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Gastrointestinal helminths in brown bears in Erzurum, Türkiye: Biological Bridge, Anthropogenic Threat

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Abstract

Changes in land use, habitat fragmentation, and global climate fluctuations are reshaping pathogen circulation dynamics by increasing the permeability of the interface among wildlife, domestic animals, and humans. In this context, wild mammals play a crucial role as natural reservoirs for parasites and sources of environmental contamination. The primary aim of this study is to microscopically and molecularly identify gastrointestinal helminth eggs detected in bear fecal samples, as well as adult parasites found in two dead bears. *Baylisascaris transfuga* (23.4%), *Uncinaria stenocephala* (3%), and *Dicrocoelium dendriticum* (19.5%) were detected in the 333 fecal samples collected from four locations. Furthermore, *B. transfuga* (in both animals), *U. stenocephala* (in one animal), and *D. dendriticum* (in one animal) were identified following post-mortem examinations. This study suggests that bears may act as reservoirs for parasitic agents, playing an active role in the persistence of pathogens in the environment and their transmission to different hosts. The findings of this study need to be examined from a One Health perspective, which focuses on biological transmission networks within ecosystems rather than on infection foci alone, to assess risks to public and animal health.

1. Introduction

Wildlife infectious diseases are a key research focus for protecting and managing wild animal populations. Additionally, the fact that some pathogens affect both pets and humans in areas where zoonotic pathogens are common underscores their significance [1]. Changes in land use, habitat fragmentation, and climate are increasing the permeability of the human-animal interface and altering the circulation of zoonotic pathogens. These changes are driven not only by direct contact with hosts but also by 'indirect spread' through environmental media such as feces, soil, and water. Therefore, understanding these risks requires a One Health approach that considers pathogen presence, environmental contamination, and the species sustaining ecological circulation [2, 3].

Brown bears (*Ursus arctos*) are Türkiye's largest carnivorous animal, and the total bear population is estimated at 17,500 [4]. It is estimated that between 2,000 and 2,400 individuals live in the most densely populated regions of eastern Anatolia and the Lesser Caucasus. This figure is believed to be increasing daily [5]. Thanks to their extensive home ranges, long lifespans, and omnivorous feeding habits, brown bears are among the 'bridge species' that connect various ecological niches. This biological mobility makes them important indicators of parasitic species and environmental contamination [6]. Although bears play a vital role in providing ecosystem services by dispersing seeds through their feces, this same fecal matter can become a major source of parasitic contamination in agricultural areas, on livestock farms, and in recreational spaces. This highlights the critical intersection between bears' restorative role in the ecosystem and the transmission of zoonotic diseases [7, 8].

Depending on biotic and abiotic factors, infectious forms exhibiting high resistance can remain viable for extended periods in these environmental matrices [2]. The integration of parasite species with high zoonotic potential into this ecological cycle poses a risk of spillover infection at the human-wildlife interface through environmental contamination, independent of direct contact [2, 8].

Studies across Europe have identified numerous helminth species in brown bears. These include *Baylisascaris transfuga*, *Uncinaria* sp., *Diphyllobothrium latum*, *Dicrocoelium* sp., and *Trichuris* sp. [9–12]. *Baylisascaris* spp. is commonly found in both captive and free-roaming bears. Currently, there is no evidence that ascarids are pathogenic or that they can infect non-bear mammals, including humans [11, 13–16]. The species *Ancylostoma* and *Uncinaria* have been found in free-roaming black and brown bears in North America and Eastern Europe, as well as in giant pandas in China [14–17. Due to widespread environmental contamination in sympatric areas, hookworm infections in bears pose a serious risk to humans [18]. There are very few studies on the presence of *Dicrocoelium* spp. in bears, and the pathogenesis of the parasite in this host is not yet fully understood [19–21].

Understanding the dynamics of wildlife-derived parasitic contamination is critical to the development of One Health-focused public health strategies [3]. There is no comprehensive study on the parasite burden of brown bears in Türkiye. This study aims to reveal the gastrointestinal system parasite diversity harbored by brown bears and the distribution of these agents in Erzurum, Türkiye, using microscopic and molecular methods, as human-wildlife interactions become increasingly common.

2. Material and Method

2.1. Study area

Erzurum (39°52'N, 41°17'E) is the largest province in the East Anatolian region (Fig. 1). The province has a predominantly continental climate, and its varied topography and vegetation provide critical habitats for wildlife. The rugged and rocky terrain in the north, combined with the high-altitude forested areas, creates an ideal environment for protecting, feeding and sustaining the region's brown bear

population. This rugged physiographic structure creates micro-ecosystems isolated from human activity and provides safe ecological corridors where the species' biological cycle can continue. The study area covers the districts of İspir, Oltu, Olur, and Tortum in northern Erzurum. These districts share similar geographical and climatic characteristics and are home to high bear populations.

2.2. Sampling

Ethical approval

was obtained from the Atatürk University Animal Research Local Ethics Committee (approval numbers 2025/37). All fieldwork was performed with ethical permits from the General Directorate of Nature Protection and National Parks (approval numbers 2025/19193491).

The sampling period was set between August and October 2025, coinciding with the fruit-ripening period in the region. This timeframe aligns with the period when bears follow their food sources closest to human habitats and use shared areas most intensively.

The sampling locations were selected based on movement routes, wildlife corridors, and feeding routes that bears actively use. In particular, land crossings with fruit trees that bears could consume and areas of shared use between humans and wildlife were prioritized. This approach reveals bears' access routes to these critical resources and allows us to analyze the risk of parasite spread in areas of intense human activity.

Fecal samples were identified by a diameter greater than 3.5 cm and by the presence of components characteristic of bears' omnivorous diet, such as wild fruit, seeds, plant fibers, and bone fragments [22, 23]. This identification was corroborated by footprints and claw marks around the feces. Samples that raised doubts about species identification were excluded from the study. Given the lack of preliminary data on parasite prevalence in brown bears in Türkiye, the study's sample size was calculated using a power analysis with a 95% confidence level, a 5% margin of error, and an expected prevalence of 50%. Based on these parameters, the ideal sample size for the target population of approximately 2,000–2,400 [5] was 323–331. As bear population data are limited, sampling areas were selected from regions with high levels of bear activity, as reported local people (e.g., by farmers and shepherds). A total of 333 fresh fecal samples were collected from the districts of Oltu, Olur, İspir, and Tortum in the northern parts of Erzurum province (Fig. 1). To minimize the risk of repeated sampling from the same individual and ensure the independence of fecal samples, a minimum distance of 2 km was maintained between sampling points, accounting for brown bears' daily movement capacity and habitat-use strategies. Fecal samples with recorded location data were transported to the laboratory in numbered ziblock bags and stored at -86°C for at least seven days.

In addition, the study also included two adult brown bears that were found dead as a result of traffic accidents in the Pasinler and Oltu districts (Fig. 1). Post-mortem examinations were conducted on both animals, and their internal organs were collected. The location and date of collection for each animal were recorded. The internal organs were placed in labeled Ziploc bags and stored at -86°C for at least seven days. This procedure was carried out to inactivate any potential zoonotic pathogens and minimize the risk of laboratory contamination for fecal samples and internal organs [24].

2.4. Microscopic examination

A total of 333 fecal samples were examined microscopically for gastrointestinal helminth eggs using the Benedict sedimentation and Fülleborn flotation methods (saturated NaCl, density: 1.27) [25]. Eggs were identified to the genus level by microscopic examination.

Following the flotation process, a 2-mL sample was carefully aspirated from the supernatant and centrifuged at 190×g for five minutes. The resulting pellet was washed twice with sterile distilled water, resuspended in 100 µl of sterile distilled water, transferred to 1.5 ml microcentrifuge tubes [26], and stored at -20°C until DNA isolation. Adult parasites were collected from the intestines by intestinal scraping and from the internal organs by macroscopic examination. They were identified at the genus and species level using stereo and light microscopes (Nikon SMZ 745T and Nikon Eclipse Ci, both from Japan) in accordance with the relevant taxonomic keys [27, 28]. The adult parasites were preserved in 70% alcohol until molecular analysis.

2.5. Isolation of Genomic DNA

To extract DNA, 25 mg of tissue was collected from the midsection of adult parasites with a sterile scalpel. Before extraction, samples were mechanically fragmented into small pieces to improve lysis efficiency. A commercial DNA extraction kit (G-spin™ Total DNA Extraction Kit, Intron, Korea) was used to extract DNA from adult parasites and eggs, following the manufacturer's recommended protocol. The total DNA was stored at -20°C for molecular analyses.

2.5. PCR Amplification

As part of the molecular characterization of *Baylisascaris* spp. isolates, universal primers (JB3 and JB4.5) targeting the partial mitochondrial COX1 region were used. However, to resolve taxonomic uncertainty arising from high sequence similarity among *Baylisascaris* species and nucleotide overlaps in the GenBank database, an additional PCR analysis targeting the partial ITS region was performed to confirm species identification. Procedures described by Bowles et al. (1994) for the partial COX1 region and by Testini et al. (2011) for the *B. transfuga* ITS region were followed. To identify *Uncinaria* species, the partial ITS-1 and partial ITS-2 regions were amplified directly using the methods of Nadler et al. (2000a, 2000b) [29–32]. The primer pairs used in the study, along with their specific PCR thermal cycling conditions, are detailed in Tables 1 and 2, respectively.

Table 1
Primer sets used for amplifying target genes.

Target gene	Primer name	Species	Sequences (5′ → 3′)	Product size (bp)	Reference
COX I	JB3	*Baylisascaris* spp.	TTTTTTGGGCATCCTGAGGTTTAT	446	Bowles et al. 1992
	JB4.5		TAAAGAAAGAACATAATGAAAATG		
ITSs	18sF	*Baylisascaris transfuga*	ACTGCTGTTTCGAGACCTTTCGAG	1177	Testini et al. 2011
	28sR		TAGCACCTTCTTTGGACTATAGCC		
ITS-1	93	*Uncinaria* spp.	TTGAACCGGGTAAAAGTCG	432	Nadler et al, 2000a
	264		CGTTTTTCATCGATACGCG		
ITS-2	623	*Uncinaria* spp.	ACGTCTGGTTCAGGGTTGTTT	274	Nadler et al, 2000b
	94		TTAGTTTTCTTTCCTCCGCT		

Table 2
Thermal profile of PCR reactions.

Target gene	Primer name	Initial denaturation/time	Denaturation/time	Annealing/time	Extension	Final extension/time	Cycles	Reference
COX I	JB3 JB4.5	94°C/5 min	94°C/30 s	50°C/30 s	72°C/45 s	72°C/7 min	35	Bowles et al. 1992
ITSs	18sF 28sR	94°C/12 min	94°C/30 s	58°C/45 s	72°C/45 s	72°C/7 min	30	Testini et al. 2011
ITS-1	93 264	95°C/5 min	95°C/1 min	54°C/1 min	72°C/1 min	72°C/5 min	33	Nadler et al. 2000a
ITS-2	623 94	95°C/5 min	95°C/1 min	54°C/1 min	72°C/1 min	72°C/5 min	33	Nadler et al. 2000b

2.6. Sequence and Phylogenetic Analysis

Bidirectional sequencing was performed commercially on an ABI PRISM 310 genetic analyzer (Applied Biosystems, Foster City, CA, USA) using PCR primers. The resulting sequences were visually inspected in Finch TV (Geospiza, Inc., Denver, CO, USA), edited, and aligned using BioEdit 7.0 (http://www.mbio.ncsu.edu/BioEdit/bioedit.html). The aligned sequences were compared with those in the GenBank database using the BLASTN program (http://www.ncbi.nlm.nih.gov/BLAST/) to identify *Baylisascaris* and *Uncinaria* species. Next, phylogenetic analyses were conducted with 1000 bootstrap replicates, and molecular characterizations were inferred using the Maximum Likelihood method in MEGA XI [33]. *Baylisascaris transfuga* sequences were registered in the GenBank database with the following accession numbers: PV662150, PV662151, PX688262, PZ245420, PZ245421, PZ383878-PZ383885 (partial COX1 region) and PZ322944-PZ322945 (partial ITSs gene region). The *Uncinaria* species sequences in this study were registered in the GenBank database under the following accession numbers: OQ773535, OQ773536, OQ773537, PZ323259-PZ323261 (partial ITS-1 gene region), OQ773547, OQ773548, OQ773549, and OQ773550 (partial ITS-2 gene region).

3. Results

Microscopic examination of the fecal samples revealed that 82 of 333 samples (24.6%) were infected with at least one species of parasite. Eggs of *Baylisascaris* spp. and *Uncinaria* spp. were detected using the Fülleborn flotation method, whereas eggs of *Dicrocoelium* spp. were detected using the Benedek sedimentation method (Figs. 2h-j). The distribution of the gastrointestinal helmint eggs are as follows: 23.4% (78/333) *Baylisascaris* spp., 3% (10/333) *Uncinaria* spp., and 19.5% (65/333) *Dicrocoelium* spp. The detailed distribution of single and mixed infections identified in the study is summarized in Table 3. All *Baylisascaris* spp. samples were subjected to PCR analysis with two primer sets, and all isolates were identified as *B. transfuga*. Similarly, all *Uncinaria* spp. samples identified microscopically were *U. stenocephala*, as confirmed by sequence analysis.

Table 3
Distribution of helminth eggs detected in fecal samples.

Parasite species	**n**	**N (%)**
Baylisascaris transfuga	333	54 (16.21)
Dicrocoelium dentriticum		40 (12.01)
Uncinaria stenocephala		6 (1.8)
Baylisascaris transfuga + Dicrocoelium dentriticum		23 (6.9)
Baylisascaris transfuga + Uncinaria stenocephala		2 (0.6)
Dicrocoelium dentriticum + Uncinaria stenocephala		2 (0.6)
n: number of fecal samples, N: number of positive samples.		

As a result of the necropsies, parasitic infections were detected in both brown bears. Following post-mortem examinations, the following parasites were identified: *Baylisascaris* spp. (in both animals), *Uncinaria* spp. (in one animal) and *Dicrocoelium* spp. (in one animal) (Figs. 2a-g). These parasites were found in the intestines and bile duct, respectively. No adult parasites were found in any of the other organs. *Dicrocoelium* spp. were identified as *D. dendriticum* based on morphological characteristics (Fig. 2a). *Baylisascaris* spp. and *Uncinaria* spp. were confirmed as *B. transfuga* and *U. stenocephala*, respectively, using morphological and molecular methods.

The Erzurum *B. transfuga* isolates were 99.2% to 100% similar to one another. Comparative analyses using GenBank reference sequences showed that the Erzurum isolates shared 99.7% homology with records from the Asiatic black bear (OR131278, South Korea), the sloth bear (KC543477, Netherlands), and the polar bear (EU628683, China) (Appendix A1). The Erzurum *U. stenocephala* isolates were 100% similar to one another and 99% similar to *U. stenocephala* isolates from island gray foxes (HQ262054 and HQ262055, USA) based on the ITS-1 region (Appendix A2). The isolates obtained in the current study showed 100% similarity to each other and 96% similarity to *U. stenocephala* isolates from wild boars (MT345056, France) in the ITS-2 region (Appendix A3).

4. Discussion

Brown bears are the largest carnivores in Türkiye [34]. With their broad trophic spectrum and high mobility across habitats, they serve as ecological reservoirs and disseminators of numerous zoonotic and non-zoonotic parasites [8]. There is very scarce literature on the gastrointestinal helminth fauna of brown bear populations in Türkiye [35]. This study aimed to investigate gastrointestinal helminths in bears in a region with a high bear population. In this context, the following were detected in fecal samples: 23.4% *B. transfuga*, 19.5% *Dicrocoelium* spp. and 3% *U. stenocephala*. Post-mortem examinations of two bears also revealed the presence of *B. transfuga*, *D. dentriticum*, and *U. stenocephala* adults.

Baylisascaris transfuga is generally considered to be low-pathogenic in bears. However, it has been reported to cause granulomatous peritonitis in a bear cub [36]. Experimental infections in susceptible rodents, such as white mice and Mongolian gerbils, have demonstrated that larvae migrate from various tissues after infection. These larvae subsequently matured to the third stage, resulting in varying degrees of visceral, neural, or ocular larva migrans [37, 38]. However, in experimentally infected chickens, no clinical signs were observed despite the presence of larvae in the tissues [39]. While the zoonotic potential of *B. transfuga* remains unconfirmed, it is thought that all nine species of *Baylisascaris* can cause visceral, ocular, and/or neural larval migration in over 100 species, including birds, mammals, and humans [13]. Since *B. transfuga* was found to cause fatal neurological diseases in a colony of Japanese macaques (*Macaca fuscata fuscata*) [40], the nematode could likely cause serious diseases in other primates, including humans [41]. *Baylisascaris transfuga* (Rudolphi, 1819) has been identified through morphological and genetic analysis in numerous bear species [10, 15, 36, 42–45]. Furthermore, infection with *B. transfuga* has been observed in zoo-kept bears [46–49]. The prevalence of *B. transfuga* in bears varies according to seasonal dynamics, with reported rates ranging from 10.7% to 90.6% [12, 50]. However, no study has examined the presence and prevalence of the

parasite in Türkiye. In this study, *B. transfuga* was detected in high abundance in all sampled regions (23.4%) and two bears subjected to necropsy. Combined with the proximity of brown bears to human habitats and their preference for anthropogenic food sources, the parasite's wide geographic distribution constitutes a strategic risk factor in the dynamics of environmental spread. The behavioral mobility of bears in peridomestic sites, beekeeping areas, and recreational sites near settlements leads to the transport of parasite eggs into these habitats, resulting in significant infection pressure [7, 8]. Given the known high resistance of *B. transfuga* eggs to environmental conditions, it is indicate that the risk of infection in contaminated areas may persist for an extended period. Therefore, *B. transfuga* is not merely a pathogen specific to wildlife, but rather a risk parameter that must be considered in regions with high levels of wildlife-human interaction due to environmental contamination.

In the study, the universal primers JB3 and JB4.5, which target the mitochondrial COX1 region, were used for the molecular diagnosis of *Baylisascaris* spp. isolates. However, it was determined that the initial sequence data exhibited high homology at critical nucleotide positions to the *B. schroederi* and *B. transfuga* reference sequences in GenBank, resulting in taxonomic ambiguity. The literature reports that *B. schroederi*, a parasite of pandas, and *B. transfuga*, a parasite of bears, are closely related at the mitochondrial genome level (particularly in the COX1 and NAD1 regions), and that standard sequence analyses make it difficult to distinguish between these two species [30, 51]. To address this taxonomic complexity and confirm definitive species-level identification of isolates from the Erzurum region, a species-specific PCR protocol was also used in our study. The data obtained using both primers were deposited in the GenBank database as *B. transfuga*.

Six species of hookworms in the genera *Ancylostoma*, *Arthrocephalus*, and *Uncinaria* have been identified in bears [52]. The most important hookworm species in bears is *U. rauschi* [15–16]. *Uncinaria* species are more common in cold climates. Their hosts are domestic and wild carnivores. Infection occurs when third-stage larvae (L3) in the soil enter a suitable host by skin penetration or orally [53]. Four species of *Uncinaria* (*U. yukonensis*, *U. rauschi*, *U. stenocephala*, and *U. ursi*) have been reported in bears [15]. *Uncinaria stenocephala* has been reported in brown bears (*Ursus arctos caucasicus*) living around the Caspian Sea. *Uncinaria yukonensis* has been described as the black bear in North America and Alaska [15, 16, 54, 55]. In addition, Olsen (1968) described a new species of hookworm, *U. rauschi*, found in Alaska in both black and grizzly bears [56]. In the present study, morphological and molecular confirmation of *U. stenocephala* in bears and in environmental fecal samples suggests that this hookworm species occurs naturally in wildlife reservoirs and can spread via environmental contamination. While *U. stenocephala* is primarily recognized as a species that infects dogs and other carnivores, there have been rare reports of cases in humans associated with cutaneous larva migrans and eosinophilic enteritis, indicating the species' zoonotic potential [57]. *Uncinaria stenocephala* adapts well to cold and temperate climates. This increases its persistence in high-altitude and cool regions, potentially raising the risk of transmission in areas where humans, domestic animals, and wildlife intersect [58]. Studies on hookworm infections in bears are limited worldwide. However, the presence of *Uncinaria* species has been reported in brown bears from various geographical regions. Parasitological studies conducted in Japan have detected *Uncinaria* spp. in brown bear feces. However, these identifications were based on morphological findings and were not confirmed at the species level using molecular methods [59]. Similarly, field studies of brown bears in Alaska revealed the presence of *Uncinaria* spp. eggs, which were identified as *Uncinaria* sp. without molecular analysis [60]. Older literature describes infections in bears in North America and Eurasia, referred to as 'northern carnivore hookworm'. It has been noted that these agents are now associated with *U. stenocephala*. However, these studies also lack molecular data [56]. A previous study of brown bears in Türkiye reported parasites only at the genus level, namely *Uncinaria* spp., based on morphological findings [35]. The presence of *Uncinaria* spp. in bears has been detected at rates ranging from 10% to 51.35% [10, 51]. In contrast, there are very few studies on the presence of *U. stenocephala* [15]. In this study, a prevalence of 3% for *U. stenocephala* was detected in the fecal samples examined; furthermore, adult forms identified in one of the two bears subjected to necropsy and the parasitic structures in the fecal samples were molecularly identified. Although the dominant hookworm species in brown bears are generally reported in the literature as *U. yukonensis* and *U. rauchi*, the detection of *U. stenocephala* in this study is particularly noteworthy for its potential public health and societal risks. The overlap between bear habitats and the shared ranges of domestic and wild carnivores creates a suitable environment for interspecies transmission (spillover) of this parasite [7–8]. In particular, this species' resistance to low temperatures allows infectious larvae to remain viable in the soil for extended periods even under the region's harsh climatic conditions, thereby establishing a persistent parasit burden [53]. This environmental risk also poses a threat of cutaneous larva migrans, which could arise from accidental human infections. Such an interaction pattern highlights that bears not only carry their own parasite load but also serve as strategic sentinel species, revealing the silent circulation within the ecosystem.

The fact that a parasite reaches sexual maturity within a host and produces eggs is considered a fundamental indicator that the biological cycle has been completed [27]. In this study, the detection of adult *U. stenocephala* in brown bears and the observation of eggs of this species in fecal samples suggest that brown bears may serve as the final host in the local life cycles of *U. stenocephala*. Although the presence of eggs in the feces of omnivores is sometimes temporary and linked to the consumption of infected prey, directly detecting

adult parasites in relevant systems increases the likelihood that the findings reflect an established host-parasite relationship. These data support the notion that bears may serve as potential reservoirs for these parasites in their wild life cycles.

Dicrocoelium dendriticum is a trematode that requires ants as an obligate second intermediate host to complete its life cycle, and it has a wide host range. The presence of *D. dendriticum* has been reported in a limited number of studies conducted on bears [19–21]. *Dicrocoelium* species were found in bear feces at rates ranging from 3.2% to 71% worldwide [19, 20]. The current study detected adult forms of *D. dendriticum* in the bile ducts of a bear that underwent a post-mortem examination, while *Dicrocoelium* spp. were found in 19.5% of fecal samples. While the morphological characteristics of the eggs were consistent with those of *D. dendriticum*, the findings were recorded as *Dicrocoelium* spp. due to the limitations of microscopic diagnosis for species identification. The involvement of brown bears in this parasitic cycle is directly linked to their opportunistic feeding habits and seasonal tendency towards myrmecophagy. The tendency of brown bears to engage in myrmecophagy is an energy-gaining strategy rather than random behavior. Noyce et al. (1997) found that the seasonal increase in ant consumption was correlated with both pupa density in nests and a decline in the nutritional quality of alternative spring food sources [62]. Studies have shown that bears rely on ants as a vital source of protein until high-energy fruits become available [62, 63]. Brown bears and domestic and wild ruminants share the same grazing areas. This facilitates bidirectional parasite transmission between the sylvatic and domestic cycles of *D. dendriticum* in these shared grazing areas. Bears are not merely passive hosts that become infected solely through myrmecophagy. They are also active biological hosts, dispersing parasite eggs over wide geographic areas thanks to their high mobility. Eggs shed into the environment via bear feces increase the infection burden on intermediate hosts in pastures, thereby ensuring the continuity of the trematode life cycle.

5. Conclusion

In conclusion, this study is the first to comprehensively investigate gastrointestinal helminths in brown bears in Türkiye. The findings suggest that, in addition to their role in ecosystem services, bears may serve as potential biomonitors for tracking the spread of parasites of zoonotic and veterinary importance. Due to their proximity to anthropogenic habitats and extensive home range capacity, bears have emerged as a potential threat in terms of spillover risk. These data underscore the strategic importance of understanding pathogen transmission dynamics in bears, as they are among the strongest biological bridges between wild and domestic life cycles from a comprehensive One Health perspective. The detection of adult worms in the intestines and of eggs in fecal samples in this study supports the conclusion that bears are definitive hosts for *U. stenocephala* rather than incidental hosts where the life cycle is completed. The central role of bears in the biological cycle of these parasites involves actively dispersing them into the environment, which poses potential risks to wildlife and public health. Therefore, the impact of bears as ecological reservoirs on environmental contamination should be considered a critical parameter in regional health management and wildlife control strategies.

Declarations

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Author Contribution

Ridvan Kirman: Conceptualization, Methodology, Formal analysis, Investigation, Data curation, Writing-original draft, Writing-review & editing, Supervision, Resources. Muzaffer Akyuz: Investigation, Formal analysis, Data curation. Salih Dombay: Investigation, Formal analysis. Aybuke Ciplak: Investigation, Formal analysis. Esin Guven: Methodology, Formal analysis, Investigation, Data curation, Writing - original draft, Writing - review & editing. Hamza Avcioglu: Methodology, Formal analysis, Investigation, Data curation, Writing-original draft, Writing-review & editing.

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Data Availability

The DNA sequences generated and analyzed during the current study have been deposited in the NCBI GenBank database under the following accession numbers: PV662150, PV662151, PX688262, PZ245420, PZ245421, PZ322944–PZ322945, PZ323259–PZ323261, PZ383878–PZ383885, OQ773535–OQ773537, and OQ773547–OQ773550.

References

1. Liatis TK, Monastiridis AA, Birlis P, Prousali S, Diakou A (2017) Endoparasites of Wild Mammals Sheltered in Wildlife Hospitals and Rehabilitation Centres in Greece. Front Vet Sci 4:220. https://doi.org/10.3389/fvets.2017.00220
2. Thompson RC (2013) Parasite zoonoses and wildlife: One Health, spillover and human activity. Int J Parasitol 43(12–13):1079–1088. https://doi.org/10.1016/j.ijpara.2013.06.007
3. Destoumieux-Garzón D, Mavingui P, Boetsch G, Boissier J, Darriet F, Duboz P, Fritsch C, Giraudoux P, Le Roux F, Morand S, Paillard C, Pontier D, Sueur C, Voituron Y (2018) The One Health Concept: 10 Years Old and a Long Road Ahead. Front Vet Sci 5:14. https://doi.org/10.3389/fvets.2018.00014
4. Gündoğdu E, Başkaya Ş (2013) Sustainable hunting management sub-working group report. – 1st Forestry and Water Council. Ankara, pp 21–23
5. International Union for Conservation of Nature (IUCN) (2016) Brown bear (*Ursus arctos*). – Red list, Supplementary Information, 26 pages.
6. Bronson E, Spiker H, Driscoll CP (2014) Serosurvey for selected pathogens in free-ranging American black bears (*Ursus americanus*) in Maryland, USA. J Wildl Dis 50(4):829–836. https://doi.org/10.7589/2013-07-155
7. García-Rodríguez A, Albrecht J, Szczutkowska S, Valido A, Farwig N, Selva N (2021) The role of the brown bear *Ursus arctos* as a legitimate megafaunal seed disperser. Sci Rep 11(1):1282. https://doi.org/10.1038/s41598-020-80440-9
8. Herrero-García G, Barroso P, Dashti A, González-Barrio D, Naves J, Fernández-Gil A, Ugarte-Ruiz M, Pérez-Sancho M, Royo LJ, Carmena D, de Miguel A, García-Rodríguez A, Gortázar C, Domínguez L, Balseiro A (2024) Non-invasive surveillance of shared pathogens in the Eurasian brown bear (*Ursus arctos*) human interface. One Health 18:100746. https://doi.org/10.1016/j.onehlt.2024.100746
9. Borka-Vitális L, Domokos C, Földvári G, Majoros G (2017) Endoparasites of Brown bears in eastern Transylvania. Romania Ursus 28(1):20–30. https://doi.org/10.2192/URSU-D-16-00015.1
10. Paoletti B, Iorio R, Traversa D, Di Francesco CE, Gentile L, Angelucci S, Amicucci C, Bartolini R, Marangi M, Di Cesare A (2017) Helminth infections in fecal samples of Apennine wolf (*Canis lupus italicus*) and Marsican brown bear (*Ursus arctos marsicanus*) in two protected national parks of central Italy. Ann Parasitol 63:205–212. https://doi.org/10.17420/ap6303.107
11. Štrkolcová G, Goldová M, Šnábel V, Špakulová M, Orosová T, Halán M, Mojžišová J (2018) A frequent roundworm *Baylisascaris transfuga* in overpopulated brown bears (*Ursus arctos*) in Slovakia: a problem worthy of attention. Acta Parasitol 63(1):167–174. https://doi.org/10.1515/ap-2018-0019
12. Molnár L, Königová A, Major P, Vasilková Z, Tomková M, Várady M (2020) Seasonal Pattern of Prevalence and Excretion of Eggs of *Baylisascaris transfuga* in the Brown Bear (*Ursus arctos*). Animals 10(12):2428. https://doi.org/10.3390/ani10122428
13. Bauer C (2013) Baylisascariosis-infections of animals and humans with 'unusual' roundworms. Vet Parasitol 193(4):404–412. https://doi.org/10.1016/j.vetpar.2012.12.036
14. Aghazadeh M, Elson-Riggins J, Reljić S, De Ambrogi M, Huber D, Majnarić D, Hermosilla C (2015) Gastrointestinal parasites and the first report of *Giardia* spp. in a wild population of European brown bears (*Ursus arctos*) in Croatia. Veterinarski Arhiv 85(2):201–210
15. Catalano S, Lejeune M, Tizzani P, Verocai GG, Schwantje H, Nelson C, Duignan PJ (2015a) Helminths of grizzly bears (*Ursus arctos*) and american black bears (*Ursus americanus*) in Alberta and British Columbia, Canada. Can J Zool 93:765e772. https://doi.org/10.1645/14-621.1
16. Catalano S, Lejeune M, van Paridon B, Pagan CA, Wasmuth JD, Tizzani P, Duignan PJ, Nadler SA (2015b) Morphological variability and molecular identification of *Uncinaria* spp. (Nematoda: Ancylostomatidae) from grizzly and black bears: new species or phenotypic plasticity? J Parasitol 101:182–192. https://doi.org/10.1645/14-621.1
17. Xie Y, Hoberg EP, Yang Z, Urban JF, Yang G (2017) *Ancylostoma ailuropodae* n. sp. (Nematoda: Ancylostomatidae), a new hookworm parasite isolated from wild giant pandas in southwest China. Parasites Vectors 10(277):1–18. https://doi.org/10.1186/s13071-017-2209-2
18. Seguel M, Munoz F, Navarrete MJ, Paredes E, Howerth E, Gottdenker N (2017) Hookworm infection in South American fur seal (*Arctocephalus australis*). Pups Vet Pathol 54:288e297. https://doi.org/10.1177/0300985816677151

19. Bugmyrin SV, Tirronen KF, Panchenko DV, Kopatz A, Hagen SB, Eiken HG, Kuznetsova AS (2017) Helminths of brown bears (*Ursus arctos*) in the Kola Peninsula. Parasitol Res 116(6):1755–1760. https://doi.org/10.1007/s00436-017-5456-4
20. Costa H, Hartasánchez R, Santos AR, Camarão A, Cruz L, Nascimento M, Gomes L, Madeira de Carvalho LM (2022) Preliminary findings on the gastrointestinal parasites of the brown bear (*Ursus arctos*) in the Cantabrian mountains, Spain. Vet Parasitol Reg Stud Rep 100681. https://doi.org/10.1016/j.vprsr.2021.100681
21. Valderrábano Cano E, Penteriani V, Vega I, Delgado MDM, González-Bernardo E, Bombieri G, Zarzo-Arias A, Sánchez-Andrade Fernández R, Paz-Silva A (2024) Influence of seasonality and biological activity on infection by helminths in Cantabrian bear. Int J Parasitol Parasites Wildl 23:100916. https://doi.org/10.1016/j.ijppaw.2024.100916
22. Murie OJ, Elbroch M (2005) Peterson Field Guide to Animal Tracks. (Third Edition). Houghton Mifflin Harcourt Company, NewYork, pp 186–189
23. De Cuyper A, Clauss M, Lens L, Strubbe D, Zedrosser A, Steyaert S, Saravia AM, Janssens GPJ (2021) Grading fecal consistency in an omnivorous carnivore, the brown bear: Abandoning the concept of uniform feces. Zoo Biol 40(3):182–191. https://doi.org/10.1002/zoo.21593
24. Deplazes P, Eckert J (1996) Diagnosis of the Echinococcus multilocularis infection in final hosts. Appl Parasitol 37(4):245–252
25. Garcia LS, Arrowood M, Kokoskin E, Paltridge GP, Pillai DR, Procop GW, Ryan N, Shimizu RY, Visvesvara G (2017) Practical Guidance for Clinical Microbiology Laboratories: Laboratory Diagnosis of Parasites from the Gastrointestinal Tract. Clin Mcrobiol Rev 31:e00025–e00017. https://doi.org/10.1128/CMR.00025-17
26. Demeler J, Ramünke S, Wolken S, Ianiello D, Rinaldi L, Gahutu JB, Cringoli G, von Samson-Himmelstjerna G, Krücken J (2013) Discrimination of gastrointestinal nematode eggs from crude fecal egg preparations by inhibitor-resistant conventional and real-time PCR. PLoS ONE 8(4):e61285. https://doi.org/10.1371/journal.pone.0061285
27. Soulsby (1986) Helminths, Arthropods and Protozoa of Domesticated Animals. 6th Edition. Bailliere Tindall, London
28. Otranto D, Traversa D (2002) A review of dicrocoeliosis of ruminants including recent advances in the diagnosis and treatment. Vet Parasitol 107(4):317–335. https://doi.org/10.1016/s0304-4017(02)00121-8
29. Bowles J, Blair D, McManus DP (1994) Molecular genetic characterization of the cervid strain ('northern form') of *Echinococcus granulosus*. Parasitology 109 (Pt 2): 215 – 21. https://doi.org/10.1017/s0031182000076332
30. Testini G, Papini R, Lia RP, Parisi A, Dantas-Torres F, Traversa D, Otranto D (2011) New insights into the morphology, molecular characterization and identification of *Baylisascaris transfuga* (Ascaridida, Ascarididae). Vet Parasitol 175(1–2):97–102. https://doi.org/10.1016/j.vetpar.2010.09.017
31. Nadler SA, Adams BJ, Lyons ET, DeLong RL, Melin SR (2000a) Molecular and morphometric evidence for separate species of *Uncinaria* (Nematoda: Ancylostomatidae) in California sea lions and northern fur seals: hypothesis testing supplants verification. J Parasitol 86(5):1099–1106. https://doi.org/10.1645/0022-3395(2000)086[1099:MAMEFS]2.0.CO;2
32. Nadler SA, Hoberg EP, Hudspeth DSS, Rickard LG (2000b) Relationships of *Nematodirus* species and *Nematodirus battus* isolates (Nematoda: Trichostrongyloidea) based on nuclear ribosomal DNA sequences. J Parasitol 86(3):588–601. https://doi.org/10.1645/0022-3395(2000)086[0588:RONSAN]2.0.CO;2
33. Tamura K, Stecher G, Kumar S (2021) MEGA 11: Molecular Evolutionary Genetics Analysis Version 11. https://doi.org/10.1093/molbev/msab120. Molecular Biology and Evolution
34. Can ÖA, Togan I (2004) Status and management of Brown bears in Turkey. Ursus 15:48–53. https://doi.org/10.2192/1537-6176(2004)015%3C0048:samobb%3E2.0.co;2
35. Kilinc O, Goz Y, Yilmaz A, Aslan L (2015) First report on heavy *Uncinaria* (*Dochmoides*) sp. (Nematoda: Ancylostomatidae) infection in brown bear (*Ursus arctos*) Cub, in Van province, eastern Anatolian region of Turkey. Kafkas Univ Vet Fak Derg 21:295e297. https://doi.org/10.9775/kvfd.2014.12260
36. Szczepaniak K, Listos P, Lopuszynski W, Skrzypek T, Kazimierczak W (2012) Granulomatous peritonitis in a European brown bear caused by *Baylisascaris transfuga*. J Wildl Dis 48(2):517–519. https://doi.org/10.7589/0090-3558-48.2.517
37. Sato H, Matsuo K, Osanai A, Kamiya H, Akao N, Owaki S, Furuoka H (2004) Larva migrans by *Baylisascaris transfuga*: fatal neurological diseases in Mongolian jirds, but not in mice. J Parasitol 90:774–781. https://doi.org/10.1645/GE-3330
38. Cho S, Egami M, Ohnuki H, Saito Y, Chinone S, Shichinohe K, Suganuma M, Akao N (2007) Migration behavior and pathogenesis of five ascarid nematode species in the Mongolian gerbil Meriones unguiculatus. J Helminthol 81:43–47. https://doi.org/10.1017/S0022149X07212118
39. Papini R, Cavicchio P, Casarosa L (1993) Experimental infection in chickens with larvae of *Baylisascaris transfuga* (Nematoda: Ascaridoidea). Folia Parasitol 40:141–143

40. Sato H, Une Y, Kawakami S, Saito E, Kamiya H, Akao N, Furuoka H (2005) Fatal *Baylisascaris* larva migrans in a colony of Japanese macaques kept by a safari-style zoo in Japan. J Parasitol 91:716–719. https://doi.org/10.1645/GE-3374RN
41. Sapp SGH, Gupta P, Martin MK, Murray MH, Niedringhaus KD, Pfaff MA, Yabsley MJ (2017) Beyond the raccoon roundworm: The natural history of non-raccoon *Baylisascaris* species in the New World. Int J Parasitol Parasites Wildl 6(2):85–99. https://doi.org/10.1016/j.ijppaw.2017.04.003
42. Johnson D, Larter NC, Elkin B, Allaire DG (2013) An opportunistic parasitological and serological examination of nuisance black bears in the Dehcho region of the Northwest Territories. Department of Environment and Natural Resources, Government of the Northwest Territories, Northwest Territories, Canada, pp 1–70
43. Hwang MH, Chin TW, Yu PH (2021) Endoparasites of Formosan black bears (Ursus thibetanus formosanus) during acorn season in Yushan National Park, Taiwan. J Wildl Dis 57:345–356. https://doi.org/10.7589/JWD-D-20-00067
44. Juránková J, Hofmannová L, Frgelecová L, Daněk O, Modrý D (2022) *Baylisascaris transfuga* (Ascaridoidea, Nematoda) from European brown bear (*Ursus arctos*) causing larva migrans in laboratory mice with clinical manifestation. Parasitol Res 121:645–651. https://doi.org/10.1007/s00436-021-07417-z
45. Li L, Chen HX (2023) Further studies on the morphology of *Baylisascaris transfuga* (Rudolphi, 1819) (Nematoda: Ascaridomorpha: Ascarididae) from the polar bear *Ursus maritimus* Phipps (Carnivora: Ursidae). Syst Parasitol 100: 283–289. https://doi.org/10.1007/s11230-023-10087-3
46. Okoshi S, Takashio M, Nakagawa S (1962) *Toxascaris transfuga* (Rudolphi, 1819) Baylis et Daubney 1922, found in captive bears in Japan. Nippon Juigaku Zasshi 24:152–155. https://doi.org/10.1292/jvms1939.24.151
47. Crum JM, Nettles VF, Davidson WR (1978) Studies on endoparasites of the black bear (*Ursus americanus*) in the southeastern United States. J Wildl Dis 14:178–186. https://doi.org/10.7589/0090-3558-14.2.178
48. Asakawa M, Sashika M, Murata K (2005) Measurements of *Baylisascaris transfuga* (Ascarididae: Nematoda) obtained from captive ursid species in a Japanese zoological Park. J Rakuno Gakuen Univ 30:99–101
49. Schaul JC (2006) *Baylisascaris transfuga* in captive and free-ranging populations of bears (family: Ursidae). PhD Thesis, Veterinary Preventive Medicine, Ohio State University, Columbus, Ohio, USA, 205 pp
50. Kim N, Nath TC, Choi T, Kim S, Choe S (2025) Infection status of Baylisascaris transfuga in captive Asiatic black bears (Ursus thibetanus) from three bile farms in South Korea, with molecular analyses. Parasitol Int 104:102992. https://doi.org/10.1016/j.parint.2024.102992
51. Xie Y, Zhang Z, Wang C, Lan J, Li Y, Chen Z, Fu Y, Nie H, Yan N, Gu X, Wang S, Peng X, Yang G (2011) Complete mitochondrial genomes of *Baylisascaris schroederi*, *Baylisascaris ailuri* and *Baylisascaris transfuga* from giant panda, red panda and polar bear. Gene 482(1–2):59–67. https://doi.org/10.1016/j.gene.2011.05.004
52. Seguel M, Gottdenker N (2017) The diversity and impact of hookworm infections in wildlife. Int J Parasitol Parasites Wildl 6(3):177–194. https://doi.org/10.1016/j. ijppaw.2017.03.007
53. Anderson RC (2000) Order Strongylida (the bursate nematodes). In: Anderson RC (ed) Nematode Parasites of Vertebrates. Their Development and Transmission, 2nd edn. CAB International, University, Wallingford, UK, pp 41–229
54. Wolfgang RW (1956) *Dochmoides yukonensis* sp. nov. from the brown bear (*Ursus americanus*) in the Yukon. Can J Zool 34:21–27. https://doi.org/10.1139/z56-003
55. Rausch RL (1961) Notes on the black bear, *Ursus americanus* Pallas, in Alaska, with particular reference to dentition and growth. Z für Saugetierkunde 26:77–107
56. Rogers LL, Rogers SM (1974) Parasites of Bears: A Review. Third International Conference on Bears. 411–430
57. Bowman DD, Montgomery SP, Zajac AM, Eberhard ML, Kazacos KR (2010) Hookworms of dogs and cats as agents of cutaneous larva migrans. Trends Parasitol 26(4):162–167. https://doi.org/10.1016/j.pt.2010.01.005
58. Traversa D (2012) Pet roundworms and hookworms: A continuing need for global surveillance. Parasites Vectors 5:91. 10.1186/1756-3305-5-91
59. Moriyoshi M, Hayashi N, Nonaka N, Nakao R, Yamanaka M, Tsubota T, Shimozuru M (2025) Patterns of intestinal parasite prevalence in brown bears (*Ursus arctos*) revealed by a 3-year survey on the Shiretoko peninsula, Hokkaido, Japan. Int J Parasitol Parasites Wildl 26:101048. https://doi.org/10.1016/j.ijppaw.2025.101048
60. Kutz SJ, Hoberg EP, Polley L, Jenkins EJ (2008) Global warming is changing the dynamics of Arctic host–parasite systems. Int J Parasitol 38(12):1361–1373. https://doi.org/10.1098/rspb.2005.3285
61. Haynes E, Coker S, Yabsley MJ, Niedrighaus KD, Ramey AM, Verocai GG, Hilderbrand GV, Joly K, Gustine DD, Mangipane B, Leacock WB, Crupi AP, Cleveland CA (2023) Survey for Selected Parasites in Alaska Brown Bears (Ursus arctos). J Wildl Dis 59(1):186–191.

https://doi.org/10.7589/JWD-D-22-00070
62. Noyce KV, Kannowski PB, Riggs MR (1997) Black bears as ant-eaters: seasonal associations between bear myrmecophagy and ant ecology in north-central Minnesota. Can J Zool 75:1671–1686. https://doi.org/10.1139/z97-794
63. Swenson JE, Jansson A, Riig R, Sandegren F (1999) Bears and ants: myrmecophagy by brown bears in central Scandinavia. Can J Zool 77(4):551–561. https://doi.org/10.1139/z99-004

Figures

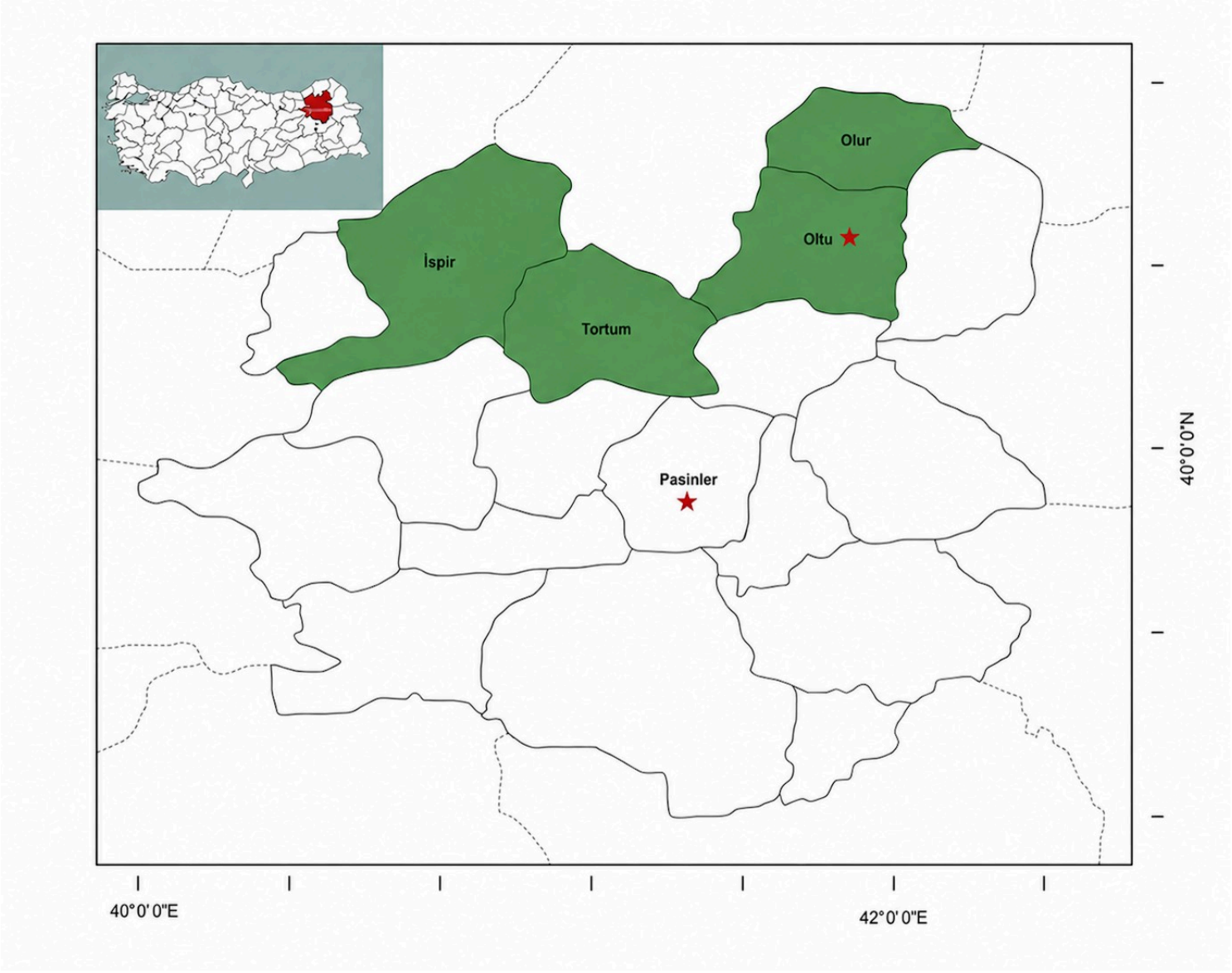


Figure 1

Study area. Green areas: fecal sampling sites, red stars: location of carcasses.

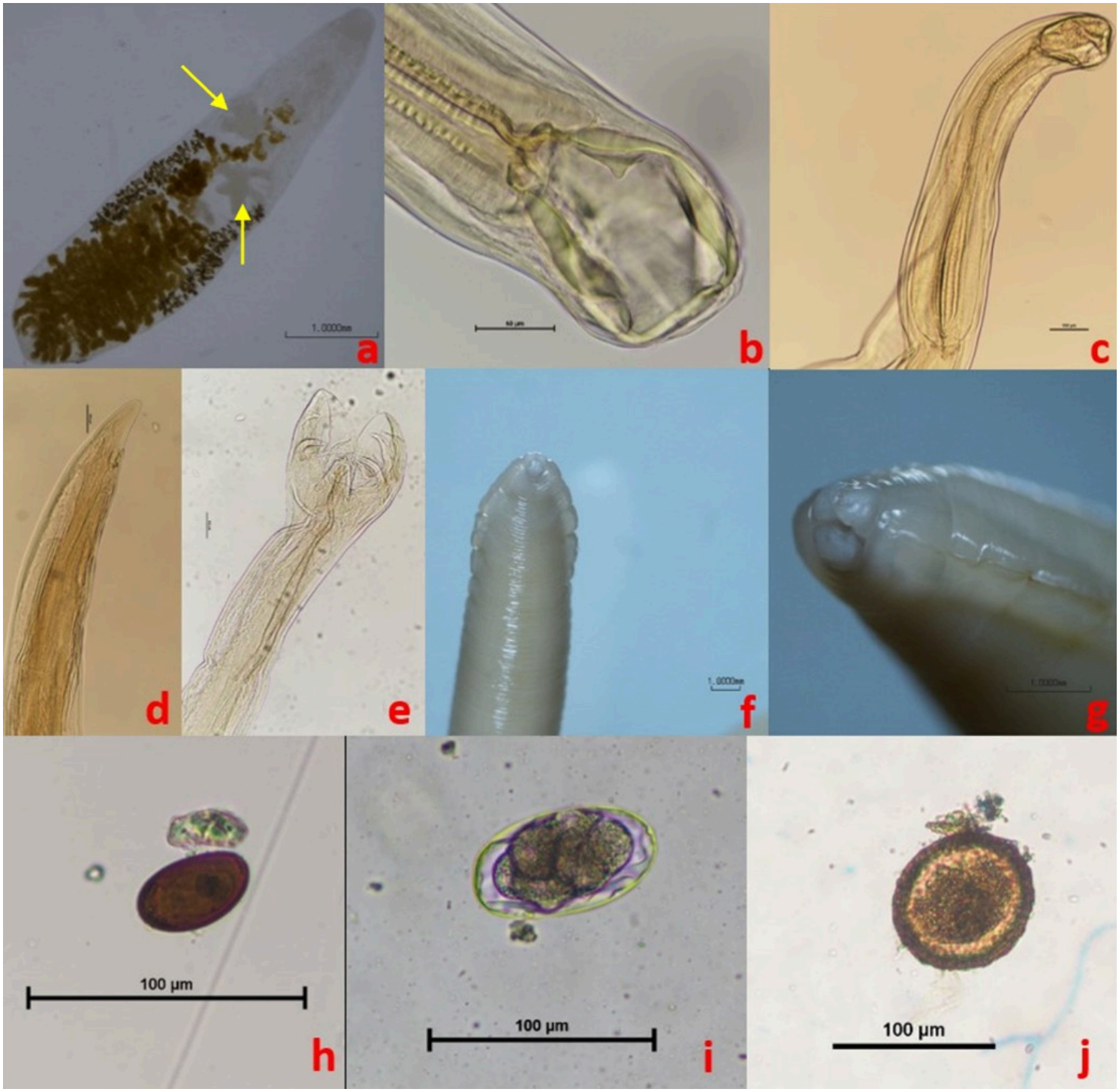


Figure 2

Adults and eggs of *Baylisascaris transfuga, Uncinaria stenocephala*, and *Dicrocoelium dendriticum*. a. *Dicrocoelium dendriticum* (yellow arrows: testes), b. *Uncinaria stenocephala*(buccal capsule, anterior end), c. *Uncinaria stenocephala* (oesophagus, anterior end), d. *Uncinaria stenocephala* (female, posterior end), e. *Uncinaria stenocephala* (male, bursa copulatrix), f. *Baylisascaris transfuga* (anterior end), g. *Baylisascaris transfuga* (lips, anterior end); h. *Dicrocoelium dendriticum* (egg), i. *Uncinaria stenocephala* (egg), j. *Baylisascaris transfuga* (egg).

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