

Does the presence of livestock in protected areas pose a risk of gastrointestinal parasite transmission to wild ungulates? A study from Bani Wildlife Sanctuary, Western Himalayas

Iyaz Quyoom Wani*, Bilal A. Bhat, Jigmet Zasay, Syed Tanveer

Department of Zoology, University of Kashmir, Srinagar-190006

*Email: Iyazquyoom@gmail.com

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Abstract

The burgeoning population of livestock within protected areas exacerbates the transmission risk of parasitic diseases among vulnerable wild ungulates. This study, conducted in the Bani Wildlife Sanctuary nestled in the western Himalayas, focused on the peak periods of livestock grazing (June-October) in 2021 and 2022 to assess the prevalence of gastrointestinal parasites in domestic sheep and goats. A comprehensive examination involved the collection of 230 faecal samples (125 from goats and 105 from sheep) from various locations within the sanctuary, followed by analysis using established sedimentation and floatation techniques. Our findings revealed the presence of 10 distinct parasite taxa, encompassing one coccidian cyst, one cestode, two trematodes, and six nematodes. Comparative analysis with documented parasites infecting wild ungulates underscores the considerable potential for cross-transmission via the faecal-oral route. Notably, the prevalence of gastrointestinal parasite taxa stood at 83.72% in goats and 74.35% in sheep, indicating their heightened susceptibility and potential contribution to pasture infectivity, surpassing that of wild ungulates. These findings suggest a significantly elevated risk of gastrointestinal parasitic transmission from domestic animals to their wild counterparts. Consistent with comparable studies, evidence suggests a correlation between parasite infection in livestock and sympatric wild ungulates, suggesting the perpetuation of these infections within the shared ecosystem. To mitigate this risk, we advocate for the regulation of anthelmintic treatment for domestic livestock and the implementation of grazing zonation strategies to curtail parasite transmission.

Keywords: Pathogens, prevalence, threats, wildlife, cross-transmission

Introduction

Interactions between livestock and wildlife have increased significantly in recent years due to increased sharing of natural habitat resulting from growing demand for agriculture, grazing, and other anthropogenic activities (Dobson and Foufopoulos, 2001). As a result of these interactions, there has been an increase in competition for food, disease outbreaks, and pathogen transmission which may lead to species hybridization (Foufopoulos et al., 2002; Lafferty, 2003). Parasites are widespread in wildlife and livestock and serve as a main factor in driving mammalian ecology and evolution (Barber and Dingemanse, 2010; Tompkins et al., 2011; Dunn et al., 2012). Even though disease transmission between livestock and wild ungulates can occur in either direction via contaminated soil, vegetation, and water sources (Nunn et al., 2011), the potential consequences of disease transmission from livestock to wildlife are of particular concern due to the threat it may pose to the survival of endangered wild species.

Contrary to the notion of parasites as harmless symbiotic organisms coexisting harmoniously with their hosts, it has been established that they significantly alter the host population by exerting a considerable impact on survival, reproductive capacity, and behaviour (Dobson, 1995). Parasitic diseases are a growing concern for conservation biologists and livestock owners (Dobson et al., 2001; Osofsky, 2005; Delahay et al., 2009, AbdulKarim et al. 2023). Gastrointestinal parasites (particularly helminths) are the leading parasites affecting wildlife and livestock (Petney and Andrews, 1998). These parasites, inhabiting the duodenum, caecum, ileum, and colon of their hosts (Soulsby, 1982) are known to consume essential nutrients, making them weak and susceptible to other diseases (Loukopoulos et al., 2007).

Pathogen transmission from domestic animals to wildlife can result in population declines and/or even local extinction of the wildlife species (Thorne and Williams, 1998; Pedersen and Fenton, 2007; Delahay et al., 2009), and this raises concern more if the species affected happens to be a vulnerable or endangered one (Altizer et al., 2003). The most common way of gastrointestinal parasitic transmission is via the faecal-oral route. The infectious stages of these parasites pass through the faecal matter of the host, survive for a considerable period in the environment, and increase the chances of transmission (Soulsby, 1982).

The detrimental impact of livestock grazing on wild ungulates within the Western Himalayan protected areas has been increasingly recognized as a significant ecological concern (Bhat et al., 2022). This region, characterised by its unique assemblage of mountain ungulates, plays a pivotal role in sustaining the area's vegetation composition and serves as a primary food source for apex predators, notably the snow leopard and common leopard (Khanyari et al., 2021). Given the herbivorous nature of both domestic livestock and wild ungulates, there exists a plausible risk of

gastrointestinal parasitic transmission between these two populations. This risk is compounded by several factors, chief among them being the seasonal habitat overlap between domestic and wild ungulates, which fosters conditions conducive to the spread of diseases.

Gastrointestinal parasitism is a major concern in the livestock industry, causing economic losses and health issues in domestic animals all over the world. However, the potential impacts of parasitic infections carried by domestic livestock on threatened wild ungulates remain an understudied and often neglected aspect of wildlife conservation. The Bani Wildlife Sanctuary (BWLS) in the western Himalayan region provides an ideal habitat for several threatened wild ungulates like Himalayan tahr, serow, goral, and musk deer (Bhatnagar et al., 2007). These ungulates face several threats to their survival, including habitat loss, hunting, and infectious diseases. Given their already critical situation, the potential threat of gastrointestinal parasitism originating from domestic livestock may pose an additional risk to the survival and well-being of these threatened ungulates.

The objective of this study was to examine the parasitic prevalence in domestic livestock and to investigate the risk of interspecific transmission by comparing these parasites with the parasitic species already known at the wildlife-livestock interface in the Himalayan region. This will help in understanding the prevalence and intensity of gastrointestinal parasitism in domestic livestock as a potential threat to wild ungulates in the BWLS. This information can be used to develop targeted interventions and management strategies to limit parasite spread and mitigate the negative effects on ungulate populations. Furthermore, by recognizing the link between domestic livestock and wildlife health, stakeholders can work together to promote sustainable practices that benefit both livestock owners and wild ungulate conservation.

Material and methods

Study area

The newly declared BWLS is nestled in the picturesque landscapes of District Kathua, Jammu and Kashmir. The sanctuary lies between the geo-coordinates ($32^{\circ}78'16''\text{N}$ to $32^{\circ} 89' 33''\text{N}$ and $75^{\circ}68'92''\text{E}$ to $75^{\circ}87'55''\text{E}$) and spans over an area of 99.67 km² encompassing a varied topography that ranges from rugged hills to lush valleys. The altitudinal range of the area is 1960 to 4000ma.s.l. contributing to its rich biodiversity influenced by different climatic zones. The sanctuary experiences a temperate type of climate and is a botanical treasure trove, featuring a diverse range of vegetation characterized by a mix of temperate, sub-alpine, and alpine types of forests (Singh and Sharma, 2022). The sanctuary is known for its diverse wildlife, providing an ideal habitat for various species. Among the notable inhabitants are the Himalayan serow,

Himalayan tahr, Himalayan brown bear, Himalayan black bear, Kashmir musk deer, Himalayan goral, common leopard and red fox. Notable avian species include western tragopan, cheer pheasant, Himalayan monal, and koklass pheasant. Domestic mammalian species that graze in the area during hotter months include domestic goats, sheep, horses, cattle, and buffalo (Bhatnagar et al., 2007; Quyoom et al., 2023).

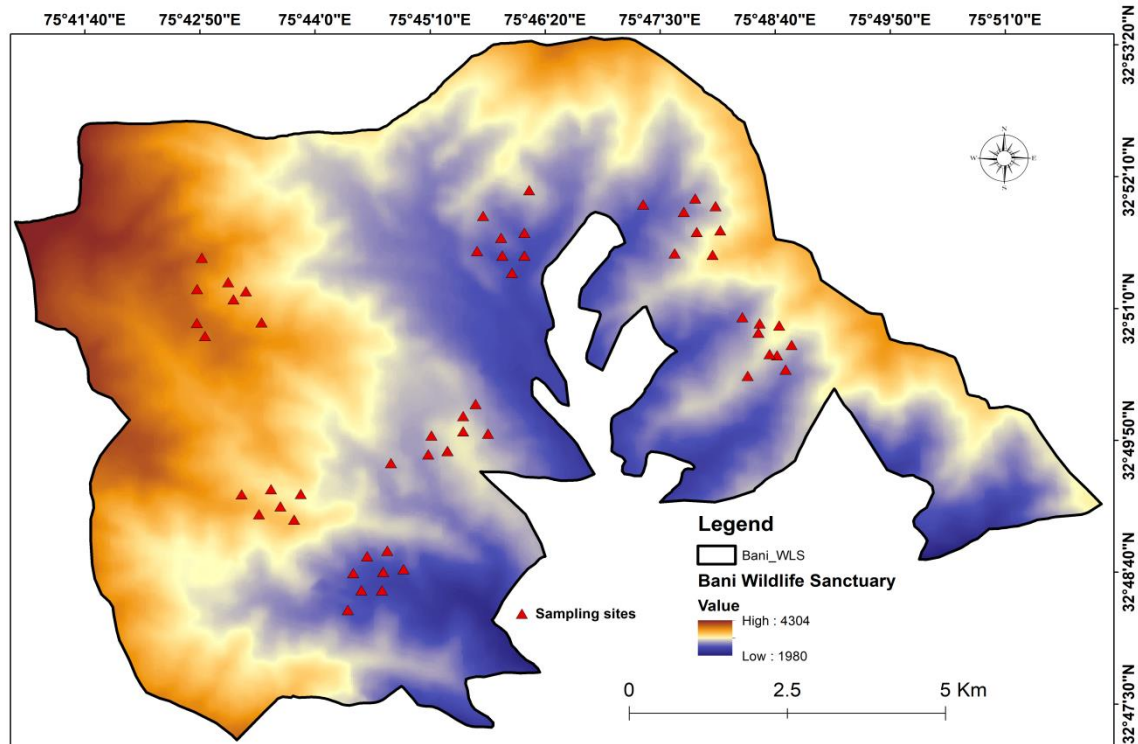


Figure 1. Map of the study area showing sampling sites

Material and methods

Faecal samples for parasitological examination were systematically collected every month basis when defecating from different herds of livestock in the BWLS. A total of 230 faecal samples of domestic livestock (goats, $n = 125$; sheep, $n = 105$) were collected at random from different sites of the study area from June to October in two years (2021 and 2022), as livestock remained prevalent in the sanctuary during these months. For coprological analysis, fresh samples were preserved in 10% formalin (Sharma and Achhami, 2022). These preserved samples were then brought to the wildlife research laboratory at the Department of Zoology, University of Kashmir. Initially, the collected samples were stored at 4°C for one week before further processing. Subsequently, the preserved faecal samples underwent examination through direct smear and standard salt sedimentation–flotation techniques (Smith et al. 2007). The Modified McMaster Technique (Coles et al., 1992) was employed to determine the eggs per gram (epg) count. The

parasite identification was based on various morphological characteristics (Soulsby, 1982), (Foreyt, 2001), and (Baker, 2007).

Additionally, online resources such as <https://parasitologycvm.ncsu.edu/mkey/ruminants/parasite/strongyle> (accessed on April 05 2022; Zajac et al., 2012; Taylor et al., 2016; Chartier and Paraud, 2012) were consulted for the identification of different parasitic stages, including oocysts, and eggs. According to the severity index defined by (Soulsby, 1982), parasitic infestations in domestic livestock (specifically sheep and goats) were classified as mild, moderate, heavy, and severe, corresponding to faecal egg counts of <500, 800-1,000, 1,100 -1,500, and >1,500, respectively. The prevalence of infestation was calculated by dividing the total number of infected samples by the total number processed and then multiplying by 100. For data analysis, the Chi-square test was applied, with a *p*-value of <0.05 deemed statistically significant.

Results

The prevalence of observed gastrointestinal parasites for each host species is summarized in Table 1. Our study reported 10 parasite taxa: one coccidian cyst, one cestode, two trematodes, and six nematodes. Overall, the prevalence of gastrointestinal parasitic taxa was 83.72% in goats and 74.35% in sheep. Among the different classes of parasites identified, the prevalence of coccidian was the highest in both hosts, followed by nematodes, cestodes, and trematodes. In both ruminants, the most prevalent nematode was *Haemonchus contortus* (55.38%), and the least prevalent nematode was *Capillaria* (3.25%). The other nematodes identified were *Trichuris* spp., *Nematodirus* spp., *Strongyloides* spp., and *Ascaris* spp. The identified trematodes were *Fasciola hepatica* and *Dicrocoelium* spp., and the identified cestode was *Moniezia* spp.

Table 1. Prevalence of gastrointestinal parasites in sheep and goats from June to October (2021 and 2022) in the BWLS

S. No.	Parasites	Class	Prevalence in goat (%)	Prevalence in sheep (%)	Overall Prevalence (%)
01	<i>Eimeria</i> spp.	Coccidian	75.41	60.51	67.96
02	<i>Moniezia</i> spp.	Cestode	23.25	30.76	27.00
03	<i>Dicrocoelium</i> spp.,	Trematodes	23.72	11.28	17.05
04	<i>Fasciola hepatica</i>		19.53	29.23	24.38
05	<i>Haemonchus contortus</i>	Nematodes	43.25	55.38	49.31
06	<i>Trichuris</i> spp.		39.53	29.74	34.63
07	<i>Nematodirus</i> spp.		37.20	47.69	42.44
08	<i>Strongyloides</i> spp.		28.83	35.38	32.10

09	<i>Capillaria</i> spp.		3.25	0	1.62
10	<i>Ascaris</i> spp.		0	5.12	2.56

Based on the severity of the infection 9% of the samples in goats were mild (epg, 0-450), 6% of the samples were moderately infected (epg, 550-950), 60% were heavily infected (epg, 1150-1500), and 25% were severely infected (epg, 1850-2750); whereas in sheep, 10% of the samples were mildly infected (epg, 50-450), 20% were moderately infected (epg, 550-1050), 25% were heavily infected (epg, 1100-1500), and 45% were severely infected (epg, 1750-2350). Chi-square analysis ($\chi^2=17.905$, $df=9$, $p<0.05$) revealed that at a 95% confidence interval, the prevalence of different parasites in both hosts was significantly different.

Table 2. Parasites reported by different workers in wild ungulates at the livestock-wildlife interface in the Himalayas region

Host	Parasites reported	Source
Himalayan tahr	<i>Eimeria</i> , <i>Moneiza</i> , <i>Oxyuris</i> , <i>Ascaris</i> , <i>Trichuris</i> , <i>Dictyocaulus</i> , <i>Haemonchus</i> , <i>Strongyloides</i> , <i>Trichostrongylus</i> , <i>Muellerius</i>	Thapa and Maharjan (2015)
Himalayan musk deer	<i>Haemonchus</i> , <i>Nematodrius</i> , <i>Trichuris</i> , <i>Strongyloides</i> , <i>Trichostrongylus</i> , <i>Moneizia</i> <i>Fasciola</i>	Bhat et al. (2021)
Himalayan goral	<i>Strongyle</i> , <i>Entamoeba</i> , <i>Strongyloides</i> <i>Cryptosporidium</i> <i>Cyclospora</i> <i>Mullerius</i> <i>Blastocystis</i>	Adhikari et al. (2021)
Domestic sheep	<i>Eimeria</i> , <i>Moniezia</i> , <i>Dicrocoelium</i> , <i>Fasciola</i> <i>hepatica</i> , <i>Haemonchus</i> <i>contortus</i> , <i>Trichuris</i> , <i>Nematodirus</i> , <i>Strongyloides</i> , <i>Ascaris</i>	Present study
Himalayan musk deer	<i>Eimeria</i> , <i>Ascaris</i> , <i>Strongyle</i> , <i>Strongyloides</i> , <i>Trichuris</i> , <i>Moneizia</i> , <i>Paramphistomium</i>	Achhane et al. (2016)
Himalayan serow	<i>Strongyle</i> , <i>Marshallagia</i> , and others (<i>Strongyloides</i> , <i>Oneizia</i> <i>Toxocara</i>)	Geladi et al. (2019)
Domestic goat	<i>Eimeria</i> , <i>Moniezia</i> , <i>Dicrocoelium</i> , <i>Fasciola</i> <i>hepatica</i> , <i>Haemonchus</i> <i>contortus</i> , <i>Trichuris</i> , <i>Nematodirus</i> , <i>Strongyloides</i> , <i>Capillaria</i>	Present study

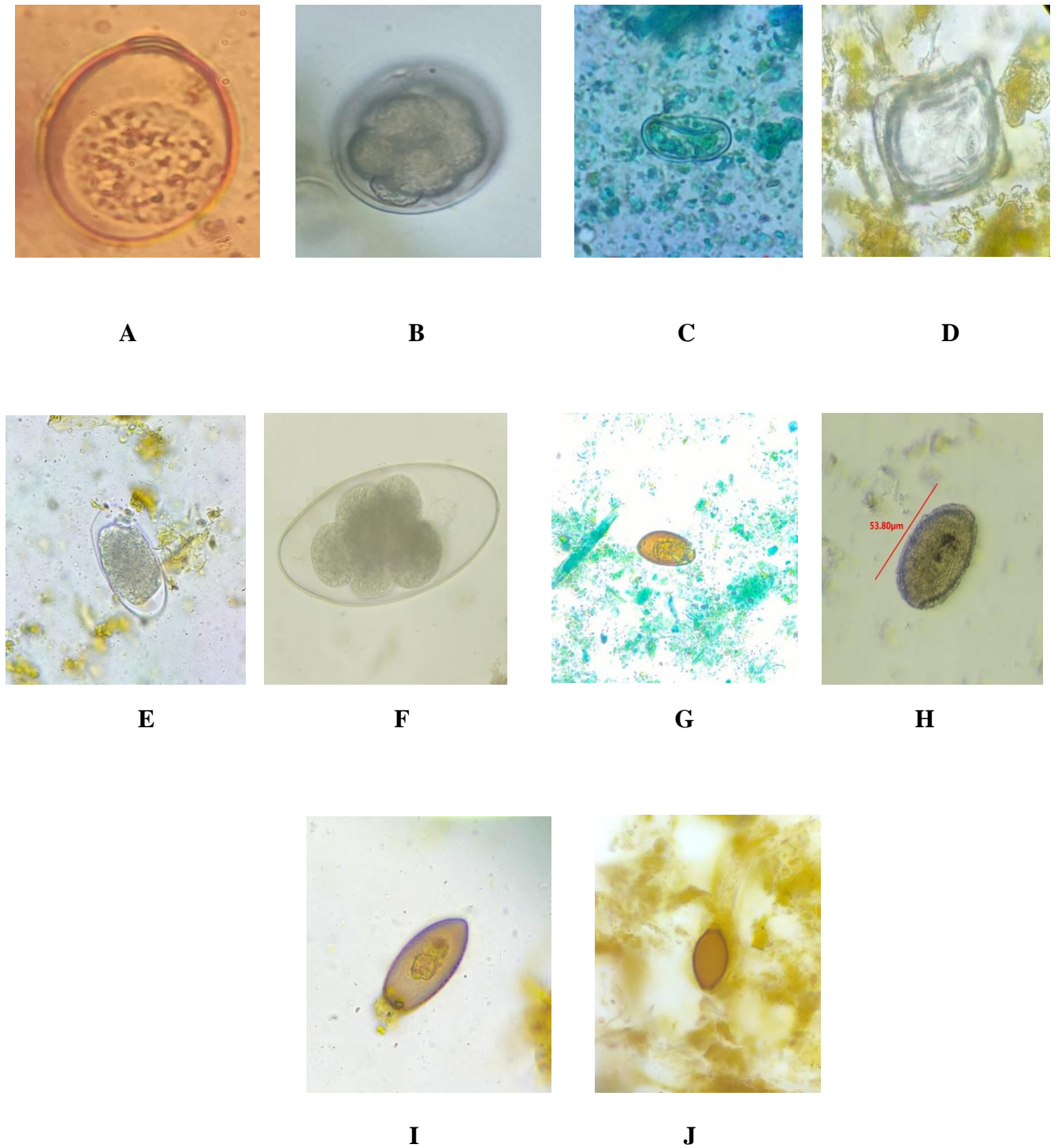


Figure 2. Eggs/oocysts of different parasites. A, *Eimeria* spp., B, *Ascaris* sp., C, *Strongyloides* sp., D, *Moniezia* sp., E, *Haemonchus* sp., F, *Naematodirus* sp., G, *Fasciola hepatica*, H, *Capillaris* spp., I, *Dicrocoelium*, J, *Trichuris* sp.

Discussion

The current study on gastrointestinal parasites (GI) in domestic livestock in the BWLS is seen as exciting research due to the area's diverse human population. The inhabitants (Zamindars) of the villages of Lawang, some from Bani and other villages have established seasonal settlements in

the area, the largest of which is the Sarthal village. The second group who use the area are the nomadic Gujjars who arrive in spring with their herds of buffaloes and some pack animals from Punjab and the plains near Kathua town. Bakkarwals, who mainly herd flocks of sheep and goats also arrive in the area in early spring and use many parts of the region (Bhatnagar et al., 2007).

The transmission of gastrointestinal parasites from domestic livestock to threatened wild ungulates is a concern for the conservation of imperilled wild ungulates in the Kashmir Himalayas, where they co-exist with livestock (Bhat et al., 2022). Studies conducted in different parts of the Himalayan region on wild ungulates have reported similar parasite taxa in different wild ungulates like Himalayan goral, Himalayan serow, musk deer, and Himalayan tahr that are also found in our study area (Quyoom et al., 2023). The parasite taxa identified during the present study were compared with those infecting wild ungulates in different parts of the Himalayan region. Comparative studies revealed that out of ten parasites reported in livestock in our study, six were common in Himalayan tahr, eight in musk deer and three in goral and serow each. From the comparison, it is clear that most of the parasite taxa are shared between domestic livestock and wild ungulates, and bi-directional transmission between the two groups is likely.

Changing environmental conditions and the grazing of livestock in common habitats may contribute to an elevated likelihood of parasite transmission between these populations. According to the findings of our study, *Eimeria* spp. was identified as the predominant gastrointestinal parasite in both hosts (goats and sheep). Furthermore, it is known that these parasites have the potential to cause significant mortality rates and a decline in milk production among the host animals (Kaur et al., 2019). The life cycle of *Eimeria* includes an exogenous phase, wherein oocysts are discharged into the shared environment, facilitating their potential cross-transmission. In this study, the prevalence of nematodes was higher than that of cestodes and trematodes. This disparity may be related to the direct life cycle of nematodes, which perhaps contributes to their elevated transmission rates and overall prevalence (Soulsby, 1982). The low prevalence of cestodes and trematodes can be related to the restricted availability of intermediate hosts, which play a key role in their transmission (Soulsby, 1982).

Consistent with previous research conducted in the Kashmir Himalaya region, the most common helminth genera were *Haemonchus* and *Nematodirus*. The observed high prevalence documented in this study can be attributed to the infectious organisms' ability to withstand adverse environmental conditions, such as extreme dryness and freezing temperatures for a longer period (Poole, 1956). The results of our study align with the observations made by (Dunn, 1978), on the parasitic nature of *H. contortus* in small ruminants, as well as the potential for transmission of *Haemonchus* spp., between domesticated livestock and wild ruminant populations. *H. contortus*,

is often associated with the occurrence of anaemia, mortality in cattle, and substantial economic and productivity losses in livestock (Zajac et al., 2006).

Parasite-sharing patterns among hosts probably originated from shared habitat and space use, given that helminths are transmitted through the environment. Previous studies conducted (Vanderwaal et al., 2014; Ezenwa, 2003; Walker and Morgan, 2014; and Morgan et al., 2006) have reported similar results implying that habitat overlap has a substantial role in promoting the transmission of gastrointestinal parasites. This could be because closely related hosts exhibit comparable patterns of resource utilization, leading to the likelihood of harbouring similar parasite assemblages (Brooks and Hoberg, 2007). According to empirical and theoretical research, it has been observed that the sharing of nematodes is more common among closely related hosts, such as bovids. This is because these species share a common ancestry and have similar adaptations in terms of ecological, physiological, and behavioural traits, which facilitate nematode transmission (Archie and Ezenwa, 2011; Ocaido et al., 2004; Gruijter et al., 2004). According to Obanda et al. (2019) the transmission of diseases among ruminants is significantly influenced by the combination of phyletic familial relatedness and spatial contiguity.

Sharma and Achhami (2022), investigated on gastrointestinal parasites in sympatric red pandas and livestock in protected areas of Nepal. They were able to identify a total of eleven parasites, with eight of them being shared between red pandas and livestock. Notably, the prevalence of shared parasite taxa was observed to be higher than that of host-specific taxa, suggesting the occurrence of cross-transmission. Out of the 11 parasites that were documented, nine exhibited similarities with our findings. Consequently, our research indicates the potential for possible cross-transmission of GI parasites between livestock and wild ungulates within our specific setting.

The transfer of diseases between domestic animals and wildlife can have significant implications for wildlife conservation (Smith et al., 2009) and the preservation of biodiversity (Daszak et al., 2000). The recent decline in the population of various mammal species, including the African wild dog, Ethiopian wolf, and black-footed ferret, has been linked to the spread of rabies and canine distemper viruses from domestic animals to wildlife (Ginsberg et al., 1995; Randall et al., 2004; Thorne and Williams, 1998). Furthermore, the transfer of the goat pox virus from domestic goats to Himalayan goral (*Naemorhedus goral*) has been documented in Arunachal Pradesh (Bora et al., 2021).

In the Himalayas, sharing grazing pastures has been recognised as conducive to parasite transmission from livestock to wild ruminants (Khanyari et al., 2021). A transmission model (GLOWORM-FL model) suggests that infective L₃h on forage peaks in summer and livestock contributes more to pasture infectivity than wild ungulates because of higher density. This suggests

that parasite transmission from domestic animals to wild ungulates is far more likely than vice versa (Khanyari et al., 2021). Gastrointestinal nematodes even at low levels have been shown to reduce fecundity and correlate with poor body conditions in wild ruminants (Irvine et al., 2006; Stien et al., 2002).

This study provides an in-depth look at the prevalence and severity of gastrointestinal parasitic infection prevalent in livestock grazing in the BWLS. The majority of these parasites have a high transmission potential to other hosts that share resources in the same area. Comparable studies show that there is a link between parasite infection in livestock and sympatric wild ungulates, indicating that these infections persist in the shared environment. The presence of parasitic infections in the shared environment may expose wild ungulates to various emerging diseases and may play a significant role in their population decline. According to this study, there are significant opportunities for parasitic transmission between domestic livestock and wild ruminants in the protected areas.

Conclusion

In shared settings, there is a substantial chance of gastrointestinal parasitic transmission between domestic and wild ungulates. Numerous animal species that are currently facing the threat of endangerment, including serow, goral, musk deer and Himalayan tahr coexist within environments that are also inhabited by livestock. This cohabitation renders these species vulnerable to the transmission of parasitic diseases that are commonly carried by domestic livestock. This study together with more investigations, on the parasites at the interface between wildlife and livestock, may offer valuable insights for making informed decisions on the management of livestock grazing activities in the protected areas. These decisions may include the regulation of anthelmintic treatment for livestock and the implementation of grazing zonation strategies. There is a need for a thorough understanding of the diversity and severity of endoparasite infection in both domestic and wild ungulates in the region. More importantly, it is imperative to evaluate the impact of these parasites on the ungulate's overall health, productivity, and fitness.

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