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# Helminth Fauna of Domestic and Wild Ruminants in Garabagh, Azerbaijan

**Elshad Ilyas Ahmadov**, **Reyhan Shoxlat Ibrahimova**, **Zhala Vasif Hasanova**, and **Farida Zohrab Mammadova**

*Living Systems Research Institute Public Legal Entity, Ministry of Science and Education, Republic of Azerbaijan, Baku, 1004, Azerbaijan*

*Corresponding author's Email: paraztitolog@mail.ru

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**ABSTRACT**

Helminth infections represent a significant constraint impacting the health and productivity of ruminants, with their distribution closely associated with ecological and management factors. The present study aimed to investigate the species composition, prevalence, and biocenological characteristics of helminths in domestic and wild ruminants in the Garabakh Economic Region of Azerbaijan. Between 2022 and 2025, a total of 760 animals were examined. Out of these, 620 were domestic ruminants such as cattle, sheep, and goats, whereas the other 140 included wild ruminants such as European roe deer, red deer, Caucasian chamois, wild sheep, and goitered gazelle. Helminth infections were evaluated through standard coprological techniques such as flotation, sedimentation, and larval recovery methods. Species identification was conducted based on morphological characteristics, and faunistic similarity was assessed using the Jaccard index. A total of 29 helminth species were identified, with 18 presented in both domestic and wild hosts. The overall prevalence was 61.7%, with goats demonstrating the highest infection rate at 74.2%. The most frequently detected species across the total examined population of domestic and wild ruminants were *Fasciola hepatica*, *Moniezia expansa*, *Moniezia benedeni*, *Haemonchus contortus*, and *Trichostrongylus axei*. The high faunistic similarity between cattle and wild sheep, and between goats and Caucasian chamois (Ij = 0.51), indicated active circulation of parasites through shared grazing areas and water sources. Out of the 16 helminth species identified in domestic ruminants, 15 were found in wild hosts. Wild sheep and chamois exhibited the most similar faunal composition. The overall prevalence did not differ significantly between domestic (63.1%) and wild (55.7%) ruminants, with *Fasciola hepatica* detected in both groups. These quantitative results indicated that wild sheep and chamois played an active role in maintaining helminths alongside livestock, highlighting the importance of ecologically integrated surveillance in shared grazing regions.

**Keywords:** Economic region, Grazing, Helminth, Ruminant

## INTRODUCTION

Wildlife populations serve as important reservoirs for a wide range of infectious agents, including zoonotic parasites. These zoonotic parasites associated with wildlife belonged to different taxonomic groups, including nematodes, cestodes, trematodes, and protozoa (Polley, 2005). Moreover, the infective stages of parasites, such as eggs and larvae, can persist for prolonged periods under suitable environmental conditions, thereby increasing the likelihood of transmission to susceptible hosts (Soulsby, 2012). The role of domestic and wild ruminants in sustaining helminth reservoirs depends on several factors, such as the types and numbers of hosts, environmental conditions, the biological traits of the habitat, and human activities. The epizootic patterns of many diseases, such as helminthiases, are affected by the natural climatic and economic-ecological factors specific to particular regions (Almaksudov et al., 2010; Atayev et al., 2022; Klimova, 2022).

Helminth infections are widespread in domestic and farm animals, causing significant economic damage to the livestock industry (de Araújo, 2023). Helminth infections can modulate host immune responses, often leading to chronic infections that negatively impact animal health and productivity (Hoerauf et al., 2005; Elliott et al., 2007; Maizels and Yazdanbakhsh, 2003).

Recent parasitological studies indicated that helminthiasis remains a major factor undermining the health and productivity of ruminants worldwide (Charlier et al., 2020; de Araújo, 2023; Mendoza-de Gives et al, 2023). Epidemiological and epizootiological screenings conducted across diverse geographical regions confirmed a high prevalence of gastrointestinal helminths in domestic and wild ruminants. A recent meta-analysis examining the global distribution dynamics of *Haemonchus contortus* (*H. contortus*) observed that this nematode exhibited considerable ecological plasticity across small (sheep, goats) and large ruminants and was a predominant species in numerous regions (Ma et al., 2025).



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The higher prevalence of helminth infections observed among juvenile animals compared to adults is generally attributed to the undeveloped acquired immunity. As hosts age and are repeatedly exposed to parasites, their immune responses become stronger, reducing the ability of infective larvae to establish and grow, and ultimately decreasing parasite survival and reproduction (Efremov, 2016). Recent monitoring of domestic ruminants highlighted the substantial economic and epizootic importance of helminthiasis. A large-scale screening in Qazvin Province, Iran, from 2024 to 2025, found helminth infections in 75.35% of sheep, 65.73% of goats, and 24.50% of cattle. The main parasites identified were *Fasciola hepatica* (*F. hepatica*), *Dicrocoelium dendriticum*, and *Nematodirus spathiger* (Hoseini et al., 2025). These findings demonstrated that helminths can cause significant economic losses in modern livestock production systems and restrict animals' ability to reach their full genetic potential. Studies of wild ruminants have demonstrated that the incidence of parasitic infestations differs significantly by host species and ecological and regional characteristics. For instance, in Sub-Saharan African countries, the prevalence rates of gastrointestinal helminths ranged from 1.4% to 100% for nematodes, 0.8% to 100% for trematodes, and 1.4% to 50% for cestodes (Phetla et al., 2024). Conversely, the prevalence of rumen trematodes in wild ruminants ranged from 0.8% to 100%, nematodes from 1.4% to 100%, and cestodes from 1.4% to 50%, indicating that wild fauna play a significant epizootiological role as natural reservoirs of helminth infections (Sibula et al., 2024).

In natural ecosystems, helminths are a key part of parasitic communities and often coexist within intricate parasite populations. Wild ruminants function as significant reservoir hosts, sustaining the circulation of helminth populations and facilitating the transmission of shared parasite species to domestic ruminants within overlapping grazing areas (Winter et al., 2018; Rossi et al., 2019). When wild and domestic ruminants share grazing areas and watering sources, the transmission and interspecific circulation of helminths are facilitated and accelerated. Epidemiological investigations confirmed that several gastrointestinal and pulmonary helminths, including *Ostertagia*, *Trichostrongylus*, and *Haemonchus* species, can be transmitted between domestic and wild ruminants in Austria, with wild ruminants acting as reservoirs within natural sites (Winter et al., 2018).

It has been established that helminth transmission can occur between wild ungulates (European bison, moose, roe deer, red deer, and sika deer) and domestic ruminants (cattle, sheep, and goats; Muromtsev, 2016). Given the shared susceptibility of domestic and wild ruminants to different helminth species and their overlapping grazing environments, comprehensive studies of host-parasite dynamics are essential. Such investigations are particularly critical as ecological and human-related factors can influence transmission patterns, host relationships, and the composition of helminth communities (Morgan and Wall, 2009; Winter et al., 2018). Based on the current study and existing literature, the species composition, prevalence, and biosenological characteristics of helminths were examined in domestic ruminants such as cattle (*Bos taurus taurus*), sheep (*Ovis aries*), and goats (*Capra hircus*), and wild ruminants, including European roe deer (*Capreolus capreolus*), red deer (*Cervus elaphus*), Caucasian chamois (*Rupicapra rupicapra*), wild sheep (*Ovis orientalis*), and goitered gazelle (*Gazella subgutturosa*) in the Garabagh economic region of Azerbaijan. The present study aimed to examine the species composition, distributional characteristics, and biocenotic relationships of helminths in domestic and wild ruminants in the Garabagh economic region of Azerbaijan, identify shared helminth species between domestic and wild hosts, and analyze the mechanisms of helminth circulation in shared grazing regions.

## MATERIALS AND METHODS

### Ethical approval

This study involved only the collection and analysis of fecal samples obtained from domestic and wild ruminants under standard management conditions. No invasive procedures, surgical interventions, experimental treatments, or therapeutic interventions were performed. The Ethics Committee of the Institute for Living Systems Research determined that the study is exempt from formal ethical approval requirements and issued an Ethics Committee Exemption Letter (Decision/Protocol No. EC-AZ-2026-002).

### Study location

The study was conducted between 2022 and 2025 in the Garabagh economic region of Azerbaijan (Figure 1), encompassing natural and anthropogenic landscapes. The region is characterized by a highly diverse landscape structure, including lowland semi-deserts, steppe ecosystems, foothill zones, broad-leaved forests, subalpine meadows, and alpine grazing areas. The altitudinal gradient ranges from approximately 100 to 3500 meters above sea level (coordinates of 39°59′21″N 46°54′00″E), creating diverse ecological conditions favorable for the circulation of numerous helminth species and their intermediate hosts. Climate conditions differ from a mild, warm, semi-arid environment in the plains to a cold mountain climate in the high-altitude areas. The annual precipitation ranges from 250 to 800 mm, while the average annual temperature varies between 6°C and 14°C.

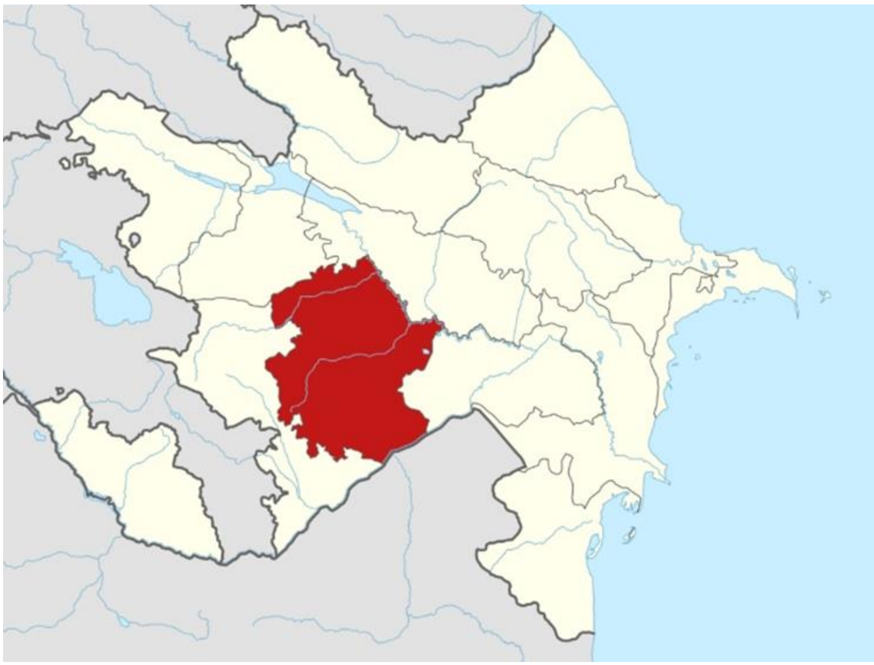

**Figure 1.** The study area of the Garabagh economic region in Azerbaijan (Designed by authors)

**Animals**

The study included 760 ruminants, consisting of 620 domestic animals sampled from farms, herds, or villages within the study area, and 140 wild animals. The domestic ruminants consisted of 220 cattle (*Bos taurus taurus*), 280 sheep (*Ovis aries*), and 120 goats (*Capra hircus*). Fecal samples from domestic and wild ruminants were collected non-invasively from freshly deposited feces in the environment. Fresh fecal samples were collected from cattle on a convenience sampling basis during visits to a total of 55 privately owned farms. Samples were collected immediately after spontaneous defecation from the first eligible animals observed, whenever possible, to minimize environmental contamination, and were transferred into sterile containers for laboratory analysis. No animals were captured, physically restrained, handled, or sedated during the sampling process.

Among the cattle, 65 were less than 1 year old, 72 were 1 to 3 years old, and 83 were over 3 years old, including 88 males and 132 females. Among the sheep, there were 90 young, 95 subadults, and 95 adults; of these, 102 were males and 178 females. The goat population included 32 young, 39 subadults, and 49 adults, with 41 males and 79 females.

The study also included 140 wild ruminants representing five species naturally occurring in the Garabagh region. These animals were represented by fecal samples collected non-invasively from naturally occurring populations during field surveys, rather than from captured or handled animals. They comprised 35 European roe deer (*Capreolus capreolus*), 20 red deer (*Cervus elaphus*), 25 Caucasian chamois (*Rupicapra rupicapra*), 30 wild sheep (*Ovis orientalis*), and 30 goitered gazelles (*Gazella subgutturosa*). Data on wild animals were obtained through field surveys and non-invasive sampling methods (fecal collection). This methodology facilitated a more comprehensive evaluation of the species composition and distribution patterns of the helminth fauna within wild ruminant populations.

**Sample collection and parasitological examination**

Field surveys were conducted across grazing areas, mountain pastures, watering points, migration routes, forest edges, and natural shelters used by domestic and wild ruminants. Fresh fecal samples from domestic ruminants were collected immediately after defecation from freshly deposited feces. For wild ruminants, samples were obtained non-invasively from freshly deposited feces identified in the field by their fresh appearance and additional field indicators (Schilling et al., 2022). Approximately 20-30 g of fecal material was placed into sterile, labeled plastic containers. Samples were transported under refrigerated conditions to the Parasitology Laboratory, Institute for the Study of Living Systems, Baku, Azerbaijan, and examined within 24-48 hours after collection.

Parasitological examinations were performed using standard qualitative and quantitative helminthological techniques widely applied in veterinary parasitology. During the initial processing of samples, sequential washing procedures were employed, followed by quantitative flotation examinations using the McMaster technique, the most widely used method for estimating parasite egg counts in feces (Gordon and Whitlock, 1939; Cringoli et al., 2004). Larval recovery was performed using the Baermann technique, a widely applied method for the isolation of nematode larvae from fecal and herbage samples based on the original description by Baermann (1917) as modified by Persson

(1974). Sedimentation procedures were conducted according to the formalin-ethyl acetate sedimentation technique, a standard concentration method in clinical parasitology first validated by Truant et al. (1981). Additionally, the pasture helminthological assessment method developed by Kotelnikov (1984) was employed to evaluate environmental contamination and the circulation of infective stages in grazing areas. Helminth eggs, larvae, and other diagnostic stages were identified under a light microscope (Carl Zeiss Axio Lab.A1, Germany) at 10x and 40x magnifications based on their morphological characteristics. Identification was performed according to established parasitological keys and published descriptions (Taylor et al., 2016).

The prevalence and abundance of helminth infections were calculated using established epidemiological indices commonly applied in parasitological studies. The faunistic similarity between helminth communities of domestic and wild ruminants was assessed using the Jaccard similarity index (Poulin, 2003).

### Statistical analysis

The prevalence (%) and abundance indices of helminths in the examined animals were calculated using standard parasitological formulas, where prevalence was defined as the proportion of infected hosts and abundance as the average number of parasites per examined host, according to Bush et al. (1997) and Rózsa et al. (2000). The similarity between the helminth faunas of domestic and wild ruminants was evaluated using the Jaccard similarity index. Differences were considered statistically significant at a p-value less than 5% ($p < 0.05$). The Wilson score method was used to calculate the 95% confidence intervals for prevalence. All statistical calculations were performed using the IBM SPSS Statistics software package (version 26, IBM Corp., Armonk, NY, USA).

## RESULTS AND DISCUSSION

In the present study, 29 helminth species were identified in domestic and wild ruminants, of which 18 species were common to both host groups (Table 1).

**Table 1.** Prevalence of helminth infections in domestic and wild ruminants examined in the Garabagh economic region of Azerbaijan (2022-2025)

| Host species | Examined (number) | Infected (number) | Prevalence (%) |
|---|---|---|---|
| Cattle | 220 | 118 | 53.6 |
| Sheep | 280 | 184 | 65.7 |
| Goats | 120 | 89 | 74.2 |
| Roe deer | 35 | 18 | 51.4 |
| Red deer | 20 | 11 | 55.0 |
| Chamois | 25 | 17 | 68.0 |
| Wild sheep | 30 | 20 | 66.7 |
| Gazelle | 30 | 12 | 40.0 |
| Total | 760 | 469 | 61.7 |

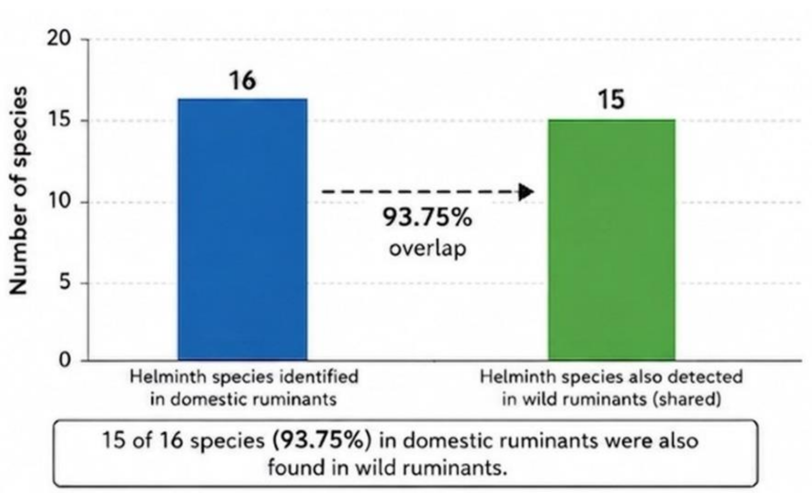


**Figure 2.** Comparison of helminth species abundance and shared taxa between domestic and wild ruminants

The high proportion of shared parasite species, given the use of common grazing areas and water sources, indicated a persistent circulation of helminths between domestic and wild ruminants. In the current study, 15 of the 16 helminth species identified in domestic ruminants were also found in wild ruminants (Figure 2), indicating a considerable level of faunistic overlap. The current findings indicated that shared grazing environments played an important role in the transmission of helminths among different host groups, as supported by Winter et al. (2018) and Rossi et al. (2019).

A total of 16 helminth species were identified in domestic ruminants and 15 in wild ruminants. Of these, 15 species were common to both domestic and wild ruminants, representing 93.75% species overlap, while one species was found exclusively in domestic ruminants. Faunistic similarity indices indicated significant overlap in helminth communities between domestic and wild ruminants, particularly between goats and Caucasian chamois (Ij = 0.51) and between cattle and wild sheep (Ij = 0.57), highlighting the importance of shared habitats in parasite transmission (Table 2).

**Table 2.** Jaccard similarity index results between helminth communities of domestic and wild ruminants in Garabagh economic region of Azerbaijan (2022-2025)

| Host pair | Shared species (number) | Jaccard index (Ij) |
|---|---|---|
| Cattle – Wild sheep | 8 | 0.57 |
| Goat – Caucasian chamois | 7 | 0.51 |
| Sheep – Roe deer | 6 | 0.43 |
| Sheep – Red deer | 5 | 0.38 |
| Goat – Gazelle | 4 | 0.31 |
| Cattle – Roe deer | 5 | 0.36 |

In total, 469 of the 760 examined ruminants (61.7%) were infected with at least one helminth species. The prevalence differed notably among host species, from 40.0% in goitered gazelles (*Gazella subgutturosa*) to 74.2% in domestic goats (*Capra hircus*). Host species and infection status were found to be highly significantly associated ($\chi^2$ = 24.546, df = 7, $p < 0.001$), indicating that helminth prevalence differed across domestic and wild ruminants within the Garabagh economic region of Azerbaijan. Pairwise comparisons, employing the Bonferroni correction, demonstrated that the prevalence in domestic goats (74.2%) was significantly greater than that observed in gazelles (40.0%; $\chi^2$ = 12.737, df = 1, $p < 0.001$). No other pairwise differences were statistically significant after correction. Notably, there was no significant difference in overall prevalence between domestic ruminants (391/620, 63.1%) and wild ruminants (78/140, 55.7%; $\chi^2$ = 2.614, df = 1, $p > 0.05$), indicating similar helminth circulation across the wildlife-livestock interface. The Jaccard similarity indices ranged from 0.31 to 0.57 (Table 2). A moderate to substantial similarity was observed between cattle and wild sheep (Ij = 0.57), and between domestic goats and Caucasian chamois (Ij = 0.51). These findings indicated that active helminth distribution occurred in shared grazing regions and at water sources.

In the current study, 16 helminth species were identified in domestic ruminants, comprising one trematode species (*F. hepatica*), two cestode species, including *Moniezia expansa* (M. *expansa*) and *Moniezia benedeni* (*M. benedeni*), and 13 nematode species. The majority of the identified species were Nematoda, including *Chabertia ovina*, *Bunostomum trigonocephalum*, *Oesophagostomum venulosum*, and *Trichostrongylus axei*, which were detected in both domestic and wild ruminants, highlighting the dominance of gastrointestinal nematodes within the studied host populations. These findings were consistent with previous reports indicating that nematodes constitute the largest component of the regional helminth fauna (Kolesnichenko, 1969). The present study indicated that many gastrointestinal nematodes were not host-specific and could circulate between wild and domestic ruminants. Similar host associations have previously been reported for ruminants in Azerbaijan, indicating that common grazing areas could promote the spread and persistence of these parasites between wildlife and livestock (Ahmedov et al., 2025). Several helminth species identified during the survey exhibited host-specific distributions and were recorded only in domestic ruminants. In contrast, most of the detected helminths were shared between domestic and wild host populations. This pattern indicated that although some host-associated species were present, the helminth communities of domestic and wild ruminants in the Garabagh region of Azerbaijan were primarily interconnected. Consistent with the current findings, Rossi et al. (2019) identified several shared parasite species, indicating that common grazing habitats facilitate parasite circulation at the wildlife-livestock interface.

In the 1960s, Kolesnichenko (1969) carried out comprehensive helminthological examinations of 75 sheep from diverse districts within the Mountainous Garabagh region of Azerbaijan, and recorded 52 helminth species, which included three trematodes, seven cestodes, and 42 nematodes. Recent helminthological investigations conducted within the Garabagh economic zone of Azerbaijan, including farms in Agjabadi and Barda districts, have identified 16 helminth species in domestic ruminants such as sheep, goats, and cattle for the first time. The identified parasite species included

*F. hepatica* (Linnaeus, 1758), *M. expansa* (Rudolphi, 1810) Blanchard, 1891, *M. benedeni* (Moniez, 1879) Blanchard, 1891, *Chabertia ovina* (Fabricius, 1788), *Strongyloides papillosus* (Wedl, 1856), *Bunostomum trigonocephalum* (Rudolphi, 1808) Railliet, 1902, *Oesophagostomum venulosum* (Rudolphi, 1809) Railliet and Henry, 1913, *Trichostrongylus axei* (Cobb, 1879), *Trichostrongylus carpicola* Ransom, 1907, *Ostertagia ostertagi* (Stiles, 1892), *Ostertagia circumcincta* (Stadelmann, 1894) Ransom, 1907, *Ostertagia occidentalis* Ransom, 1907, *H. contortus* (Rudolphi, 1803), *Nematodirus spathiger* (Railliet, 1896), *Trichocephalus* (*Trichuris*) *ovis* (Abildgaard, 1795), and *Trichocephalus* (*Trichuris*) *skrjabini* (Baskakow, 1924). Among the examined domestic ruminants, cattle demonstrated the greatest helminth species diversity, hosting all 16 species identified in the present study.

According to the helminthological investigations in the Agjabadi and Barda districts of Azerbaijan, the following species were identified in cattle, including *F. hepatica*, *M. expansa*, *M. benedeni*, *Strongyloides papillosus*, *Ostertagia ostertagi*, *Nematodirus spathiger*, *Chabertia ovina*, and *Trichostrongylus axei*. In the present study, *F. hepatica*, *Strongyloides papillosus*, *M. expansa*, *M. benedeni*, *Trichostrongylus capricola*, *H. contortus*, *Trichocephalus* (*Trichuris*) *skrjabini*, and *Trichocephalus* (*Trichuris*) ovis were recorded in sheep. In goats, *Ostertagia occidentalis*, *Oesophagostomum venulosum*, *Chabertia ovina*, *Bunostomum trigonocephalum*, *Ostertagia circumcincta*, *H. contortus*, and *Trichostrongylus axei* were detected during the present study.

*Fasciola hepatica*, a zoonotic parasite associated with human fascioliasis, was among the helminths identified in the present study, thereby posing a considerable public health concern. Its detection in both domestic and wild ruminants confirmed that these host populations served as vital reservoirs for the maintenance and distribution of *F. hepatica* within the study area. Additionally, *Strongyloides papillosus* was detected in the present study, a parasite with a broad host range that could have implications for veterinary and public health. The presence of these parasites in domestic ruminants that share grazing areas with wild ruminants underscored the potential epidemiological importance of the wildlife–livestock interface in maintaining parasite transmission cycles (Viney and Lok, 2015; Moreira et al., 2023).

Different helminth groups exhibited distinct transmission strategies, ecological requirements, and distribution patterns determined by host specificity, life-cycle characteristics, and environmental factors (Taylor et al., 2016). However, many helminth species have free-living larval stages that are strongly influenced by climate factors, particularly temperature and humidity, which affect their development, survival, and transmission (O'Connor et al., 2006; Taylor et al., 2016). Consequently, seasonal patterns of helminth infection are commonly observed in grazing animals. The spatial and temporal distribution of these parasites may be shaped by the abundance and dispersal of intermediate hosts and vertebrate reservoir hosts (Morgan and Wall, 2009). Elevations in ambient temperature are expected to alter ecological conditions and accelerate the development of environmentally transmitted parasite stages (Kutz et al., 2005; Fischlin et al., 2007). These changes may promote parasite transmission, ultimately leading to increased infection and reduced productivity in grazing livestock.

The environment in extensively grazed regions could have influenced the *Moniezia* spp. life cycle, thereby sustaining parasite populations in local ruminants. This finding indicated that grazing areas and ecosystems play a vital role in maintaining cestode circulation among domestic and wild ruminant species. The relatively high densities of oribatid mites recorded in the present study, which ranged from 170-350 and 550-1200 individuals/m², indicated that suitable intermediate hosts for *Moniezia* spp. were readily available in the Garabagh economic region of Azerbaijan. The concurrent detection of *M. expansa* and *M. benedeni* in grazing ruminants supported the importance of pasture ecosystems in maintaining parasite transmission. These results indicated that environmental factors and host overlap contributed to the circulation of monieziosis within the Garabagh economic region of Azerbaijan.

In the present study, *M. expansa* and *M. benedeni* were identified in domestic ruminants (sheep, goats, and cattle) from the Garabagh economic region of Azerbaijan. Additionally, these cestodes were identified in wild ruminants, including *Ovis orientalis*, indicating that wild herbivores served as potential reservoirs for *Moniezia* spp. within natural ecosystems. A comparative analysis of host–parasite relationships indicated that wild herbivores, including wild sheep and gazelles, helped maintain helminth transmission in shared grazing areas (Modabbernia et al., 2021). The results of the present study demonstrated that helminth transmission in the Garabagh economic region occurred in mixed grazing areas that included both domestic and wild ruminants. Furthermore, the study of helminth fauna in the Garabagh economic region of Azerbaijan identified 87 helminth species, comprising 19 biohelminths and 68 geohelminths (Asadov, 1960; Kolesnichenko, 1969), reflecting the diversity of parasite transmission strategies in the region. The relatively high prevalence of trematodes and nematodes in domestic ruminants, compared with wild hosts, indicated that livestock played a critical role in maintaining parasite populations in grazing regions.

In domestic ruminants, helminth communities were recorded, ranging from three-species and five-species to multi-species associations. Similarity analysis revealed notable overlap in helminth fauna between goats and Caucasian chamois and between cattle and wild sheep, indicating ecological relatedness among parasite communities across host groups. Lower helminth prevalence was observed in wild ruminants compared with domestic sheep and goats, reflecting differences in host density, grazing intensity, and exposure to contaminated pasture environments. The co-occurrence of domestic and wild ruminants in shared high-mountain summer grazing regions created favorable conditions for parasite transmission and helped maintain helminth circulation in both natural and semi-natural ecosystems. The present findings revealed substantial overlap in helminth species between domestic and wild ruminants, highlighting ecological connectivity among host populations within shared grazing ecosystems.

## CONCLUSION

Among the 16 helminth species recorded in domestic ruminants, 15 were recorded in wild ruminants as well. The most prevalent parasites identified in the present study included *F. hepatica*, *M. expansa*, *M. benedeni*, *H. contortus*, and *Trichostrongylus axei*. The current findings demonstrated that wild ruminants could serve as significant reservoirs of helminths in natural biosemiotic systems, thereby facilitating their transmission to domestic animals. Since ecological and climatic factors greatly influence helminth distribution in biocenoses, it is recommended to regularly monitor helminth infections in both wild and domestic ruminants to effectively manage these infections levels. Additionally, further studies focusing on long-term seasonal patterns and pathways of parasite transmission between domestic and wild ruminants are recommended.

## DECLARATIONS

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### Authors' contributions

Elshad Ilyas Ahmadov conceptualized and designed the study, conducted the field investigations, analyzed the data, and drafted the manuscript. Reyhan Shoxlat Ibrahimova contributed to sample collection, laboratory examinations, and the literature review. Zhala Vasif Hasanova participated in laboratory analyses, data processing, and manuscript editing. Farida Zohrab Mammadova assisted with field investigations, data collection, and manuscript editing. All authors have read, reviewed, and approved the final edition of the manuscript.

### Availability of data and materials

The datasets generated and analyzed during the current study are available upon reasonable request from the corresponding author.

### Competing interests

The authors declare no financial or non-financial competing interests regarding the publication of this article.

### Ethical considerations

The authors confirmed that the present study is original, has not been previously submitted for publication or under review elsewhere, and adheres to ethical standards regarding data integrity and the avoidance of plagiarism. The authors also affirmed that no artificial intelligence tools were used in the writing and preparation of the manuscript. The authors accept full responsibility for the originality of the study before submission and before publication.

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