94), suggesting adaptation to ruminant hosts.

Interestingly, the *T. muris* sample joined the *T. ovis* and *T. globulosa* clades, contributing to the formation of a larger subclade. This pattern may indicate phylogenetic proximity or evolutionary relationships among these species.

All major nodes were supported by high or satisfactory bootstrap values (≥85), with no weak nodes (<70). Overall, the phylogenetic tree clearly illustrates the internal relationships among *Trichuris* species, demonstrating both host-specific clustering and intraspecific genetic diversity. Notably, the close clustering of *T. discolor* and *T. muris*, which is somewhat unusual compared to previous phylogenetic studies, may result from the short ITS2 sequence used. Therefore, using longer sequences or multiple genetic markers is recommended to enhance phylogenetic resolution.

DISCUSSION

The morphometric differences observed between *Trichuris discolor* from Bukhara deer and domestic sheep likely reflect host-specific adaptations, individual variation, or environmental influences. These findings underscore that *T. discolor* may exhibit plasticity in body morphology depending on the host, consistent with previous reports on host-associated variation in parasitic nematodes (Gasser *et al.*, 2008).

Molecular-genetic analysis revealed two nucleotide substitutions (T ↔ C) at positions 43 and 128 between *T. discolor_Cb* and *T. discolor_Oa*, indicating relatively close genetic relationships. The *T. discolor_Cb* sequence showed complete identity with the reference database isolate (OP824836), demonstrating a highly conserved nucleotide composition typical of the species. In contrast, 15–17 nucleotide differences were found when comparing *T. discolor* to *T. ovis*, confirming clear phylogenetic separation and evolutionary independence. The integration of morphometric and genetic data, along with the observation that these variants occur across different geographic regions and host species, supports the biological significance of even minimal nucleotide differences. This suggests host-specific evolutionary adaptation, a pattern widely observed in parasitic nematodes (Hoberg and Brooks, 2008).

Phylogenetic analysis placed *T. discolor* isolates in a well-supported monophyletic clade, while occasional grouping with *T. muris* may reflect rare host-switching events. Overall, *T. discolor* demonstrates both genetic stability and host-associated morphological adaptability, highlighting the need for further studies on host-specific evolutionary processes to understand species diversity and epidemiology.

CONCLUSION

Morphometric differences observed between male and female *Trichuris discolor* individuals from two different hosts (Bukhara deer and sheep) can be explained by the host species, living conditions, and ecological environment.

Molecular-genetic analyses suggest that *T. discolor_Cb* and *T. discolor_Oa* are closely related but represent strain-level differentiation, both showing high similarity to *Trichuris discolor* (OP824836) from the international bioinformatics database.

Compared to *T. ovis*, both isolates show significant genetic divergence, confirming their independent phylogenetic positions.

Identified SNP (Single Nucleotide Polymorphism) variations serve as early biomarkers of genetic diversification and may play a critical role in the parasite's adaptation process to the host organism.

This study's phylogenetic tree demonstrated the monophyletic origin of the genus *Trichuris* and its independent evolutionary lineage separate from other nematodes. The analysis especially highlighted that *T. discolor* isolates have low genetic divergence within the species and phylogenetically close populations. Additionally, the grouping of *T. muris* with *T. discolor* indicates possible host-switching events among parasites.

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NOVELTY STATEMENT

This study provides the first integrated morphological and molecular-genetic characterization of Trichuris discolor from Uzbekistan, combining detailed morphometric analysis with mitochondrial DNA sequencing. The findings contribute new regional genetic data and improve taxonomic resolution within the genus *Trichuris*.

AUTHOR'S CONTRIBUTION

The materials were collected, morphologically studied, and statistically analyzed by Seytveliyeva Sevilya, Daminov Asadullo, Vladimir Turytsin, Natalya Marmazinskaya, and Anvarbek Ibrokhimov. Oybek Amirov and Azamat Yuldoshkhonov carried out molecular analyses. Oybek Amirov analyzed the collected materials and the preparation of the manuscript. The authors read and approved the manuscript.

Generative AI and AI-assisted technology statement

The authors confirm that no generative AI or AI-assisted technologies were used in the design, data analysis, or interpretation of results.

Conflict of interest

The authors have declared no conflict of interest.

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