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RESEARCH ARTICLE

Helminth fauna of odd-toed ungulates in Central Uzbekistan

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Abstract

Helminth infections of odd-toed ungulates represent one of the most significant parasitological problems in livestock production in the arid regions of Central Asia. However, studies of the helminth fauna of odd-toed ungulates in Central Uzbekistan have been virtually absent to date. The present study aimed to investigate the species composition, prevalence, and infection intensity of helminths in horses and donkeys from Central Uzbekistan during 2025–2026. The study was conducted on horses and donkeys from livestock farms in districts of the Central region of Uzbekistan using a combination of parasitological methods, including diagnostic deworming and complete and incomplete helminthological necropsy. A total of 24 helminth species were identified in horses and 19 species in donkeys. The dominant species in horses were *Parascaris equorum* (prevalence 46.7%), *Triodontophorus serratus* (43.3%), *Strongylus edentatus* (36.6%), and *Oxyuris equi* (33.3%). In donkeys, representatives of Cyathostominae predominated, including *Cyathostomum catinatum* (prevalence 42.2%; infection intensity 87.5±41.3 specimens; OR=1.85), *Cyathostomum coronatum* (40.0%; 47.0±7.6 specimens; OR=2.97), *Cylicocyclus auriculatus* (35.5%; 92.0±41.5 specimens; OR=2.76), and *Cylicocyclus nassatus* (33.3%; 130.5±59.8 specimens; OR=2.00). Molecular genetic identification of the dominant species *Cyathostomum catinatum* was performed based on ITS-2 sequences of ribosomal DNA. The isolates obtained from a horse and a donkey from Central Uzbekistan confirmed their species identity as

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C. catinatum and formed a common phylogenetic cluster with reference sequences from China and Iran.

Keywords
Central Uzbekistan, donkeys, horses, helminth fauna, *Parascaris*, prevalence, *Strongylus*, intensity

Introduction

The study of the helminth fauna of odd-toed ungulates in Central Uzbekistan is a relevant field of research IN parasitology and veterinary science due to the widespread occurrence of parasitic infections, their substantial effects on the physiological condition of animals, the circulation of pathogens between domestic and wild animals, as well as the potential reduction in livestock productivity and economic efficiency. The order Perissodactyla represents a phylogenetically ancient and ecologically significant group of mammals, including both widespread domestic species and wild species, many of which are rare and endangered. The formation of the helminth fauna of odd-toed ungulates in Central Uzbekistan is determined by specific arid climatic conditions, including high temperatures, low humidity, and pronounced seasonality, which substantially affect parasite life cycles and patterns of distribution. Despite the availability of studies on the parasite fauna of domestic and wild animals in Uzbekistan, the helminth fauna of odd-toed ungulates remains insufficiently studied. Recent studies of domestic and wild animals in the country have largely focused on artiodactyls, for which considerable helminth species diversity has been established, including representatives of Cestoda, Trematoda, and Nematoda (Akramova et al. 2025). At the same time, information on the species composition, prevalence, and intensity of helminth infections in horses and donkeys, particularly under the conditions of Central Uzbekistan, remains considerably less comprehensive. The study of the helminth fauna of horses and donkeys is of particular interest because these animals are of important economic value, are widely used in rural areas, and are kept under conditions that facilitate the circulation of various groups of parasites. Therefore, the aim of the present study was to investigate the species composition, prevalence, and intensity of helminth infections in horses and donkeys in Central Uzbekistan, as well as to perform molecular genetic identification of one of the dominant species – *Cyathostomum catinatum*.

Materials and methods

The material for the present study consisted of helminth collections from horses and donkeys bred on livestock farms in Bukhara, Navoi, and Samarkand regions of the Republic of Uzbekistan during 2025-2026. In Bukhara Region, the study was conducted on farms located in the Gulobod, Jondor, Kagan, Alat, Peshku, Karakul,

Karaulbazar, Romitan, Vobkent, and Gijduvan districts. In Navoi Region, material was collected in the Karmana, Kanimekh, Navbahor, Nurata, Kyzyltepa, Tamdy, Uchkuduk, Khatyrchi districts, as well as in the vicinity of the cities of Navoi and Zarafshan. In Samarkand Region, the study was conducted in the Bulungur, Ishtikhan, Jomboy, Kattakurgan, Nurabad, Payarik, and Urgut districts, as well as in the settlements of Oktash, Laish, and Juma (Fig. 1).

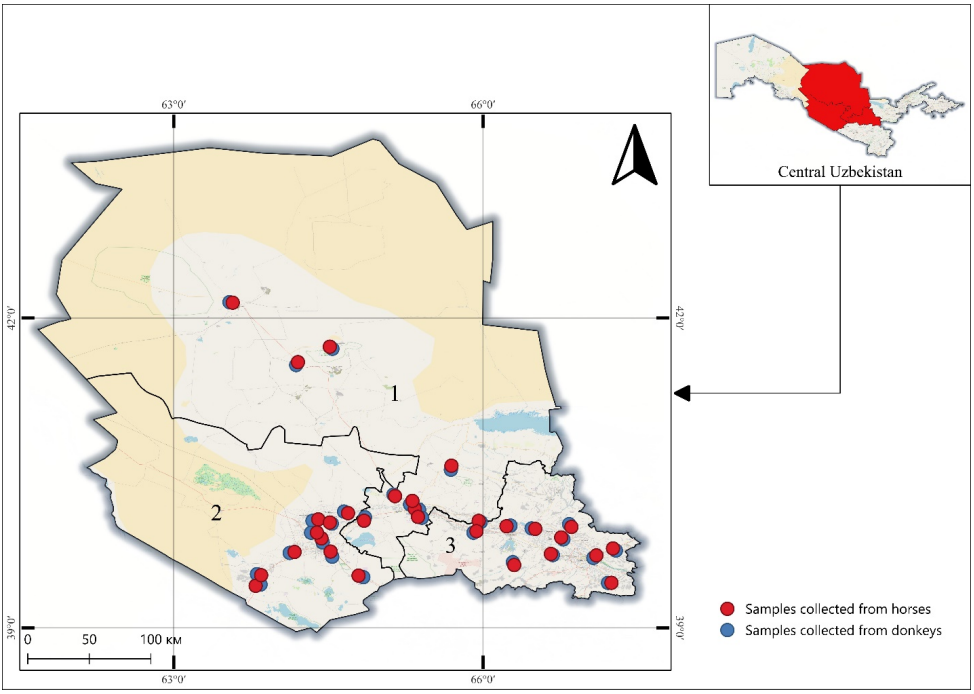


Figure 1. Sampling sites of horses and donkeys in Central Uzbekistan: 1 – Navoi Region; 2 – Bukhara Region; 3 – Samarkand Region.

To study the helminth fauna of odd-toed ungulates, a set of parasitological methods was applied, including diagnostic deworming and helminthological necropsy. Helminthological material from horses and donkeys was collected throughout all seasons of the year. The study was conducted on horses (n=60) and donkeys (n=45). Of the total number of horses, 45 animals underwent diagnostic deworming, while 15 animals were examined by complete helminthological necropsy, involving a thorough examination of the gastrointestinal tract, liver, and other organs to detect both luminal and tissue-dwelling parasite forms (Taylor et al. 2015). In addition, 32 liver samples and 32 lung samples from horses were examined using incomplete helminthological necropsy. Among donkeys, 30 animals were examined by diagnostic deworming, and 15 animals were examined by necropsy.

The diagnostic deworming method consisted of a single oral administration of ivermectin at a dose of 0.2 mg/kg body weight, followed by the collection of expelled helminths over a period of 24–72 hours, in accordance with current recommendations for the control of helminth infections in odd-toed ungulates (Rendle et al. 2019; Nielsen 2012). Diagnostic deworming with ivermectin and complete or incomplete helminthological necropsy were used complementarily for helminth detection. Nematodes were recovered by both diagnostic deworming and necropsy, whereas cestodes, trematodes, and tissue-dwelling helminth stages reported in this study were detected during necropsy. The collected material was washed, fixed in 70% ethanol, and identified based on morphological characteristics (Taylor et al. 2015). Helminths were identified morphologically using standard taxonomic keys (Lichtenfels et al. 2008; Boev et al. 1962, 1963; Ivashkin and Dvoinos 1984). Morphological examination and species identification of helminths were performed on temporary and permanent preparations using modern equipment: EMZ-5TRD stereoscopic microscope (MEIJI TECHNO, Japan, 2010), an inverted CK-53 microscope (Olympus, Japan, 2015) and a binocular NLCD-307 B microscope (Motic, Japan, 2020).

To confirm the species identity of the nematodes under study, a molecular genetic method based on amplification and subsequent sequencing of the ITS-2 (Internal Transcribed Spacer 2) region of ribosomal DNA was applied. DNA was extracted from individual nematode specimens using the DNeasy Blood & Tissue Kit (Qiagen). Prior to DNA extraction, the parasites were mechanically disrupted using sterile instruments and subsequently lysed in the presence of ATL buffer and Proteinase K according to the manufacturer's protocol. The extracted DNA was used as a template for subsequent polymerase chain reaction (PCR). The ITS-2 region was amplified using the primers ITS2F (5′-TAGCTTCAGCGATGGATCGGT-3′) and ITS2R (5′-CTTTTCCTCCGCTAAATGATATGC-3′). PCR was performed in a 25 μL reaction mixture containing 12.5 μL of 2×Taq DNA Polymerase Master Mix, 1 μL of each primer (10 μM), 2 μL of extracted DNA, and 8.5 μL of sterile deionized water. Amplification was performed in a thermocycler under the following conditions: initial denaturation at 95 °C for 8 min, followed by 35 cycles consisting of denaturation at 94 °C for 30 s, primer annealing at 55 °C for 30 s, and extension at 72 °C for 40 s; a final extension was performed at 72 °C for 7 min. The amplification products were analyzed by electrophoresis in a 2% agarose gel to confirm the presence of a PCR fragment of the expected size. Positive amplicons were purified and submitted for sequencing. The obtained nucleotide sequences were edited and compared with reference sequences available in the international GenBank database using the BLAST algorithm. Species identity was determined based on the degree of similarity between the obtained sequences and published sequences of the corresponding species. The obtained sequences were also used for phylogenetic analysis. The phylogenetic tree was constructed using the Maximum Likelihood method, and the statistical support of individual branches was assessed using bootstrap analysis with 1000 replicates. The analysis was performed using the MEGA software package.

Statistical analysis of the obtained data was performed using methods of variation statistics and epidemiological analysis commonly used in parasitology (Upjohn et al. 2010; Tedla & Abichu 2018). The prevalence of infection (EI, %) was calculated as the proportion of infected animals among the total number of animals examined. The results were presented as the mean and standard error of the mean (M±m). The intensity of infection (II) was expressed as the mean value with standard deviation and range: M±SD; min–max (Levy et al. 2015; Tedla & Abichu 2018). To assess the strength of the association between host species and the probability of infection, the odds ratio (OR) was calculated, as widely applied in epidemiological studies of parasitic infections (Neuhaus et al. 2010; Fritzen et al. 2010). All calculations were performed using standard statistical methods.

Results

During the study, 25 helminth species were recorded in equids. Of these, 20 species – *Cyathostomum catinatum*, *Cyathostomum coronatum*, *Parapoteriostomum euproctus*, *Cylicocyclus auriculatus*, *Cylicocyclus nassatus*, *Cylicocyclus insigne*, *Cylicocyclus leptostomum*, *Triodontophorus serratus*, *Triodontophorus brevicauda*, *Triodontophorus tenuicollis*, *Strongylus equinus*, *Strongylus edentatus*, *Delafondia vulgaris*, *Parascaris equorum*, *Oxyuris equi*, *Habronema muscae*, *Habronema microstoma*, *Drascheia megastoma*, *Physocephalus sexalatus*, and *Gongylonema pulchrum* – were identified by diagnostic deworming and complete and incomplete helminthological necropsy. Five species – *Echinococcus granulosus* larvae, *Taenia hydatigena* larvae, *Anoplocephala magna*, *Fasciola gigantica*, and *Setaria equina* – were detected exclusively by complete and incomplete helminthological necropsy.

The indicators of helminth infection intensity in equids from Central Uzbekistan are presented in the Table 1. A total of 24 helminth species were identified in horses, whereas 19 species were recorded in donkeys. Thus, helminth species diversity was slightly higher in horses than in donkeys.

The prevalence patterns differed between the two host groups. In horses, *Parascaris equorum* (46.7%) and several large strongylid species were among the most frequently detected helminths, whereas several Cyathostominae species, particularly *Cyathostomum catinatum* (42.2%), *C. coronatum* (40.0%), *Cylicocyclus auricu-latus* (35.5%), and *C. nassatus* (33.3%), were more frequently detected in donkeys.

The mean infection intensity also varied depending on the parasite species and host. In horses, the highest infection intensity values were recorded for *Fasciola gigantica* (81.0±28.0 specimens), *Delafondia vulgaris* (74.5±12.0 specimens), *Cyathostomum catinatum* (69.5±29.8 specimens), and *Strongylus edentatus* (61.5±30.3 specimens). In donkeys, the highest infection intensity was recorded for *Cylicocyclus nassatus* (130.5±59.8 specimens), *C. auriculatus* (92.0±41.5 specimens), and *Cyathostomum catinatum* (87.5±41.3 specimens). Overall, in donkeys, several Cyathostominae species were characterized not only by higher prevalence but also by higher mean infection intensity compared with horses.

Table 1. Prevalence and intensity of helminth infections in horses and donkeys from Central Uzbekistan

No	Helminth species	Detection method	Horse		Donkey		OR donkey vs. horse
			Prevalence % (95% CI)	Mean intensity±SD (range)	Prevalence % (95% CI)	Mean intensity±SD (range)	
1	*Echinococcus granulosus* larvae	N	24.1 (16-35)	6.0±2.5 (1-11)	20.0 (18-45)	4.0±1.5 (1-7)	0.82
2	*Anoplocephala magna*	N	13.3 (11-23)	38.00±19.80 (24-52)	13.3 (11-30)	32.3±2.55 (3-58)	1.00
3	*Taenia hydatigena* larvae	N	20.0 (16-45)	2.5±0.8 (1-4)	-	-	-
4	*Fasciola gigantica*	N	25.5 (15-40)	81.0±28.0 (25-137)	26.7 (11-52)	10.0±3.5 (3-17)	1.09
5	*Cyathostomum catinatum*	DD+N	28.3 (18-43)	69.5±29.8 (10-129)	42.2 (27-61)	87.5±41.3 (5-170)	1.85
6	*Cyathostomum coronatum*	DD+N	18.3 (12-31)	46.50±38.89 (19-74)	40.0 (25-58)	47.0±7.60 (3-86)	2.97
7	*Parapoteriostomum euproctus*	DD+N	15.0 (11-29)	36.0±2.70 (23-49)	15.5 (12-34)	37.2±8.10 (3-64)	1.04
8	*Cylicocyclus auriculatus*	DD+N	16.6 (12-31)	12.5±5.3 (2-23)	35.5 (22-55)	92.0±41.5 (9-175)	2.76
9	*Cylicocyclus nassatus*	DD+N	20.0 (11-34)	20.0±7.5 (5-35)	33.3 (19-51)	130.5±59.8 (11-250)	2.00
10	*Cylicocyclus insigne*	DD+N	21.6 (13-36)	28.5±11.8 (5-52)	17.7 (15-34)	66.5±29.3 (8-125)	0.78
11	*Cylicocyclus leptostomum*	DD+N	13.3 (9-26)	32.4±4.50 (28-36)	-	-	-
12	*Triodontophorus serratus*	DD+N	43.3 (31-59)	51.0±24.5 (2-100)	31.1 (17-48)	53.5±18.3 (17-90)	0.59
13	*Triodontophorus brevicauda*	DD+N	23.3 (13-36)	23.7±3.20 (15-28)	-	-	-
14	*Triodontophorus tenuicollis*	DD+N	11.6 (10-23)	33.4±5.09 (18-43)	-	-	-
15	*Strongylus equinus*	DD+N	31.6 (20-46)	51.5±24.3 (3-100)	-	-	-
16	*Strongylus edentatus*	DD+N	36.6 (23-50)	61.5±30.3 (1-122)	-	-	-
17	*Delafondia vulgaris*	DD+N	18.3 (11-31)	74.50±12.02 (66-83)	13.3 (12-30)	45.0±12.5 (6-92)	0.69
18	*Parascaris equorum*	DD+N	46.7 (33-61)	2.0±0.5 (1-3)	22.2 (12-41)	1.5±0.3 (1-2)	0.33
19	*Oxyuris equi*	DD+N	33.3 (21-48)	3.5±0.8 (2-5)	26.7 (14-44)	1.5±0.3 (1-2)	0.73
20	*Habronema muscae*	DD+N	20.0 (11-34)	20.50±23.33 (4-37)	15.5 (11-34)	20.3±2.69 (6-42)	0.74
21	*Habronema microstoma*	DD+N	15.0 (10-29)	26.0±9.68 (9-43)	11.1 (9-30)	24.6±4.33 (3-55)	0.71

№	Helminth species	Detection method	Horse		Donkey		OR donkey vs. horse
			Prevalence % (95% CI)	Mean intensity±SD (range)	Prevalence % (95% CI)	Mean intensity±SD (range)	
22	*Drascheia megastoma*	DD+N	8.3 (6-21)	32.5±6.26 (21-44)	6.7 (7-21)	32.4±4.85 (5-60)	0.79
23	*Physocephalus sexalatus*	DD+N	-	-	20.0 (10-37)	3.5±2.68 (2-19)	-
24	*Gongylonema pulchrum*	DD+N	15.0 (9-26)	22.5±7.20 (7-38)	11.1 (9-26)	16.7±3.60 (3-36)	0.71
25	*Setaria equina*	N	20.0 (13-45)	2.5±0.8 (1-4)	13.3 (12-38)	5.0±2.0 (1-9)	0.62
Total number of species:		-	24		19		-

Note: "-" OR not calculated due to zero prevalence in one host group; DD – diagnostic deworming; N – necropsy.

The odds ratios (ORs) were used to descriptively characterize the association between host group and the prevalence of individual helminth species. The highest OR values were observed for *Cyathostomum coronatum* (OR=2.97), *Cylicocyclus auriculatus* (OR=2.76), and *Cylicocyclus nassatus* (OR=2.00), indicating higher observed prevalence of these species in donkeys than in horses. An OR below 1 was observed for several species, with the lowest value recorded for Parascaris equorum (OR=0.33), reflecting lower observed prevalence in donkeys. Several helminth species were detected exclusively in one host group: *Taenia hydatigena* larvae, *Cylicocyclus leptostomum*, *Triodontophorus brevicauda*, *T. tenuicollis*, *Strongylus equinus*, and *S. edentatus* were detected only in horses, whereas *Physocephalus sexalatus* was detected only in donkeys. For these species, OR was not calculated because of zero prevalence in one host group.

The results demonstrate distinct differences in the helminth fauna of horses and donkeys from Central Uzbekistan. Horses were characterized by greater species diversity and higher observed prevalence of several large strongylids and *Parascaris equorum*, whereas several small strongylid species, particularly *Cyathostomum coronatum*, *Cylicocyclus auriculatus*, and *Cylicocyclus nassatus*, were more frequently detected in donkeys.

Given the large number of species identified, representatives of the most widespread genera characteristic of the helminth fauna under study were selected to illustrate their morphological features. The anterior ends of representatives of the examined genera differ in the structure of the buccal apparatus. In *Cylicocyclus*, the posterior margin of the buccal capsule has a ring-shaped thickening, whereas this structure is absent in *Cyathostomum*. In *Triodontophorus*, the buccal capsule is well developed and contains three prominent teeth projecting into the buccal capsule from the esophageal funnel. In *Strongylus*, the buccal capsule is large and thick-walled, with four well-developed teeth. In *Habronema*, the mouth opening is surrounded by two trilobed lips that are not separated from the body by a constriction.

In *Setaria*, the anterior end bears four prominent cephalic papillae, and the mouth is surrounded by a chitinous ring (Fig. 2).

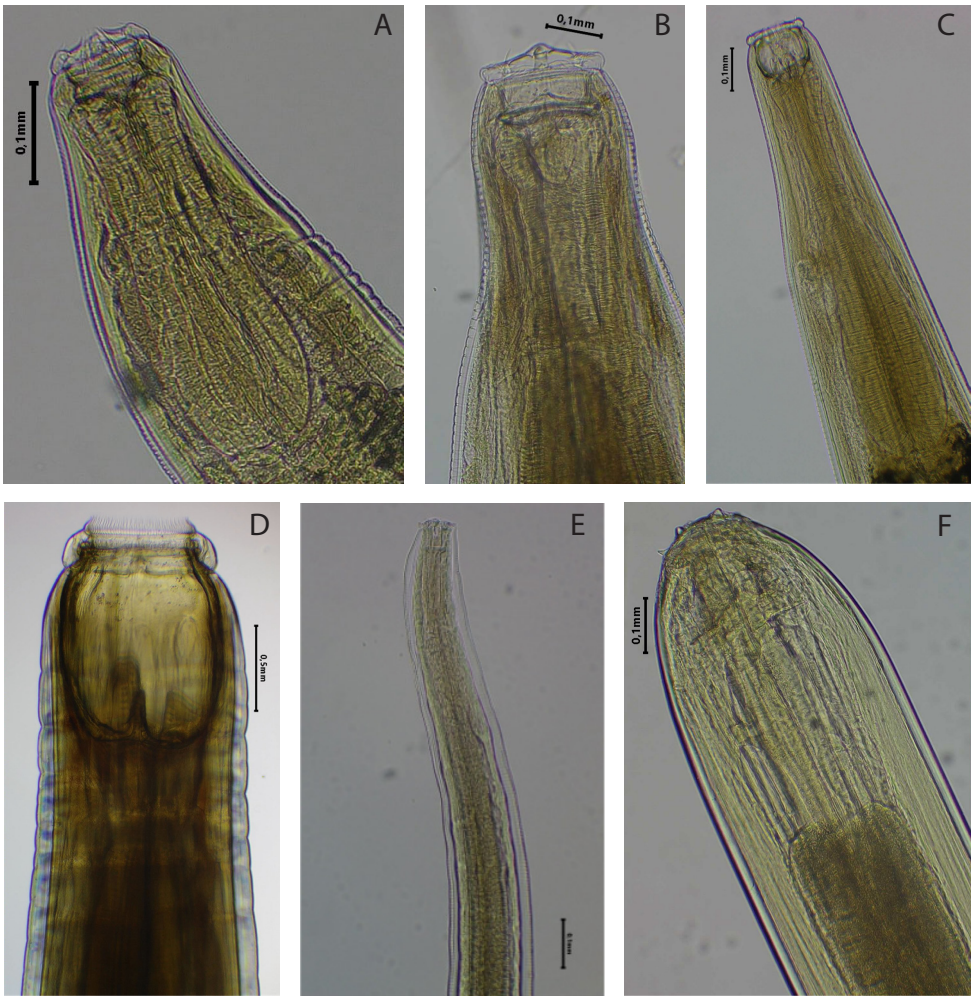


Figure 2. **A** – Cyathostomum Molin, 1861; **B** – Cylicocyclus Ihle, 1922; **C** – Triodontophorus Looss, 1902; **D** – *Strongylus* Mueller, 1861; **E** – *Habronema* Diesing, 1861; **F** – *Setaria* Viborg, 1795.

Because *Cyathostomum catinatum* was characterized by high prevalence and infection intensity and was one of the dominant species in donkeys, this species was selected for molecular genetic analysis, despite the higher prevalence of *Parascaris equorum* (46.7%) in horses. The selection of *C. catinatum* was based on its detection in both horses and donkeys, which allowed a comparative molecular genetic analysis of isolates obtained from the two host species. In addition, *C. catinatum* (42.2%)

was the dominant species in donkeys, further supporting its selection for molecular genetic analysis. (Fig. 3).

To confirm the species identity of *Cyathostomum catinatum* collected from a horse and a donkey in Central Uzbekistan, a phylogenetic analysis based on ITS-2 sequences of ribosomal DNA was performed. The obtained sequences were compared with reference sequences of *C. catinatum* available in the GenBank database, including isolates from Uzbekistan, Iran, and China obtained from horses (*Equus caballus*) and donkeys (*Equus asinus*). In the resulting phylogenetic tree, the analyzed sequences of *C. catinatum* formed a common species-specific cluster, separated from the other investigated representatives of the subfamily Cyathostominae.

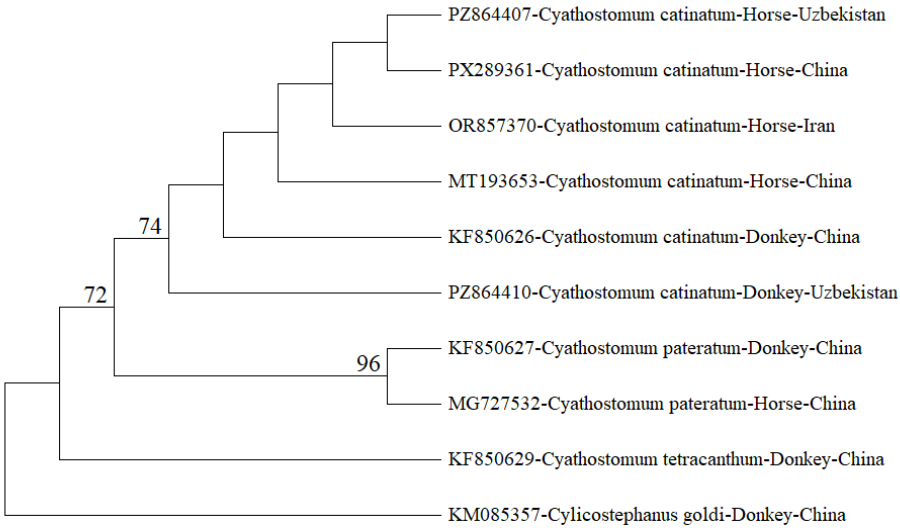


Figure 3. Phylogenetic tree of *Cyathostomum catinatum* constructed using the Maximum Likelihood method.

The sequence obtained from a horse in Uzbekistan (PZ864407) was located within the *C. catinatum* cluster and showed close phylogenetic relationships with sequences of *C. catinatum* obtained from horses in China (PX289361) and Iran (OR857370). The sequence obtained from a donkey in Uzbekistan (PZ864410) was also positioned within the *C. catinatum* cluster, together with reference sequences obtained from horses and donkeys in China. The Uzbek sequences therefore remained within the same species-specific phylogenetic group despite occupying different positions within the cluster. The sequences of *Cyathostomum pateratum* from a donkey and a horse in China formed a separate, well-supported clade with a bootstrap value of 96%. *Cyathostomum tetracanthum* occupied a separate position relative to the *C. catinatum* and *C. pateratum* groups. *Cylicostephanus goldi* formed the most distinct branch and was used as an outgroup for phylogenetic analysis.

The bootstrap values of 72% and 74% supported the major internal nodes separating the principal groups. Thus, the phylogenetic analysis based on ITS-2 sequences supported the species identification of the investigated Uzbek isolates as *Cyathostomum catinatum*.

Discussion

The obtained results indicate a high diversity of helminth species in equids from Central Uzbekistan. A total of 25 helminth species were recorded in the studied sample, of which 24 species were identified in horses and 19 in donkeys. The parasite community was characterized by a predominance of nematodes, particularly representatives of the family Strongylidae and subfamily Cyathostominae, as well as the presence of *Parascaris equorum*, *Oxyuris equi*, representatives of Habronematidae, *Anoplocephala magna*, *Fasciola gigantica*, *Echinococcus granulosus* larvae, and *Setaria equina*. The observed structure of the helminth fauna generally corresponds to the characteristic features of parasite communities of equids described for Central Asia and other regions.

In horses, the highest prevalence was recorded for *Parascaris equorum* (46.7%), *Triodontophorus serratus* (43.3%), *Strongylus edentatus* (36.6%), *Oxyuris equi* (33.3%), and *Strongylus equinus* (31.6%). In donkeys, representatives of Cyathostominae predominated, including *Cyathostomum catinatum* (42.2%), *C. coronatum* (40.0%), *Cylicocyclus auriculatus* (35.5%), and *C. nassatus* (33.3%).

The obtained molecular genetic data support the phylogenetic relatedness of *Cyathostomum catinatum* detected in equids from Central Uzbekistan. In the present study, the *C. catinatum* sequences obtained from a horse and a donkey from Central Uzbekistan (PZ864407 and PZ864410, respectively) were positioned within the same *C. catinatum* cluster together with reference sequences of this species from Iran and China. The position of the investigated sequences within the phylogenetic tree supports their affiliation with *C. catinatum* and indicates their phylogenetic relatedness to isolates from different geographic regions. A similar molecular genetic approach was previously applied in the study of nematodes of domestic dogs and cats in Karakalpakstan, where differences among isolates of the dominant species Toxascaris leonina from different hosts were identified and their phylogenetic relationships were established (Akramova et al. 2024).

The obtained data are preliminary with regard to the population structure of *C. atinatum* isolates obtained from horses and donkeys. The phylogenetic tree demonstrates that the Uzbek isolates occupy different positions within the *C. catinatum* cluster, while remaining within the same species-specific group.
Molecular analyses are ongoing. The obtained results on the helminth fauna of equids show considerable similarity to data reported from Kazakhstan. In the northern and central regions of Kazakhstan, nematodes of the suborders Strongylata, Ascaridata, and Oxyurata also predominate in horses. In a recent study the prevalence of strongylid infections ranged from 54.5-78.7%, that of Pa-

rascaris equorum from 9.1-44.6%, and that of *Oxyuris equi* reached up to 32.4% (Zhanabayev et al. 2026). The prevalence of *P. quorum* in horses in Central Uzbekistan (46.7%) slightly exceeded the maximum value reported for the surveyed regions of Kazakhstan. At the same time, the prevalence of *O. equi* in our study (33.3%) was practically comparable to the maximum values reported for Kazakhstan.

The helminth fauna of horses in Tajikistan is characterized by an even higher representation of gastrointestinal nematodes. According to published data, horses were found to harbor *Parascaris equorum*, *Strongyloides westeri*, *Strongylus equinus*, *Alfortia edentatus*, *Delafondia vulgaris*, representatives of Cyathostominae, as well as *Anoplocephala magna* and *A. perfoliata* (Shodmonov 2019).

For Turkmenistan, published quantitative data specifically on the helminths of domestic horses remain considerably limited. However, studies of the helminth fauna of the Turkmen kulan are important for understanding the regional structure of parasite communities. A study of kulans from Badhyz and Askania-Nova identified 42 helminth species, of which 34 belonged to the family Strongylidae. The authors noted considerable similarity between the helminth fauna of the kulan and the parasite communities of other representatives of the Equidae (Dvoinos et al. 1992). This finding indicates similarities in the ecological conditions governing the circulation of major soil-transmitted helminths in the steppe and semi-desert regions of Central Asia. Overall, the comparison demonstrates that the parasite community of horses and donkeys in Central Uzbekistan shows pronounced similarity to the helminth fauna of Equidae from other regions of Central Asia. The main common components include Strongylidae, Cyathostominae, *Parascaris equorum*, *Oxyuris equi*, *Anoplocephala* spp., and some representatives of Habronematidae. At the same time, the prevalence of individual species varied considerably among regions. The most pronounced differences were observed for *P. equorum*.

An important feature of our study was the difference in prevalence patterns between the two host groups. In horses, *P. equorum*, *T. serratus*, *S. edentatus*, and *S. equinus* were among the more frequently detected species, whereas *C. coronatum*, *C. auriculatus*, *C. nassatus*, and *C. catinatum* were more frequently detected in donkeys.

Conclusion

As a result of the study, 25 helminth species were identified in equids from Central Uzbekistan. A total of 24 species were recorded in horses and 19 species in donkeys, indicating a higher species diversity of the helminth fauna in horses.

The helminth fauna of equids was predominantly composed of nematodes of the order Strongylida. In horses, the highest prevalence values were recorded for

Parascaris equorum (46.7%), *Triodontophorus serratus* (43.3%), and *Strongylus edentatus* (36.6%), whereas in donkeys, *Cyathostomum catinatum* (42.2%), *Cyathostomum coronatum* (40.0%), and *Cylicocyclus auriculatus* (35.5%) predominated. The highest infection intensity in horses was recorded for *Fasciola gigantica* – 81.0±28.0 specimens (25-137), *Delafondia vulgaris* – 74.5±12.02 specimens (66-83), and *Cyathostomum catinatum* – 69.5±29.8 specimens (10-129). In donkeys, the highest infection intensity was recorded for *Cylicocyclus nassatus* – 130.5±59.8 specimens (11-250), *Cylicocyclus auriculatus* – 92.0±41.5 specimens (9-175), and *Cyathostomum catinatum* – 87.5±41.3 specimens (5-170).

Molecular genetic analysis confirmed the species identity of *Cyathostomum catinatum* isolated from a horse and a donkey in Central Uzbekistan. The obtained sequences clustered within a single phylogenetic group with reference sequences of *C. catinatum* from China and Iran, confirming the genetic similarity of the Uzbek isolates to representatives of this species from other regions of Asia. The distinct positions of the *C. catinatum* isolates obtained from the horse and donkey within the common species cluster indicate the presence of intraspecific genetic variability.

The obtained data contribute to the knowledge of the helminth fauna of equids in Uzbekistan and may be used in the development of regional measures for the diagnosis, prevention, and control of helminth infections.

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