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Occurrence and risk factor assessment of infectious diseases in domestic livestock at the livestock–Wildlife Interface of Ramnagar Wildlife Sanctuary (RWLS)

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ABSTRACT

This study, conducted between April 2024 and July 2025, assessed the prevalence and risk factors of infectious diseases at the livestock–wildlife interface of Ramnagar Wildlife Sanctuary (RWLS), Jammu. Domestic livestock from fringe villages and migratory Bakarwal herds were surveyed using community interviews, local veterinarian interviews and laboratory diagnostics. High levels of overlap between domestic and wild animals were reported, particularly near shared water sources and forest edges. Villagers noted tick infestation, Lumpy Skin Disease (LSD), reproductive disorders, and diarrhoea, while Bakarwal herds exhibited sore mouth lesions, diarrhoea, and tick infestation. Laboratory surveillance revealed gastrointestinal parasitism in 42.5% of cattle, 46.67% of buffaloes, 39.58% of sheep, and 38.0% of goats. Brucella seroprevalence was 18.18% in cattle and 10.34% in goats, while LSDV was detected in 15.15% of cattle. Risk factors included irregular deworming and vaccination, lack of mineral supplementation, limited veterinary access for pastoralists, and shared grazing and water resources with wildlife. Seasonal overlap—defined as the convergence of migratory livestock herds with wildlife populations during grazing and water availability periods—was also identified as a potential driver of exposure. Although chisquare analysis ($\chi^2 = 0.2$; $p > 0.05$) did not show a significant statistical association between wildlife interaction and disease occurrence, ecological evidence indicated that shared environments and overlapping seasonal movements created opportunities for indirect transmission. The identified factors were interpreted as potential ecological and management related exposure conditions rather than statistically confirmed predictors of disease transmission. The findings underscored the need for integrated management strategies, improved veterinary outreach, community awareness, and coordinated surveillance to mitigate disease risks at the livestock–wildlife interface.

Keywords*:* Bakarwal pastoralists, Disease prevalence, Risk factors, Wildlife-livestock interface

In India, livestock production forms an important component of the agricultural economy and rural livelihood. Open grazing of domestic animals in or near natural wildlife habitats creates zones of overlap between livestock and wild species, forming the domestic–wildlife interface (DWI), which represents the physical space where they share range and may interact directly or indirectly (Huyvaert *et al.* 2018). The DWI is a recognised hotspot for disease emergence, with many pathogens exhibiting multi-host and bi-directional transmission between domestic and wild animal populations (Phukon, 2015). In natural conditions, indirect contact is the most common mode of disease transmission (Kukielka *et al.* 2013) which includes aerosols, contaminated soil, water, mucus and faeces (Franklin *et al.* 2011). Environmental pressures, like seasonal droughts, can force both groups to converge on limited resources, temporarily increasing the risk of outbreaks. The livestock–wildlife interface is a critical zone for disease emergence, and Booma *et al.* (2025), studying frontier landscapes under land-use change, found that cross-species transmission contributed substantially to disease dynamics, with ~34% of new livestock infections originating from wildlife and ~47% of new wildlife infections traced back to livestock. Jammu and Kashmir is inhabited by pastoralist communities such as the Bakarwals, a migratory tribe rearing sheep and goats, seasonally move between the plains of Jammu in winter and the high-altitude pastures of Kashmir and Kishtwar in summer (Sharma *et al.* 2003). Ramnagar Wildlife Sanctuary (RWLS) in the Jammu district is surrounded by villages

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with dense livestock population and receives seasonal influx of Bakarwal herds during winters (September–March). The shared use of grazing areas and water resources by livestock and wildlife in and around the sanctuary creates a potential risk for disease transmission, although systematic scientific information on such risks in this region remains limited. Given the substantial ecological, economic, and public health implications, diseases emerging at the livestock–wildlife interface warrant urgent and sustained attention from veterinary and conservation authorities alike (Siembieda *et al.* 2011). No comprehensive study has been undertaken to assess the disease dynamics or risk factors at the domestic-wildlife interface of RWLS.

MATERIALS AND METHODS

Study area: The present study was conducted around RWLS, located in the Jammu district of Jammu and Kashmir, India. The sanctuary lies on the outskirts of Jammu city along NH-1A, between 32°44′ N latitude and 75°20′ E longitude, and covers an area of approximately 31.32 km². It comprises a mosaic of protected forested areas interspersed with human settlements, making it a significant domestic–wildlife interface. The terrain is predominantly hilly, and is characterised by mixed deciduous forests and subtropical vegetation. The sanctuary supports diverse wildlife, including Leopard, Barking Deer, Cheetal, Wild Boar, Nilgai, Jackal, Jungle Cat, Rhesus Macaque, and Langur.

Transect-based mapping of domestic-wildlife interaction hotspots near RWLS: An on-foot transect survey was conducted near RWLS to identify and map potential domestic–wildlife interaction zones. Transects were designed to locate animal congregation points, including natural waterholes, man-made water ditches, open grazing clearings, and feeding sites, which are considered potential interaction hotspots. Visual observations were made along transects to record signs of animal activity, such as tracks, dung/droppings, evidence of grazing/browsing. All observations were geotagged using a GPS Map Camera Application (Version 2.1.0.0). A range finder was used to measure distance and angle for animals or indirect signs detected away from the transect line. The collected GPS coordinates, distance–angle measurements, and field observations were compiled and shared with the Wildlife Institute of India (WII), where the data were integrated into a spatial database to identify and map domestic–wildlife interaction hotspot zones near RWLS.

Field surveys: Field surveys were conducted to assess domestic–wildlife interactions and associated disease risks around RWLS. Data were collected from three key stakeholder groups: livestock herders residing in fringe villages, migratory Bakarwal pastoralists, and local veterinarians.

Survey of livestock farmers: Questionnaire-based surveys were conducted among livestock herders within and around RWLS to document livestock management practices and potential disease transmission risks at the domestic–wildlife interface. Face-to-face interviews were conducted with 27 livestock-owning households (n = 27) located within a 5 km buffer zone of RWLS. Five migratory Bakarwal pastoralist households (n = 5) were surveyed within the forested interior of the sanctuary during their seasonal stay from February to March 2025. Information collected from both groups included livestock species and herd size, feeding practices (stall feeding, free grazing, or mixed systems), frequency and type of wildlife interactions (direct sightings, shared grazing areas, and common water sources), and livestock health status during the preceding year, including morbidity, mortality, and access to veterinary services. For Bakarwals, additional data on seasonal movement patterns and herd composition were recorded to reflect their migratory and high-contact pastoral system.

Data collection from local Veterinarians: Data were collected through informal discussions during field visits to veterinary dispensaries and outreach camps, as well as telephonic interactions. The discussions focused on commonly reported livestock diseases, seasonal disease patterns, recent outbreaks, and veterinarian observations regarding wildlife–livestock interactions.

Sample Collection: Blood and faecal samples were collected from livestock during community-based field surveys conducted in fringe villages surrounding RWLS. Blood samples were collected aseptically by jugular venepuncture and transferred into plain and EDTA-coated vacutainer tubes. Whole blood collected in EDTA tubes was stored for further analysis. Blood collected in vacutainers was centrifuged at 3000 rpm for 10 min to obtain serum/plasma, which was transferred into sterile, labelled vials and stored at −20 °C until analysis.

Faecal samples were collected directly from the ground using disposable gloves, ensuring selection of freshly voided droppings, and placed in labelled zip-lock polythene bags indicating species, location and date of collection. All samples were transported to the laboratory under cold chain conditions and stored at 4 °C until subjected to parasitological examination.

Faecal examination: A total of 301 faecal samples were screened from different livestock species, comprising 40 from cattle, 15 from buffalo, 96 from sheep, and 150 from goats. Faecal examination was done as per the method given by Soulsby (1982).

Serological testing for diseases in domestic animals: Appropriate biological samples, viz., whole blood, serum or plasma, were subjected to different serological tests for screening suspected diseases (Brucellosis and Lumpy Skin Disease (LSD) using standard methods.

Brucellosis: A total of 79 serum samples from domestic animals, including cattle (n=33), sheep (n=17) and goats (n=29), were screened for Brucella infection using the Rose Bengal Plate Test (RBPT) as a rapid agglutination screening test (Alton *et al.* 1988).

Lumpy Skin Disease (LSD): Animals were clinically examined for lesions suggestive of LSD, and apparently

healthy in-contact cattle from the same herds were also sampled to assess subclinical infection or recent exposure. Whole blood samples from suspected cattle (n = 33) were screened for Lumpy Skin Disease Virus (LSDV) by conventional polymerase chain reaction (PCR). Viral DNA was extracted using the QIAamp DNA Mini Kit (Qiagen, Hilden, Germany) as per the manufacturer's protocol and stored at −20 °C until analysis. PCR targeting the LSDV P32 gene was performed using primers described by Ireland and Binepal (1998) and recommended by the World Organization for Animal Health (OIE, 2018). The PCR reaction was carried out in a 25 µl volume containing GoTaq® Green Master Mix, forward and reverse primers (10 µM each), template DNA, and nuclease-free water. Thermal cycling consisted of an initial denaturation at 95 °C for 5 min followed by 40 cycles of denaturation at 95 °C for 10 s, annealing at 56 °C for 30 s, and extension at 72 °C for 30 s. PCR products were resolved on a 1% agarose gel in 1× TAE buffer and visualised under UV illumination using a gel documentation system (VilberLourmat, Eberhardzell, Germany).

Statistical analysis: The data were analysed using the Chi-square test (Snedecor and Cochran, 1991).

RESULTS AND DISCUSSION

The RWLS and its adjoining areas constitute an active domestic–wildlife interface marked by substantial overlap in land and resource use. Field surveys and community interactions revealed frequent livestock movement into forest fringes, particularly along the southern and south-eastern boundaries of the sanctuary. Livestock grazing and shared use of water sources were commonly observed, indicating regular indirect contact between domestic animals and wild species.

Spatial mapping identified multiple high-interaction zones near forest edges and water points, confirming concentrated areas of overlap between livestock and wildlife. Occasional sightings of wild boar and jackals near agricultural fields further indicated permeability of the sanctuary boundary. Similar interface conditions have been recognised as key drivers of pathogen spillover due to shared grazing grounds and congregation at water sources (Jones *et al.* 2013).

Seasonal migration of Bakarwal pastoralists emerged as an important factor intensifying the interface. Sheep, goats and Bhakarwali dogs accompanying nomadic groups were observed grazing and utilising earthen water ditches constructed for wildlife near RWLS. Earlier reports indicate the seasonal entry of approximately 30–40 nomadic families with 800–1000 livestock into the sanctuary (Atri, 2020), increasing pressure on limited resources and the likelihood of disease transmission. Limited access to veterinary care for migratory livestock may further facilitate persistence of infectious agents.

The small area of the sanctuary (12.75 km²), absence of permanent water sources, and fragmentation of the Eco-Sensitive Zone (ESZ), including zero buffer stretches along the southern and western boundaries due to urban expansion, exacerbate livestock intrusion and unregulated grazing (MoEFCC, 2018). Seasonal drying of waterholes leads to congregation of animals at a few sites, increasing contact rates. Grazing pressure exceeding carrying capacity of the forest has also been reported to impair natural regeneration and degrade habitat quality (Atri, 2020).

The observed spatial pattern demonstrated a high-risk domestic–wildlife interface characterized by shared resources, weak physical separation and intensive anthropogenic pressure, which was consistent with documented scenarios where these interactions contributed to disease transmission and habitat degradation (Gortazar *et al.* 2007).

Field survey: A field survey of 32 respondents, (27 villagers, 5 migratory Bakarwal pastoralist). The survey fetched information on herd composition, feeding practices, herd size, wildlife interaction, and livestock health, providing insight into management systems operating at the DWI.

The village households were characterized by small, mixed herds, with cattle being the most commonly reared species, followed by sheep, goats, and buffaloes (Table1). In contrast, migratory Bakarwals maintained small-ruminant-based herds, with goats forming the largest proportion (Table1). This herd structure reflected the adaptive advantages of goats and sheep in mobile pastoral systems, where resilience, browsing ability, and ease of movement were essential (Sharma *et al.* 2003).

Feeding practices differed markedly between the two groups. Most village households relied primarily on open

Table 1. Distribution of animal types owned by villagers (n=27) and migratory Bakarwal pastoralists (n=5)

Livestock Type	Villagers – Frequency (n=27)	Villagers – Percentage (%)	Bakarwal Pastoralists – No. of Animals (n=280)	Bakarwal Pastoralists – Percentage (%)
Cattle	8	29.63%	–	–
Buffalo	3	11.11%	–	–
Sheep	5	18.52%	91	32.50%
Goat	4	14.81%	105	37.50%
Kid/Lamb	–	–	84	30.00%
Mixed	7	25.93%	–	–
Total	27	100%	280	100%

grazing (77.78%; 21/27), while a smaller proportion practiced stall feeding (22.22%). Migratory Bakarwal herds depended exclusively on free grazing, consistent with their traditional pastoral livelihood. Heavy dependence on grazing in forest fringes and open landscapes has been identified as a major driver of livestock–wildlife overlaps near RWLS (Atri, 2020), particularly around shared resources such as water points and grass patches.

Herd size distribution indicated contrasting management systems. Village households mainly maintained small herds (70.37%; 19/27), with only few keeping medium-sized herds (29.63%), reflecting subsistence-oriented livestock rearing. Bakarwals, on the other hand, managed medium to large, mobile herds, typical of nomadic aligning with pastoral systems across India where mobility, flexibility, and resource use efficiency favour smaller-bodied livestock (Sharma *et al.* 2003). Larger herd sizes and small-ruminant dominance increase animal congregation at grazing and water points, potentially elevating disease transmission risk at the domestic–wildlife interface.

Chisquare analysis ($\chi^2 = 0.2$; $p > 0.05$) showed no significant association between wildlife–livestock interactions and disease occurrence. Nevertheless, respondents reported encounters with wild boar and deer near grazing and water sources. Shared pasture, soil, water, faecal material and vectors might have provided opportunities for indirect exposure but, the present study did not establish pathogen spillover or spillback. Thus, interface contact should be interpreted as a potential exposure condition rather than evidence of transmission

Health problems reported by livestock owners (Table 2) reflected these interface conditions. Tick infestation and lumpy skin disease (LSD) were the most frequently reported issues among village herds, indicating high ectoparasite pressure and circulation of vector-borne viral diseases. Among Bakarwal herds (Table 2), sore mouth, diarrhoea, and tick infestation were common, likely associated with prolonged grazing, animal movement, nutritional stress, and limited access to veterinary services. The coexistence of infectious, parasitic, and reproductive disorders suggested ongoing health challenges in both sedentary and migratory livestock systems.

Table 2. Reported health issues in domestic animals by villagers (n=27) and Bakarwal pastoralists (n=5)

Villagers – Health Issue	Frequency (n)	Bakarwal – Health Issue	Frequency (n)
Tick infestation	13	Tick infestation	3
Lumpy Skin Disease (LSD)	10	Oculo-nasal discharge	1
Diarrhoea	4	Diarrhoea	3
Repeat breeding	4	Interdigital dermatitis	1
Abortion	3	Sore mouth and muzzle	3
Mastitis	3	Mastitis	1
Silent heat	2	Silent heat	–
Anestrus	4	Anestrus	–
Total	43	Total	12

Information obtained from local veterinarians corroborated the field-level observations. Tick infestation, gastrointestinal parasitism, Peste des Petits Ruminants (PPR), Orf, enterotoxaemia, and metabolic disorders were commonly encountered, with recent outbreaks of LSD and Orf reported during the study period. Although veterinarians did not report direct wildlife involvement in clinical cases, this mostly likely reflected the indirect and environmentally mediated nature of most interface interactions rather than absence of risk.

The presence of diseases such as PPR and Orf is of particular concern, given their high transmissibility and potential spillover into wild ungulates under shared grazing systems (Mahapatra *et al.* 2015). Similarly, the persistence of tick-borne and metabolic disorders highlights gaps in preventive healthcare, nutrition, and parasite control, especially among migratory pastoral communities.

Overall, the field survey indicated that livestock management practices around RWLS—characterised by open and unregulated grazing, mixed and mobile herds, and shared use of natural resources—created conditions conducive to habitat degradation, competition for forage, and maintenance and transmission of diseases at the domestic–wildlife interface, supporting earlier observations by Atri (2020). These findings highlighted the need for regulated grazing, designated grazing zones, strengthened veterinary outreach, improved vaccination coverage, and enhanced community awareness within an integrated One Health framework.

Gastrointestinal parasitism (GIT) at the domestic–wildlife interface: GIT-parasitism was detected in buffaloes (46.67%), cattle (42.5%), sheep (39.58%), and goats (38%) (Table 3). Parasites detected included amphistomes, Strongyles, Strongyloides, Trichuris, Moniezia, coccidia, and Balantidium, indicating prevalence of both helminthic and protozoan infections Differences among species might be attributed host susceptibility, grazing behaviour, and management.

These findings aligned with earlier reports of GIT parasitism in domestic livestock and wildlife species inhabiting or frequenting interface areas. For instance, Allwin *et al.* (2016) reported a prevalence of 80% in domestic cattle and 63.3% in wild gaur sharing grazing spaces in the Nilgiri Hills, with common parasites including Strongyle, Trichuris, Moniezia and amphistomes, many of which were also observed in the present study. Similarly, Talukdar *et al.* (2020) documented parasite overlap between livestock and Swamp Deer in conservation reserves, identifying Strongyle, Trichostrongylus, Fasciola, and Moniezia spp. in both host types, highlighting the role of shared environments in facilitating parasite transmission.

The presence of strongyle, trichuris, and amphistome eggs in domestic livestock in this study echoed the findings

Table 3. Species-wise prevalence and parasitic forms detected in domestic livestock based on faecal examination

Species	n	Detected Parasites	Parasitic egg (+ve)	Prevalence (%)
Cattle	40	Amphistome egg, Strongyloides egg, Coccidia oocyst, Trichuris, *Moniezia benedeni*, Strongyle egg	17	42.5
Buffalo	15	Coccidia oocyst, Balantidium trophozoites egg, Amphistome egg	7	46.67
Sheep	96	Amphistome egg, Strongyloides egg, Strongyle egg	38	39.58
Goat	150	Trichuris egg, Strongyloides egg, Strongyle egg, *Moniezia expansa*	57	38

Table 4. Species-wise helminth in domestic livestock on faecal examination.

Specie	n	+ve	AMP	MON	COC	BAL	STR	STL	TR	M*
Cattle	40	17	4	1	1	0	6	1	1	3
Buffalo	15	7	2	0	1	2	1	0	0	1
Sheep	96	38	12	0	0	0	14	7	0	5
Goat	150	57	0	4	0	0	20	11	9	13

AMP: Amphistome, MON: Moniezia, COC: Coccidia, BAL: Balantidium, STR: Strongyle, STL: Strongyloides, TR: Trichuris, M: Mixed

* Mixed infections are included in parasite counts and total positives

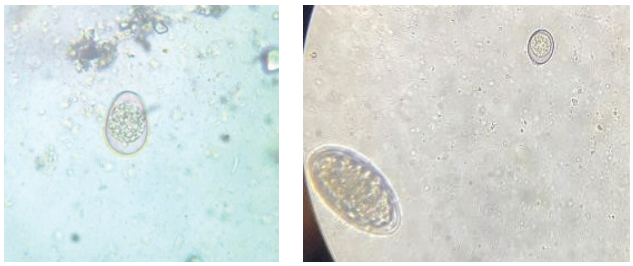
of Sapkota *et al.* (2022), who reported high prevalence of Paramphistomum, Strongyle and Trichuris spp. in both deer and livestock in buffer zones of Chitwan National Park, Nepal. However, detection of parasites belonging to the same genus or morphologically similar groups in different host populations does not by itself establish cross-species transmission. Shared grazing and defaecation areas can increase opportunities for parasite exposure but confirmation of cross-transmission would require species level identification and molecular characterization such as DNA Barcoding or metabarcoding. (McFarland *et al.* 2024).

Studies from various wildlife reserves and zoos emphasized the ubiquity of gastrointestinal parasites in wild herbivores. Lone *et al.* (2016) found over 53% of endangered Hangul deer in Dachigam National Park infected with helminths such as Trichuris and Moniezia spp., while Shirbhate and Shrirbhate (2022) reported Strongyle and Strongyloides spp. as dominant parasites in Blackbuck populations in Rajasthan.

Further, the findings of Khattak *et al.* (2023), showing a parasite prevalence exceeding 60% in sheep and goats and around 43% in cattle and buffaloes, reinforced the view that GIT parasitism is a widespread and significant issue among ruminants in South Asia. Risk factors identified in that study, poor deworming practices, inadequate management, and rural settings, mirrored the conditions observed in the villages surrounding RWLS.

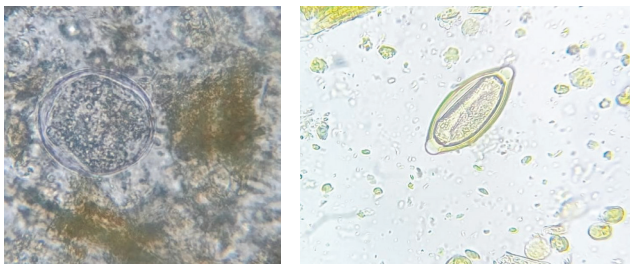
The detection of *Balantidium coli* in buffaloes, although less commonly reported in wildlife, was notable due to its zoonotic potential and has also been found in captive primates (Das *et al.* 2024), raising concerns about environmental contamination and interspecies transmission within shared ecosystems.

Serological examination in domestic animals: *Rose Bengal Plate Test (RBPT) for brucellosis*: The results



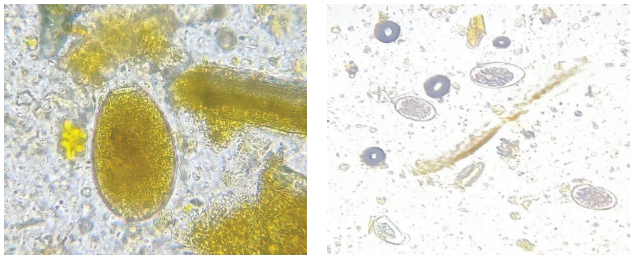
1a 1b

Fig. 1. (a) Coccidian oocyst in buffalo; (b) Mixed infection in cattle showing bothStrongyle egg and Coccidian oocyst.



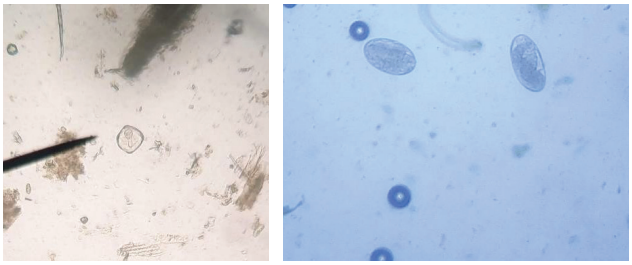
2a 2b

Fig. 2. (a) *Balantidium* cyst observed in buffalo faecal samples; (b) *Trichuris* egg in goat



3a 3b

Fig. 3. (a) *Amphistome* egg in sheep; (b) *Strongyle* eggs in goat.



4a 4b

Fig. 4. (a) *Moniezia* egg in cattle; (b) *Strongyloides* eggs in sheep.

Table 5. Screening of brucellosis by RBPT

Species	n	Positive	Negative	Prevalence (%)
Cattle	33	6	27	18.18
Sheep	17	0	17	0.00
Goat	29	3	26	10.34

of RBPT screening indicate the presence of Brucella antibodies in cattle and goats in the study area, suggesting ongoing or prior exposure to the pathogen, with cattle showing the highest prevalence among the tested species Table 5.

The higher seroprevalence in cattle was consistent with their role as the primary hosts for *Brucella abortus*, the predominant agent of bovine brucellosis. Caprine and ovine brucellosis is endemic in India (Saxena and Joshi, 2021). Risk factors include livestock production systems, cattle breed and management practices like transhumance and pastoralism, which facilitated frequent herd mingling and enhance transmission potential (Makwavarara, 2018). Shared access to grazing areas and water points near wildlife habitats increased the likelihood of contact with infected animals and contributes to pathogen circulation at the domestic–wildlife interface (Treanor *et al.* 2010). The detection of brucellosis near RWLS underscored the livestock–wildlife interface as a hotspot for Brucella spillover and maintenance (Godfroid and Kasbohrer, 2013). Similar patterns have been reported in the Serengeti, where *Brucella abortus* was detected in African buffaloes and lions sharing grazing areas with livestock, indicating a possible wildlife reservoir role (Sambu *et al.* 2021). In the RWLS context, overlapping use of grazing and water resources might have increased opportunities for cross-species pathogen exposure, however, the present study did not establish direct transmission between livestock and wildlife. Goats, while less frequently infected than cattle, still showed notable seropositivity (10.34%), underscoring their vulnerability and possible role in sustaining the infection chain, particularly for *Brucella melitensis*, which is more commonly associated with small ruminants. Brucellosis is an important zoonosis of public health significance.

Lumpy Skin Disease Virus (LSDV) screening in cattle (Conventional PCR): Conventional PCR targeting the P32 gene confirmed Lumpy Skin Disease Virus (LSDV) infection in 5 of 33 cattle (15.15%), indicating active or recent circulation of the virus in the study area. Detection of the expected ~100 bp amplicon, along with clinical signs such as ulcerated nodules and healed lesions in some animals, suggested both ongoing and past infections within affected herds. LSDV is known to persist in endemic regions and is primarily transmitted mechanically by blood-feeding vectors, including Stomoxys, Aedes spp., and ticks (Amblyomma and Rhipicephalus) (Tuppurainen *et al.* 2013). The warm and humid conditions of the RWLS region might have favoured vector abundance and facilitate transmission. Indirect spread through contaminated secretions and shared water or feeding sources further increased exposure risk under free-grazing and communal management systems prevalent in the study area.The role of wildlife in LSD epidemiology is not fully understood; however, susceptibility has been reported in several wild ruminants, including African buffalo, giraffe, and antelope species (WOAH, 2024). Thus, LSDV detection at RWLS indicated continued circulation and warrants surveillance at the domestic–wildlife interfaces.

The present study demonstrated that the RWLS represented an important domestic–wildlife interface characterized by shared grazing lands, water resources and seasonal livestock movement. Field observations and laboratory investigations confirmed the occurrence of gastrointestinal parasites, brucellosis seropositivity and lumpy skin disease among domestic livestock. Although wildlife-livestock overlap was evident, the study did not establish direct pathogen transmission or spillover between wildlife and livestock. Nevertheless, shared environmental resources and seasonal animal movements represented potential exposure pathways that require further investigation through pathogen specific surveillance and molecular characterization. Poor livestock management practices, limited veterinary access and unregulated resource sharing further amplify transmission risks. These findings supported the need for further strengthening of the integrated One Health–based surveillance, improved livestock management, and coordinated action between veterinary and wildlife authorities to mitigate disease risks at the RWLS interface.

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