

REVIEW ARTICLE

Emerging Infectious Diseases at the Wildlife and Livestock Interface: A One Health Perspective from the Saiga Antelope and Domestic Sheep System

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ABSTRACT

The wildlife-livestock interface is an important setting for the emergence and transmission of infectious and parasitic diseases, driven by environmental change, animal movement, shared grazing resources and livestock management practices. Central Asian rangelands, particularly those in Kazakhstan, provide an important context for examining these dynamics because migratory saiga antelopes (*Saiga tatarica*) share habitats with domestic livestock, including sheep. This review examines the ecological, epidemiological, host-related and molecular factors influencing disease emergence at the wildlife–livestock interface, using the saiga–sheep system as a case study within a One Health framework. Particular attention is given to *Pasteurella multocida*, gastrointestinal nematodes and *Coenurus cerebralis*, alongside the potential influence of host genetic susceptibility, climatic variability and shared environmental exposure. Available evidence indicates that spatial overlap and the occurrence of related pathogens in wildlife and livestock provide opportunities for cross-species transmission but do not, in themselves, establish transmission or its direction. The review highlights the importance of integrating ecological surveillance, molecular characterization, genomic epidemiology and temporally matched sampling to distinguish shared exposure from genuine pathogen exchange and sustained transmission. It further discusses the role of livestock management, conservation-based veterinary interventions and coordinated institutional collaboration in mitigating disease risks. An integrated One Health approach combining movement ecology, molecular diagnostics, host susceptibility assessment and targeted preventive measures is essential to strengthen disease surveillance, protect wildlife populations and support sustainable livestock production in shared rangeland ecosystems.

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INTRODUCTION

The interactions between people, domestic animals and wild animals are still undergoing changes due to emerging diseases. Many of these diseases are rooted in the interface of wild and domestic populations at places where they use the same water, graze on the same land, share migration routes and/or come into contact when

resources are scarce (Rulli *et al.*, 2025). The wildlife and livestock interface is an area of contact that is a major issue for veterinary epidemiologists, conservation biologists and public health officials as it serves as a two-way traffic zone through which pathogens can cross from one species to another with different immune systems and livestock management history (Miller *et al.*, 2025). In recent decades, the rate of emergence of new and re-

emerging pathogens at this interface has greatly increased, because of the increase in both livestock populations and the spread of agricultural and grazing land into wildlife habitat, and the demographic recovery by some populations of wildlife ungulates from past declines (Usmani *et al.*, 2023). Wild and domestic animals are coming into increasing contact, and at times in a more stressed condition, than in the past when densities of humans and livestock were lower compared to grazing resources (Malhi *et al.*, 2022). Therefore, diseases that were previously confined to a single host species have more opportunity to spread across species and gain the potential to cause a sustained transmission cycle involving both wildlife and livestock (Fagre *et al.*, 2022).

The One Health concept provides the most coherent framework for understanding and addressing disease emergence at this interface (Hernandez *et al.*, 2025; Hossain *et al.*, 2025). One Health does not view wildlife disease, livestock disease and human health as distinct areas to be managed but seeks a unified approach in surveillance, a unified diagnostic capacity, and a coordinated policy response that considers the drivers of disease in all three that are ecological and social in nature (Ahmed *et al.*, 2025). This is especially applicable to areas where wide-spread pastoralism shares the rangelands with large numbers of migratory wild ungulates as it is the same rangelands that are being used for livestock economies that are critical habitat for wildlife conservation (Teague, 2023).

Central Asia, and Kazakhstan in particular, offers an instructive setting in which to examine these dynamics. Saiga antelope is a migratory ungulate of critical importance for the western parts of Eurasia, sharing large parts of their grazing area with domestic sheep and other livestock (Khanyari *et al.*, 2022a). Spatial and temporal overlap between saiga and domestic animals may be greater in such areas during seasonal migration, resulting in possible common environmental exposures or contact with other species. This overlap should not, however, be taken as an indicator of pathogen exchange; rather, epidemiological or molecular evidence should be used (Khanyari *et al.*, 2022a). Kazakhstan also has a long history of sheep keeping, where many of the breeds are adapted to steppe and desert environments, and have unique genetic traits for disease susceptibility and resistance (Orkara *et al.*, 2025). The extent of these intermingled uses, as well as the conservation value of this species of saiga that has suffered large population declines in the past that can be linked, in part, to outbreaks of infectious and parasitic diseases (Khanyari *et al.*, 2022a). It makes this an area of interest about understanding and predicting the distribution of these diseases between the wildlife and livestock markets and to the management of these diseases at that interface (Hayes *et al.*, 2023).

This review uses the saiga antelope and domestic livestock system of Kazakhstan as a case study to examine disease emergence as a multistage process rather than as a simple consequence of contact between host species. We suggest an integrated One Health approach that considers how environmental and climatic change affect wildlife movement, livestock grazing patterns, water use and spatial overlap among wildlife and livestock. The ability to progress from exposure to infection, through host

switching, onward transmission to clinical disease further depends on host immunity, genetic susceptibility, physiological stress and pathogen characteristics. Molecular epidemiology and genomic surveillance can then be used to differentiate shared exposure from true pathogen transmission. The framework is applied throughout the review to incorporate ecological, epidemiological, evolutionary and molecular evidence, and to highlight opportunities for surveillance and preventive actions to limit disease emergence at wildlife–livestock interfaces.

Review Methodology: Relevant studies were retrieved from the PubMed, Google Scholar, Scopus and Web of Science databases, and the period covered studies up to 2026. The following search terms were used in a combination of Boolean operators: “saiga”, “*Saiga tatarica*”, “wildlife livestock interface”, “wildlife livestock transmission”, “wild ungulates”, “domestic sheep”, “Kazakhstan”, “*Pasteurella multocida*”, “pasteurellosis”, “gastrointestinal nematodes”, “*Coenurus cerebralis*”, “*Taenia multiceps*”, “spillover”, “reverse transmission”, “host switching”, “One Health”, “molecular epidemiology”, “whole genome sequencing”, “genomic surveillance”, “PCR”, “climate”, “migration”, and “disease surveillance”. The reference lists of key articles and recent reviews were consulted for additional relevant publications.

Integrated One Health Framework for Disease Emergence at the Wildlife and Livestock Interface:

Epidemiologically relevant contact at the wildlife and livestock interface can range from indirect environmental exposure through shared pasture, water sources or contaminated substrates to direct spatial and temporal contact between host species. However, contact is not a sufficient criterion for the demonstration of pathogen transmission. Emergence of a disease can, on the contrary, be considered as a succession of events: ecological overlap, pathogen exposure, successful infection of a recipient host, and, in certain instances, intra-host transmission. Opportunities for exposure are predominantly dictated by environmental factors, animal movement and livestock management, whilst host immunity, genetic susceptibility and pathogen characteristics will determine whether exposure leads to infection and disease. They are interacting processes that constitute the disease emergence pathway (Fig. 1) and are used throughout this review to assess evidence from the saiga and livestock interface.

Within this framework, disease emergence is considered to occur through five interconnected stages. First, environmental and anthropogenic factors, including climate variability, land use and land cover, availability of water, as well as livestock management and pressure, change the distribution and mobility of wildlife and livestock. Second, the changes in the movement and resource exploitation result in spatial and temporal overlap of host populations and their environments. Thirdly, this overlap creates opportunities for direct exposure, environmental exposure, vector mediated or scavenger mediated pathogen exposure. Fourth, host related factors and pathogen characteristics will influence whether exposure is followed by transient contamination, infection, host switching or sustained transmission. Finally, the expression of disease and further transmission will decide

whether an isolated single spill over will culminate in an outbreak or continue to be sustained in a new host population. Therefore, epidemiological, ecological and genomic evidence should be considered together.

At the interface, there are three interlinked pillars that are emphasized by One Health approaches (Gwakisa *et al.*, 2023). The first is the surveillance, which involves periodic sampling of an animal population so that pathogens can be identified before they attain large scale outbreaks (Cardoso *et al.*, 2022). The second is diagnostics, which is becoming more and more dependent on molecular tools like the polymerase chain reaction assays and phylogenetic analysis to determine the geographic and species origin of the strain of the pathogen (Schmitz *et al.*, 2022). The third component is intervention, which may include vaccination, livestock movement management, biosecurity, parasite control, habitat management and targeted veterinary measures. The surveillance, diagnostics and intervention processes are not autonomous in the proposed framework. Surveillance detects shifts in the ecological contacts and occurrence of pathogens; molecular diagnostics assesses the identity and relatedness of pathogens; the evidence from these two activities informs interventions at various points along the transmission pathway where risk can be most effectively reduced (Nuvey *et al.*, 2022).

One of the distinguishing characteristics of interface disease dynamics is that in addition to livestock, wildlife populations can only be managed with certain tools not available for livestock (Karmacharya *et al.*, 2024). Vaccination, treatment and quarantine are practices that are common in domestic animals, but difficult to be applied to free-ranging animals, especially those of conservation concern like the saiga antelope (Kock *et al.*, 2010). This imbalance often means that disease control measures at the livestock side are aimed at livestock, such as enhanced biosecurity, targeted use of anthelmintics, selection of breeds or developments for wildlife (only in very unusual circumstances, targeted veterinary care for

al., 2021b). Bovine tuberculosis (BTB) caused by the bacterium *Mycobacterium bovis* has long been known to be maintained by wildlife reservoirs, and in parts of the UK, badger populations and in New Zealand (Justus *et al.*, 2024). Brushtail possum populations are well characterized examples of wild maintenance hosts which can persist infection in cattle herds despite intensive control activity aimed at eradication in cattle (Byrne *et al.*, 2024). A similar situation exists with *Brucella abortus* infection in elk and bison in the Greater Yellowstone Ecosystem of the United States, with elk and bison populations harboring the infection which occasionally spill over into cattle grazing on the margins of protected areas (Cotterill *et al.*, 2018). And decades of debate over the effectiveness of and need for vaccination, fencing and population control as complementary responses to *Brucella* control (Zhang *et al.*, 2018).

Another example of an interface is avian influenza, where many subtypes of influenza A virus are found in wild waterfowl that can infect domestic poultry flocks and, in rare cases, cause zoonotic health effects in humans, with often catastrophic economic and sometimes zoonotic consequences (Bruno *et al.*, 2026). African swine fever, which is sustained in a wild boar population in certain parts of Europe and Asia, is another example of how the control of the virus primarily in commercial pig production (Cadenas-Fernández *et al.*, 2022). It can be complicated by the spread of the virus across the landscape, via infected wild boar, despite successful eradication on individual farms (Makovska *et al.*, 2023).

The examples from around the world have some similarities with the saiga and sheep system in Central Asia analyzed in this review (Kushaliyev *et al.*, 2023). A pathogen of immediate concern for the health of livestock is present in each of these cases and is found in a wildlife population, which in addition to livestock has an immediate host or reservoir (Libera *et al.*, 2022). The contact between wildlife and livestock is affected by environmental and seasonal factors; and control measures must involve more than just conventional livestock-focused veterinary medicine (Timsina, 2024). The saiga antelope and sheep system in Kazakhstan thus can be seen as a well-documented example of a pattern that is occurring across the region with emerging infectious diseases and, by extension, an example of a pattern that is seen globally (Table 1) (Abdybekova *et al.*, 2023). endangered wildlife populations) (Gortazar *et al.*, 2015).

Global comparisons of wildlife and livestock interface dynamics: It is helpful to first understand the nature of wildlife-livestock interactions in the broader context of the world, as similar interactions have been observed in many other disease types and ecosystems; the Central Asian case studies that make up the core of this review provide illustrative examples of these interactions (Jori *et*

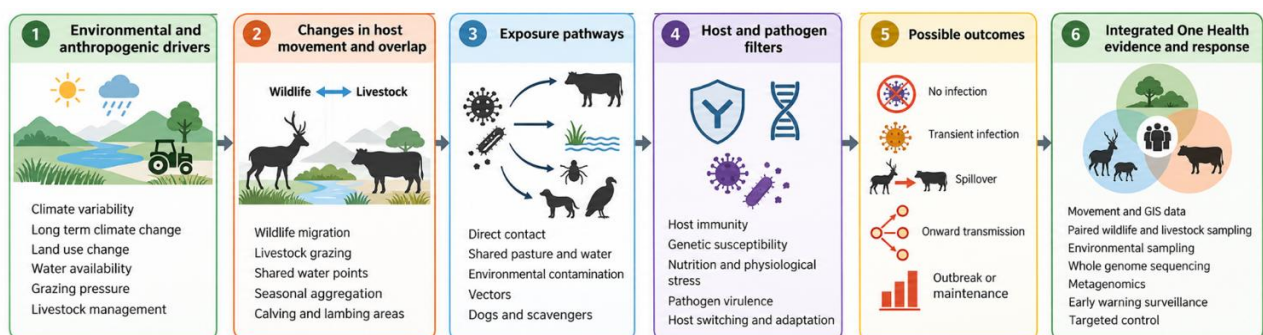


Fig. 1: One Health approach to Emerging diseases at the Wildlife-Livestock interface. Changes in the environment and anthropogenic conditions affect wildlife movement, livestock management and overlap, which in turn affects the direct and indirect exposure pathways. Host susceptibility and pathogen characteristics are responsible for the progression from exposure to disease emergence/host switching/onward transmission. Ecological, epidemiological and genomic surveillance are feasible means of evidence for pathogen exchange and opportunities for One Health interventions at the target level.

Table 1: Representative global wildlife and livestock systems providing comparative evidence for cross-species disease dynamics

Pathogen or disease	Wildlife host	Livestock host	Setting	Main interface mechanism	Evidence available	Interpretation of Evidence level	Relevance to saiga-livestock review	Reference
<i>Mycobacterium bovis</i>	European badger	Cattle	Ireland and UK	Direct and indirect environmental contact	Long term epidemiology, movement studies, surveillance and molecular evidence	Wildlife contribution to cattle epidemiology is well established, although individual transmission events may remain difficult to assign	Strong	Demonstrates how reservoir status (Byrne <i>et al.</i> , 2024) requires population level evidence, not simple co-occurrence
<i>Brucella abortus</i>	Elk, bison also important in the Greater Yellowstone ecosystem	Cattle	USA	Aggregation, reproductive materials and shared range	Long term ecological and epidemiological evidence	Spillover from infected cattle and elk populations to cattle has been documented	Strong	Illustrates how host aggregation and management can modify spillover risk (Cotterill <i>et al.</i> , 2018)
Peste des petits ruminants virus	Mongolian saiga and other wild ungulates	Sheep and goats	Mongolia	Spatial overlap between infected livestock and wild ungulates	Clinical, spatiotemporal and molecular evidence including related viral sequences	Evidence strongly supports livestock to wildlife spillover during the 2016 to 2017 outbreak	Strong	Closely relevant saiga (Pruvot <i>et al.</i> , 2020) example showing the level of evidence needed to support transmission direction
African swine fever virus	Wild boar	Domestic pigs	Europe and Asia	Animal movement, contaminated environments and carcasses	Surveillance, epidemiology and molecular evidence	Direction varies by epidemiological setting	Strong interface evidence	Demonstrates that wildlife and livestock roles may change (Cadenas Fernández <i>et al.</i> , 2022) among settings and should not be assumed in advance
Influenza viruses	A Wild aquatic birds	Domestic poultry	Global	Migration, shared environments and indirect contamination	Extensive surveillance and molecular evidence	Repeated wildlife and poultry introductions occurs, although transmission can be more complex in some systems	Strong	Illustrates the importance of movement ecology and molecular surveillance (Blagodatski <i>et al.</i> , 2021)

Drivers of pathogen emergence at the interface:

Multiple ecosystem and human factors exacerbate the risk of the spread of pathogens at the intersection of animals and humans (Esposito *et al.*, 2023). Land use change is also one of the most important, with a decline in spatial separation between the ranges of wild ungulates and livestock due to the expansion of grazing areas and development of agriculture (Barroso and Gortázar, 2024). In areas where pastoralism has a low density, the rise in pastoralism density and the change of grazing patterns puts domestic livestock closer to the wildlife corridors, especially during migration. Transmission mechanics can be affected by variations in precipitation and temperature, or climate variability, which is different from long-term climate change (Stavi *et al.*, 2022). Short droughts cause domestic and wild ungulates to gather within certain patches of green forage and water which artificially increase host density and contact rates. In contrast, long-term climate change can alter the geographic distribution of habitats for vectors, and can affect the seasonal timing of saiga migration routes (Khanyari *et al.*, 2022a). Drought can drive together wild and domestic animals at such high densities that contact rates increase and the chance of a pathogen spread through shared environmental reservoirs are greatly increased (Tomori and Oluwayelu, 2023).

In addition to demographic factors, there are limiting factors within the wildlife populations which further influence disease dynamics (Almberg *et al.*, 2022). Declines in populations during history can be recovered and result in increased densities of the population, as has happened with several populations of saiga in Kazakhstan after interventions for their conservation can be implemented, which can increase

the possibility of pathogen transmission within or between populations (Serikbayeva *et al.*, 2023). Likewise, the genetic homogeneity which can be caused by population bottlenecks can lead to lack of immunological diversity in recovering wildlife populations, which may lead to increased susceptibility to some pathogens (Gibson, 2022). Differences in indigenous breeds across pastoral areas also add to variability of susceptibility of livestock to diseases, which are not always fully characterized (Velado-Alonso *et al.*, 2022). When this is considered in conjunction with pathogen specific surveillance, understanding the genetic background of livestock populations, such as their genetic predispositions to specific diseases (Struelens *et al.*, 2024). Therefore, an important complement to pathogen specific surveillance and knowledge of the role host genetics play in the probability of infection, as well as the severity of clinical outcomes (Vashisht *et al.*, 2023).

It is also important to remember that as well as being shaped by ecological drivers, contact at the interface is also shaped by socioeconomic factors in pastoral communities that are often overlooked when considering only ecological drivers (Sharifian *et al.*, 2022). Many factors affecting the occurrence of domestic sheep and migrating saiga herds, such as herding practices, sheep stocking densities, and the adoption of biosecurity measures like controlled watering points or fencing, affect how often domestic sheep will encounter migrating saiga herds (Hatami *et al.*, 2022). In a community which has livestock as an important livelihood, it is not always easy to distinguish between the need to find forage and the need to consider the risk of disease when choosing where and when to graze (Horn and Isselstein, 2022). Direct

epidemiological consequences of the latter are understandable considering the economic pressures and are not always ignored. Having a grasp of these livelihood constraints instead of assuming that if herders are not in contact with wildlife migration routes, they will readily adopt effective disease mitigation measures, is more likely to lead to long-term adoption of practical strategies (Yeshey *et al.*, 2023).

Most importantly, the flow of pathogens is bidirectional at this interface. Domestic livestock also have been recognized as important sources of infection for susceptible wildlife species (known as spillback or reverse transmission). In addition, the presence of common parasite species in the pasture suggests co-occurrence and environmental contamination but does not guarantee the direction of cross-transmission. True transmission would involve epidemiological association (spatial as well as molecular) and molecular identity of parasite populations (Fig. 2). Interfacial disease transmission should also be recognized as being facilitated by scavenging and predator species especially in the case of parasites with indirect life cycles (Newsome *et al.*, 2024). Domestic and semi wild dogs that are involved with the saiga herding community can be parasites of natural dead, predation or disease saiga antelope, allowing completion of parasite life cycles that require carnivores as definitive hosts (Khanyari *et al.*, 2022a). Cestode parasites are also of particular interest for this pathway as they are transmitted in the carcasses of infected wildlife that are available to dogs, and that these

infected carcasses are a major component of the wildlife mortality events that can result in infection in livestock (Rojas *et al.*, 2024).

Bacterial Diseases at the Interface: Pasteurellosis in Wild and Domestic Ungulates

Pasteurella (P.) multocida has been a focus of attention in Central Asia because of its reported link to mass mortality of saiga antelope populations and its importance to livestock health (Akçakavak *et al.*, 2024; Nikolaenko, 2024). *P. multocida* is a gram-negative coccobacillus that can be commensally carried in the upper respiratory tract and can also act opportunistically as a pathogen if physiologic stress occurs or the environment is altered (Piorunek *et al.*, 2023; Shahzad *et al.*, 2024). So that the clinical significance of this organism is highly dependent on the host's status and environment (Woelfel *et al.*, 2024).

This has been confirmed in the western Kazakhstan region where investigations of the carrier state of pasteurellosis in apparently healthy saiga antelopes have shown that a proportion of the animals are carriers of the organism sub-clinically, meaning the bacterium can be present in a herd and not overtly disease causing until under the right conditions (Amirgazin *et al.*, 2025). This carrier phenomenon is of epidemiological importance because it does not imply that wild populations are not infected with a disease-causing pathogen, but rather that the infection is not visible from the outside.

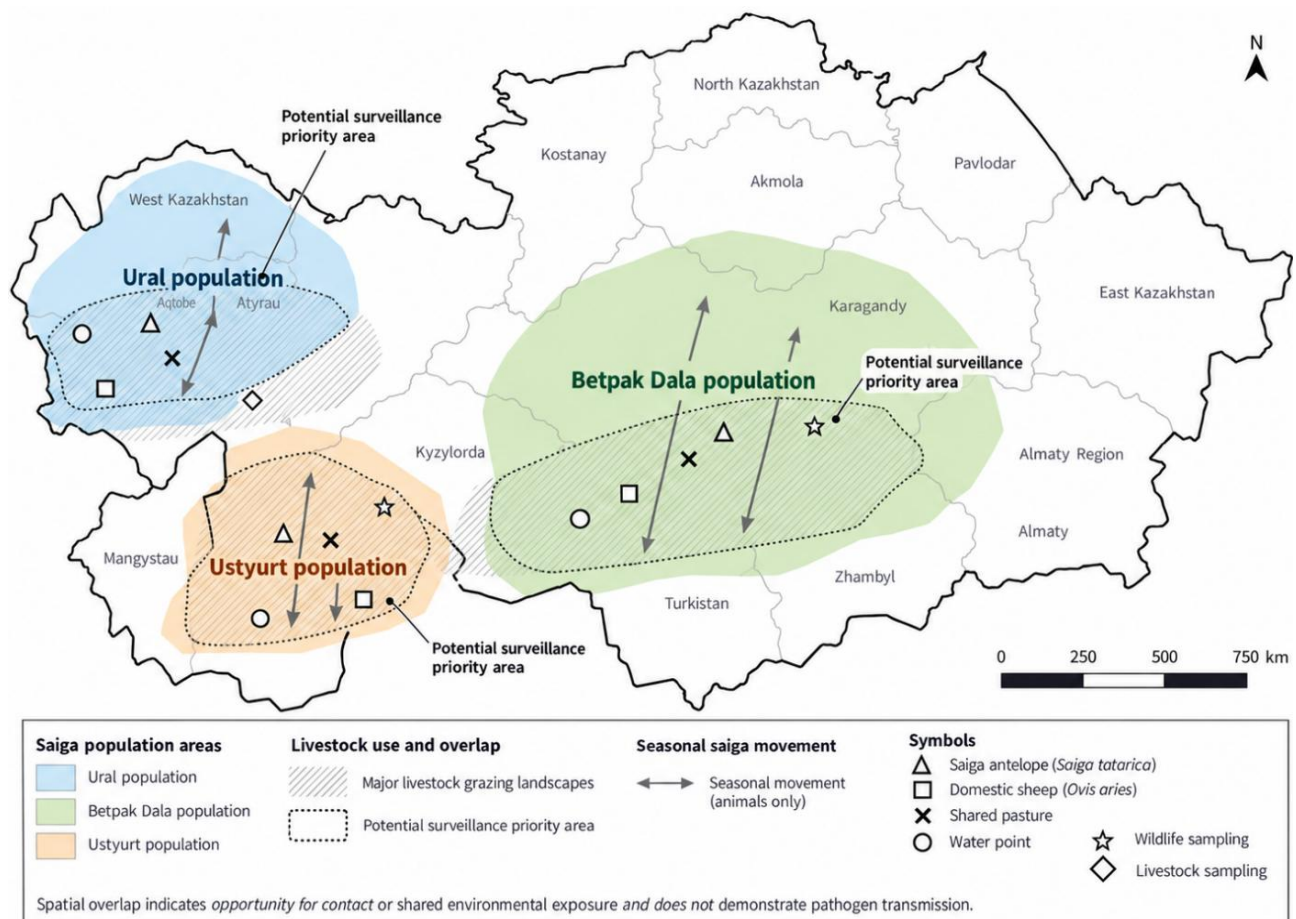


Fig. 2: The spatial setting of the interface between saiga and livestock in Kazakhstan. The areas of major saiga populations and movement areas are represented with respect to the landscapes of livestock use relevant to implementation of interface surveillance.

In Kazakhstan, there is a better basis for comparison of *P. multocida* from wildlife and livestock which are associated with hemorrhagic septicemia based on recent genomic evidence. Whole genome sequencing of 22 isolates from saiga and livestock revealed closely related hemorrhagic septicemia lineages and showed phylogenetic clustering of isolates from outbreaks (Amirgazin *et al.*, 2025). Importantly, the isolates grouped by specific outbreaks, and not by a single mixed wildlife-livestock transmission cluster. The genomic results, therefore, support the presence of related *P. multocida* lineages in both wildlife and livestock disease systems in Kazakhstan, but do not confirm evidence of direct transmission between saiga and domestic animals, or direction of transmission. The genomic relatedness should thus be considered in conjunction with the host sampling contemporarily performed, geographical overlap and epidemiological contact data before inferring cross-species transmission. Thus, the available migration-associated studies demonstrate temporal and ecological opportunity for contact and provide isolates from both saiga and livestock, but they do not constitute direct evidence of a transmission event from one host population to the other.

Another aspect of the epidemiology of pasteurellosis at this nexus is the impact of seasonality on the transfer of pathogens (Balta *et al.*, 2024). The presence of *P. multocida* in migration periods suggests that the bacterium is present when there is a potential for high spatial overlap between wildlife and livestock. But no temporal association proves that migration is connected to bacterial exchange between saiga and domestic animal. Migration corridors should therefore be considered as priority areas for coordinated surveillance and not as proven transmission corridors. To assess if pathogen exchange is happening within these zones, it is important to sample saiga and livestock simultaneously, and to conduct high resolution molecular or genomic comparisons and spatial epidemiological analyses (Khanyari *et al.*, 2022a; Taubaev *et al.*, 2024).

The outbreak of pasteurellosis in saiga antelope is of particular concern from a clinical and pathogenesis perspective as outbreaks are historically linked to large-scale and sudden mortalities occurring over a short timeframe to affect a large percentage of a herd (Orkara *et al.*, 2025). It is believed that a normally commensal or sub-clinically carried organism becomes pathogenic and systemic when host stress, environmental factors. And perhaps additional physiological changes which occur around calving or nutritional factors combine to trigger the infection, but the exact sequence of events is still under study. A stable carrier state in apparently healthy populations means the pathogen is always present at some baseline level in saiga herds and the central epidemiological question is not whether it is present or not, but what factors lead to the manifestation of a disease outbreak (Khanyari *et al.*, 2022a).

The potential implications of saiga carriage to domestic sheep sharing the same rangelands are not clear. Shared range use does not mean that sheep are acquiring *P. multocida* from saiga as there are opportunities for exposure to a common environmental source or infected host. So, livestock that are on a seasonal basis in the same

areas as saiga should be assumed as suitable targets for paired surveillance and not assumed to be continuously exposed to saiga. Using a coordinated sampling program of wildlife, livestock and environmental sources would identify if genetically related strains exist throughout the compartments (Taubaev *et al.*, 2024). Second, veterinary services monitoring of livestock health in these regions could benefit from using molecular surveillance data from wildlife as an early indicator of strains that might have emerging risk in co grazing sheep, a sentinel system for livestock health protection (Marzouk and Alajaji, 2025).

All evidence taken together shows that *P. multocida* can be carried by saiga, that outbreaks of saiga disease have occurred and that molecular characterization of bacterial lineages is useful for comparisons. While there could be a spatial overlap with livestock during the migration season, which could increase the risk of cross-species transmission of *P. multocida*, there is no current evidence that *P. multocida* can be transmitted through migration itself. Genomic relatedness, migration data and temporally matched sampling from both saiga and livestock would be required to determine whether direct pathogen exchange occurs and, if so, its direction (Kamath *et al.*, 2016). The results from this work highlight the need for continued surveillance of both domestic and wild host populations, and to not consider pasteurellosis as a solely wildlife health issue, as these lineages of bacteria can be present within the entire interface ecosystem (Bravo *et al.*, 2022).

Parasitic diseases at the interface: In Kazakhstan, helminth infection has been found in saiga antelope as well as domestic livestock, and the opportunity for helminth exposure can be through shared rangelands, where infective stages of the parasites may be deposited in the pasture or water. However, the presence of the same taxa of parasite in wildlife and livestock does not confirm cross-species transmission (Abdybekova *et al.*, 2023). Parasite fauna of Ural saiga antelopes and Turkmenian kulan (wild horses) in Kazakhstan have been surveyed, and a variety of helminth species found in these wild equid and antelope populations have been recorded, with baseline data on the helminth fauna of wildlife living on a rangeland shared with domestic herds in Kazakhstan (Kushaliyev *et al.*, 2024). This survey work confirms that the area's wild animal herd supports a wide range of parasites, some of which have also been reported in domestic sheep. This overlap demonstrates compatible host ranges and potential shared environment exposure but does not independently establish transmission between wildlife and livestock (Khanyari *et al.*, 2022b).

Comparative study of helminths of saiga antelope and Ural sheep from western Kazakhstan has shown that there is a similarity in parasites of wild and domestic animals living in the same landscape. Similarity is epidemiologically relevant as it points out parasites that can occur in both host populations. However, the mere fact that two species are taxonomically similar does not indicate if infections were directly transmitted from one species to another, indirectly acquired from contaminated pasture, or from an independent transmission cycle. Stronger inference demands that consideration be given to the life cycles of parasites, the temporal and spatial

overlap of the parasites and hosts, the persistence of infective stages in the environment, and, ideally, molecular or population-genetic comparison of parasites sampled from the two populations at the same time (Kushaliyev *et al.*, 2023).

In addition to gastrointestinal (GI) nematodes, infections at the interface have also been reported for cestodes, notably the larval stage of *Taenia multiceps*, known as *Coenurus cerebralis* which causes a neurological disease in sheep known as gid or staggers (Varcasia *et al.*, 2022). In Kazakhstan, molecular study of neurological sheep revealed the presence of *Coenurus cerebralis* in the studied animals using molecular diagnosis, which provided updated data on the prevalence of the condition based on the current state of the condition in Kazakhstani sheep flocks (Kozhayeva *et al.*, 2025).

The intensity of GI nematode transmission at the interface is greatly affected by seasonal and environmental conditions, as most nematode species have free living larval stages that are best developed and live on pasture in moist, moderate temperatures (Jas *et al.*, 2022). Therefore, when rainfall or irrigation-induced pasture moisture increases, the risk of parasite burden in both the saiga antelope and co grazing sheep also increases, whereas when these times of drought happen, the potential for parasite burden in the sheep is reduced, but the hosts are concentrated around existing water sources and green forage patches, which may be at risk for a higher parasite load. The relationship of the climate, pasture condition and host aggregation is vital to predicting when transmission pressure is likely to be high and when parasite control measures applied to the livestock are likely to be most effective (Table 2) (Dickinson *et al.*, 2024).

The pathophysiological effects of GI nematode infection in the saiga antelope, as summarized in recent review articles, do not just include effects on body condition (Bautista-Garfias *et al.*, 2022). But may also have an impact on reproductive capacity and susceptibility to co-infections, relevant considering the historical susceptibility of saiga populations to mass mortality events. It is important to note that the physiological effects on infected animals when combined with nutritional stress or concurrent bacterial infection can be significantly greater than either of these alone (Gaudino *et al.*, 2022). Thus, integrated rather than pathogen-specific

monitoring programs are increasingly recommended for this species as part of conservation veterinary programs (Heiderich *et al.*, 2024).

Host genetics and breed susceptibility in livestock:

Although pathogen characteristics and environmental drivers are well studied components in interface disease research, the genetic background of livestock populations is another crucial factor in disease outcomes and is sometimes overlooked in studies of interface disease between wildlife and livestock (Hassell *et al.*, 2017). Kazakhstan has several native sheep breeds that have been adapted to climatic conditions and forage resources of various steppe and desert regions, and, as a result, have unique profiles of hereditary traits important for disease resistance and susceptibility (Orkara *et al.*, 2025). A detailed examination of the Kazakh sheep breeds has laid a foundation to understand breed specific genetic factors, their history and genetic characteristics, as well as important hereditary diseases and disorders that are present in these populations, which can help in understanding how these factors may modify susceptibility to the infectious and parasitic diseases that circulate at the wildlife livestock interface (Taubaev *et al.*, 2024). To determine susceptibility, investigations will be conducted on specific genomic markers including polymorphisms in the Major Histocompatibility Complex (MHC) and Toll-like receptor (TLR) genes in indigenous Kazakh sheep breeds. These loci are known to modulate innate immune responses and cytokines and may account for the clinical variability in severity and shedding rates among different breeds with the same exposures to parasites.

The practical implications of host genetics to interface disease research are also important for breeding and management decisions (Robinson *et al.*, 2023). Some local indigenous breeds are more resistant to common diseases and parasites, and selective breeding programs based on this information might help to improve the resiliency of livestock without the need for high levels of chemical or pharmaceutical management. This strategy is also in line with One Health principles as it will decrease the use of antimicrobial and anthelmintic therapy, thus limiting the potential for antimicrobial resistance to develop that may impede future disease management at the interface (Endale *et al.*, 2023).

Table 2: Representative pathogen systems relevant to wildlife and livestock interfaces and the strength of evidence for cross species transmission

Pathogen/disease	Wildlife host	Livestock host	Geographic relevance	Principal pathway	Evidence available	Strength of cross species evidence	Zoonotic significance	References
<i>Pasteurella multocida</i>	Saiga	Cattle/livestock	Kazakhstan	Respiratory/contact; shared interface	Carriage, outbreaks, WGS	Moderate; unresolved	direction Limited	(Amirgazin <i>et al.</i> , 2025)
Gastrointestinal nematodes	Saiga	Sheep	Kazakhstan	Shared contaminated pasture	Shared taxa, ecological overlap	Plausible; direct transmission demonstrated	cross incompletely low	(Kushaliyev <i>et al.</i> , 2023)
<i>Taenia multiceps</i>	Potential wild intermediate hosts	Sheep	Kazakhstan/global	Canid faecal contamination	Established livestock cycle; molecular detection	canid life saiga role uncertain	Dog sheep cycle strong; Rare zoonotic relevance	(Varcasia <i>et al.</i> , 2022)
<i>Mycobacterium bovis</i>	Badgers and other wildlife	Cattle	Europe	Direct/indirect environmental	Epidemiological and molecular	Strong in well studied systems	Yes	(Justus <i>et al.</i> , 2024)
<i>Brucella abortus</i>	Elk/bison	Cattle	North America	Reproductive materials/contact	Epidemiological and molecular	Strong in defined systems	Yes	(Cotterill <i>et al.</i> , 2018)
PPR virus	Mongolian saiga/wild ungulates	Sheep/goats	Mongolia	Direct/close contact	Spatiotemporal and molecular	Strong livestock to wildlife spillover	No direct zoonotic risk	(Pruvot <i>et al.</i> , 2020)
African fever virus	swine Wild boar	Domestic pigs	Europe/Asia	Contact, carcasses, environment	Epidemiological/molecular	Strong; direction varies	No	(Cadenas Fernández <i>et al.</i> , 2022)

Conservation management and preventive veterinary measures: Control of the disease at the wildlife/livestock interface must be based on interventions that are suitable to the ecological and logistical situation of free-ranging wildlife populations (Jori *et al.*, 2021a). For the saiga antelope, a species of high conservation value with large historical population changes, veterinary preventive measures have been increasingly included in the conservation program for both the Betpakdala and Ural population in Kazakhstan (Serikbayeva *et al.*, 2023). Dedicated nurseries and coordinated veterinary preventive measures for these saiga populations is a practical example of how conservation and veterinary health goals can be integrated to aid in the recovery of the populations while also decreasing the risk of disease. Nursery based approaches also provide an opportunity for increased control over vulnerable age classes, especially the young animals which may be more susceptible to bacterial and parasitic infection. It is as well as the opportunity to provide targeted veterinary care to young animals that would not be possible over the vast expanse of open rangeland used by free ranging herds (Schlecht *et al.*, 2020).

The preventive measures discussed in this review are best understood and applied in the context of overall surveillance and diagnostic results (Akindahunsi *et al.*, 2024). For instance, an understanding of seasonal transmission of *P. multocida* with migration timing can help schedule monitoring to coincide with the highest period of transmission risk and GI nematode epidemiology can help determine pasture rotation or additional nutritional support to reduce any peak periods of nematode transmission. Conservation veterinary programmes thus provide an operational link between epidemiology research and disease management on the ground, with the potential to transform the research into action that could safeguard wildlife populations and the livestock economies on which they depend (Marzouk and Alajaji, 2025).

Surveillance, Diagnostics, and Molecular Epidemiology: The above studies collectively show a trend towards the growing use of molecular tools for surveillance of diseases in wildlife and livestock (Tigistu-Sahle *et al.*, 2023). Polymerase chain reaction (PCR) methods for detection and phylogenetic sequence analysis have been especially useful for two different, but complementary, applications. They enable the correct

identification of the species and strains of pathogenic bacteria which can be hard to discriminate by conventional culture based or biochemical identification, as shown in comparative tests of *P. multocida* identification techniques (Panwar *et al.*, 2023). Second, they allow genetic relationships to be established between strains recovered from various hosts, locations and time periods, a genetic approach that would not be possible by using traditional epidemiological approaches (Hill *et al.*, 2026).

Whole genome sequencing (WGS) and metagenomics should be integrated with standard PCR to advance advancing molecular epidemiology at the wildlife-livestock interface. These contemporary genomic surveillance tools generate accurate granular information to monitor pathogen evolution, genomic adaptation and host-switching mechanisms in real-time. WGS can be used to compare virulence factor polymorphisms and genomic drift for the ability to distinguish between transient environmental contamination and ongoing spillovers of pathogens, moving interface management from reactive diagnostics to proactive surveillance (Fig. 3).

In the case of parasitic diseases, molecular diagnosis has also helped to enhance the accuracy of prevalence estimates, as with the case of *Coenurus cerebralis* in Kazakhstani sheep (Kiyan *et al.*, 2025). It is where the molecular diagnosis would provide greater certainty of the diagnosis than clinical presentation alone, as there can be several causes of neurological signs compatible with coenurosis (Abbas *et al.*, 2024). Such a diagnostic precision is fundamental not only for the proper reporting of the disease, but also for the choice of the proper treatment and the selection of the right disease control measures based on the right cause (Fabre *et al.*, 2023). A significant area of future surveillance research is to expand molecular characterization programs to allow for more comprehensive coverage of the pathogens circulating at the interface, and more systematic sampling plans to better reflect seasonal and geographical variation in the prevalence of pathogens (Vashisht *et al.*, 2023). The coordinated sampling of both wildlife and livestock populations, based on a standard molecular protocol would greatly improve the evidence base for making decisions on disease control and could facilitate the detection of emerging pathogen strains before the outbreak of large numbers of wildlife or livestock hosts (Keusch *et al.*, 2022).

Integrated One Health surveillance framework for the wildlife and livestock interface.

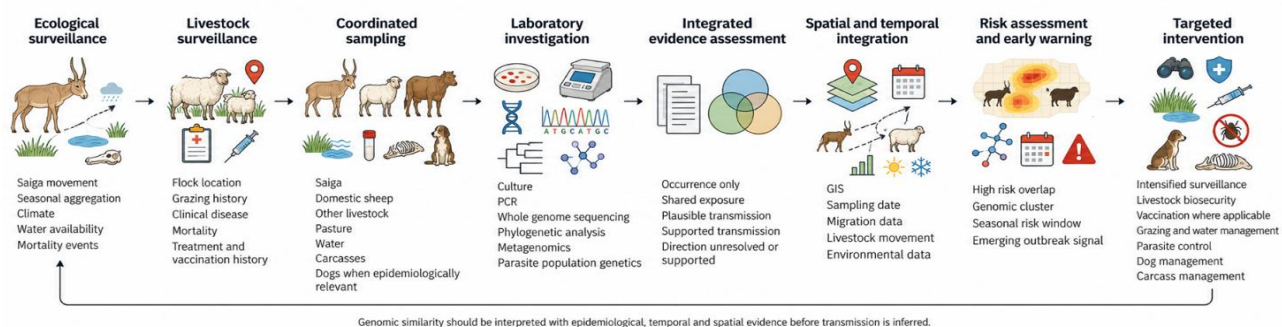


Fig. 3: One Health interface with wildlife and livestock surveillance and evidence-assessment framework. Coordinated sampling and molecular investigation are directed by ecological and livestock and environmental surveillance. Coordinated sampling and molecular investigation is directed by ecological, livestock and environmental surveillance.

One Health response: policy and practice: To convert the scientific information that is summarized in this review into the development of effective disease control policy, there needs to be close working between veterinary services, wildlife conservation authorities and livestock producing communities (Jori *et al.*, 2021b). This collaboration is especially significant in Kazakhstan because of the use of shared rangeland by saiga antelope and domestic sheep and the known potential for pathogen exchange between the saiga and domestic sheep species as shown in the literature reviewed here (Khanyari *et al.*, 2022c). An operational One Health framework must integrate spatial movement data, Geographic Information Systems (GIS), and veterinary surveillance into early-warning systems (Zinsstag *et al.*, 2023). Pathogen monitoring of wild animals for carrier states, like *P. multocida*, can be used in regular monitoring to give early warning of a situation that is likely to lead to disease outbreaks, and in turn allow for preventive measures to be taken before the onset of mass mortality events (Boulianne *et al.*, 2020). Effective programs for managing parasites will take into consideration the overlapping use of the same pastures by both wildlife and livestock, and the importance that guard dogs play in controlling transmission of cestodes and will lessen the overall parasite exposure of both wild and domestic species (Dixit *et al.*, 2024). Incorporation of host genetic information into livestock management decisions can help develop more resilient domestic livestock populations, decreasing reliance on reactive livestock treatment approaches. The ongoing investing in the nursery-based conservation veterinary programmes for vulnerable wildlife populations can help support populations of conservation concern, as well as minimize disease risk at the wider interface.

Realizing these policy goals will depend on the continued cooperation of institutions across sectors, which typically have lacked close collaboration in the past. Such as those providing veterinary services for livestock production, those managing wildlife populations and those conducting the epidemiology and molecular research (Lane *et al.*, 2025). Enhancing the institutional linkages between the fields of wildlife and livestock diseases and making sure that the results of wildlife disease studies are shared with livestock health authorities (Thompson *et al.*, 2024). That livestock health data is shared with wildlife disease authorities are important practical steps towards achieving One Health goals at the wildlife-livestock interface (Karmacharya *et al.*, 2024).

Challenges and future directions: While important advances have been made towards understanding the dynamics of disease transmission between wildlife and livestock in Kazakhstan and similar rangeland systems, disease surveillance and control efforts remain constrained by several challenges. Due to logistical challenges of sampling free-ranging populations of wildlife in large areas, often remote, across the steppe regions, current surveillance information is informative but likely a partial picture of the level of pathogen circulation throughout the region. Resource constraints also inhibit the ability of veterinary and conservation institutions to perform the molecular diagnostic testing increasingly identified as vital to proper pathogen

characterization. Increased availability of sequencing and phylogenetic analysis capacity and training of personnel who can perform and interpret these analyses is an important investment priority to support the enhanced interface disease surveillance in the future.

Changes in migration timing and route driven by climate further complicate future disease management planning, as history may provide for changes in contact between saiga antelope and livestock populations that are hard to predict, and that can impact the spread of diseases like *P. multocida*, which are thought to be strongly associated with migration behavior. Monitoring the migration routes and watching for diseases will continue to be important to identify and address potential changes in migration patterns as they arise. Moreover, future disease management needs to become more data-driven and integrate predictive modelling in a One Health approach. Combining spatial movement data, climate forecasting and genomic surveillance with machine learning models can highlight high-risk spatial-temporal nodes for pathogen spillover, enabling proactively taking action for veterinary and conservation actions before an outbreak happens. The genetic susceptibility of wildlife and livestock populations to disease should be given additional research attention. Similarly, detailed genetic characterisation of saiga antelope populations, including with regards to immune related genetic diversity, would give valuable additional understanding into why some populations seem more susceptible to specific disease-causing pathogens or parasites than others, and thus start to document hereditary factors relevant to disease resistance in the Kazakh sheep breed.

Conclusions: The system of saiga antelope and domestic sheep in Kazakhstan is an important example for studying the complex system of emerging infectious diseases at the wildlife-livestock interface. Current knowledge shows considerable spatial overlap and common environmental reservoirs for pathogens like *P. multocida*, GI nematodes, and *Coenurus cerebralis*, but great epidemiological uncertainty exists. If identical parasite species are found on the same range lands, this does not necessarily mean that the parasites are being transmitted to each other. Future comparative studies should incorporate high-resolution genomic epidemiology with contemporized wildlife, livestock and environmental sampling, movement and spatial epidemiology to differentiate shared exposure from likely cross-host transmission and to assess the direction of transmission when there is sufficient evidence. In addition, intermediate hosts, like shepherd dogs, and changing climatic factors play a key role and need to be explicitly included in disease models. To go forward, a strong, effective One Health approach is needed. Integrated veterinary-conservation policies, combined with spatial GIS movement tracking, targeted molecular diagnostics, predictive disease modelling and integrated veterinary-conservation policies, can help authorities move from reactive outbreak management to proactive risk mitigation. These are all integrated practices that are necessary to ensure the sustainable living of vulnerable wildlife populations along with the livelihoods that rely on these shared ecosystems.

REFERENCES

- Abbas I, Tamponi C, Madau G *et al.*, 2024. Treatment and management of coenurosis by *Taenia multiceps*: field data from outbreaks in endemic regions and literature review. *Parasites & Vectors* 17(1):335.
- Abdybekova AM, Zhaksylykova AA, Kushaliyev KZ *et al.*, 2023. A survey of the parasites of Ural saiga antelopes and Turkmenian kulans of Kazakhstan. *International Journal for Parasitology: Parasites and Wildlife* 21:232-236.
- Ahmed MM, Okesanya OJ, Othman ZK *et al.*, 2025. Holistic approaches to zoonoses: integrating public health, policy, and one health in a dynamic global context. *Zoonotic Diseases* 5(1):5.
- Akcakavak G, Karataş Ö, Tuzcu N *et al.*, 2024. Determination of apoptosis, necroptosis and autophagy markers by real-time pcr in naturally infected pneumonic pasteurellosis caused by *Pasteurella multocida* and *Mannheimia haemolytica* in cattle. *Pakistan Veterinary Journal* 44(2):483-489.
- Akindahunsi T, Olulaja O, Ajayi O *et al.*, 2024. Analytical tools in diseases epidemiology and surveillance: A review of literature. *International Journal of Applied Research* 10(9):155-161.
- Almberg ES, Manlove KR, Cassirer EF *et al.*, 2022. Modelling management strategies for chronic disease in wildlife: Predictions for the control of respiratory disease in Bighorn sheep. *Journal of Applied Ecology* 59(3):693-703.
- Amirgazin A, Yessembekova G, Akhmetova A *et al.*, 2025. Genomic Insights into *Pasteurella multocida* Serotype B: 2 from Hemorrhagic Septicemia Outbreaks in Wildlife and Livestock in Kazakhstan. *Pathogens* 14(12):1273.
- Balta I, Lemon J, Murnane C *et al.*, 2024. The One Health aspect of climate events with impact on foodborne pathogens transmission. *One Health* 19:100926.
- Barroso P and Gortázar C, 2024. The coexistence of wildlife and livestock. *Animal Frontiers* 14(1):5-12.
- Bautista-Garfias CR, Castañeda-Ramírez GS, Estrada-Reyes ZM *et al.*, 2022. A review of the impact of climate change on the epidemiology of gastrointestinal nematode infections in small ruminants and wildlife in tropical conditions. *Pathogens* 11(2):148.
- Blagodatski A, Trutneva K, Glazova O *et al.*, 2021. Avian influenza in wild birds and poultry: dissemination pathways, monitoring methods, and virus ecology. *Pathogens* 10(5):630.
- Boulianne M, Blackall PJ, Hofacre CL *et al.*, 2020. Pasteurellosis and other respiratory bacterial infections. *Diseases of Poultry*:831-889.
- Bravo M, Combes T, Martínez FO *et al.*, 2022. Wildlife symbiotic bacteria are indicators of the health status of the host and its ecosystem. *Applied and Environmental Microbiology* 88(1):e01385-01321.
- Bruno L, Nappo MA, Ferrari L *et al.*, 2022. Nipah virus disease: epidemiological, clinical, diagnostic and legislative aspects of this unpredictable emerging zoonosis. *Animals* 13(1):159.
- Bruno L, Nappo MA, Frontoso R *et al.*, 2026. Avian Influenza Viruses: Global panzootic, host range expansion and emerging ONE-HEALTH THREATS. *Veterinary Sciences* 13(1):67.
- Byrne AV, Allen A, Ciuti S *et al.*, 2024. Badger ecology, bovine tuberculosis, and population management: lessons from the island of Ireland. *Transboundary and Emerging Diseases* 2024(1):8875146.
- Cadenas-Fernández E, Ito S, Aguilar-Vega C *et al.*, 2022. The role of the wild boar spreading African swine fever virus in Asia: another underestimated problem. *Frontiers in Veterinary Science* 9:844209.
- Cardoso B, García-Bocanegra I, Acevedo P *et al.*, 2022. Stepping up from wildlife disease surveillance to integrated wildlife monitoring in Europe. *Research in Veterinary Science* 144:149-156.
- Cotterill GG, Cross PC, Cole EK *et al.*, 2018. Winter feeding of elk in the Greater Yellowstone Ecosystem and its effects on disease dynamics. *Philosophical Transactions of the Royal Society B: Biological Sciences* 373(1745):20170093.
- Dickinson ER, McFarland C, Toigo C *et al.*, 2024. Host movement dominates the predicted effects of climate change on parasite transmission between wild and domestic mountain ungulates. *Royal Society Open Science* 11(1):230469.
- Dixit B, Kumar R, Dixit AK *et al.*, 2024. Risk factors associated with parasitic diseases in dogs and cats. *Principles and Practices of Canine and Feline Clinical Parasitic Diseases*:19-30.
- Endale H, Mathewos M and Abdeta D, 2023. Potential causes of spread of antimicrobial resistance and preventive measures in one health perspective-a review. *Infection and Drug Resistance*:7515-7545.
- Espósito MM, Turku S, Lehrfield L *et al.*, 2023. The impact of human activities on zoonotic infection transmissions. *Animals* 13(10):1646.
- Fabre V, Davis A, Diekema DJ *et al.*, 2023. Principles of diagnostic stewardship: a practical guide from the Society for Healthcare Epidemiology of America Diagnostic Stewardship Task Force. *Infection Control & Hospital Epidemiology* 44(2):178-185.
- Fagre AC, Cohen LE, Eskew EA *et al.*, 2022. Assessing the risk of human-to-wildlife pathogen transmission for conservation and public health. *Ecology Letters* 25(6):1534-1549.
- Gaudino M, Nagamine B, Ducatez MF *et al.*, 2022. Understanding the mechanisms of viral and bacterial coinfections in bovine respiratory disease: a comprehensive literature review of experimental evidence. *Veterinary Research* 53(1):70.
- Gibson AK, 2022. Genetic diversity and disease: The past, present, and future of an old idea. *Evolution* 76(s1):20-36.
- Gortázar C, Barroso P, Nova R *et al.*, 2022. The role of wildlife in the epidemiology and control of Foot-and-mouth-disease And Similar Transboundary (FAST) animal diseases: a review. *Transboundary and Emerging Diseases* 69(5):2462-2473.
- Gortazar C, Diez-Delgado I, Barasona JA *et al.*, 2015. The wild side of disease control at the wildlife-livestock-human interface: a review. *Frontiers in Veterinary Science* 1:27.
- Gwakisa P, George J, Sindato C *et al.*, 2023. Pillars for successful operationalization of one health as an ecosystem approach: experience from a human-animal interface in the Maasai steppe in Tanzania. *One Health Outlook* 5(1):11.
- Hassell JM, Begon M, Ward MJ *et al.*, 2017. Urbanization and disease emergence: dynamics at the wildlife-livestock-human interface. *Trends in Ecology & Evolution* 32(1):55-67.
- Hatami Z, Laven RA, Jafari-Gh S *et al.*, 2022. Factors affecting the perception and practice of Iranian nomadic and semi-nomadic pastoralists in regard to biosecurity practices in sheep and goat farms: a cross-sectional and prospective study. *Ruminants* 2(1):54-73.
- Hayes BH, Vergne T, Andraud M *et al.*, 2023. Mathematical modeling at the livestock-wildlife interface: scoping review of drivers of disease transmission between species. *Frontiers in Veterinary Science* 10:1225446.
- Heiderich E, Keller S, Pewsner M *et al.*, 2024. Analysis of a European general wildlife health surveillance program: Chances, challenges and recommendations. *Plos One* 19(5):e0301438.
- Hernandez A, Lee J and Kang H, 2025. Navigating the interconnected web of health: a comprehensive review of the one health paradigm and its implications for disease management. *Yonsei Medical Journal* 66(4):203.
- Hill V, Dellicour S, Giovanetti M *et al.*, 2026. Phylogenetic insights into the transmission dynamics of arthropod-borne viruses. *Nature Reviews Genetics* 27(1):47-61.
- Horn J and Isselstein J, 2022. How do we feed grazing livestock in the future? A case for knowledge-driven grazing systems. *Grass and Forage Science* 77(3):153-166.
- Hossain H, Chowdhury MSR, Khan SS *et al.*, 2025. Emerging Zoonotic Diseases: Epidemiology, Public Health Impact, and the Urgent Need for a Unified "One Health" Approach. *Pakistan Veterinary Journal* 45(1):36-47.
- Jas R, Hembram A, Das S *et al.*, 2022. Impact of climate change on the free-living larval stages and epidemiological pattern of gastrointestinal nematodes in livestock. *Indian Journal of Animal Health* 61(2):83-94.
- Jori F, De Nys H, Faye B *et al.*, 2021a. Characteristics and perspectives of disease at the wildlife-livestock interface in Africa. *Diseases at the Wildlife-Livestock Interface: Research and Perspectives in a Changing World*:181-215.
- Jori F, Hernandez-Jover M, Magouras I *et al.*, 2021b. Wildlife-livestock interactions in animal production systems: what are the biosecurity and health implications? *Animal Frontiers* 11(5):8-19.
- Justus W, Valle S, Barton O *et al.*, 2024. A review of bovine tuberculosis transmission risk in European wildlife communities. *Mammal Review* 54(3):325-340.
- Kamath PL, Foster JT, Drees KP *et al.*, 2016. Genomics reveals historic and contemporary transmission dynamics of a bacterial disease among wildlife and livestock. *Nature Communications* 7(1):1448.
- Karmacharya D, Herrero-García G, Luitel B *et al.*, 2024. Shared infections at the wildlife-livestock interface and their impact on public health, economy, and biodiversity. *Animal Frontiers* 14(1):20-29.
- Keusch GT, Amuasi JH, Anderson DE *et al.*, 2022. Pandemic origins and a One Health approach to preparedness and prevention: Solutions based on SARS-CoV-2 and other RNA viruses. *Proceedings of the National Academy of Sciences* 119(42):e2202871119.

- Khanyari M, Milner-Gulland EJ, Oyanedel R *et al.*, 2022a. Investigating parasite dynamics of migratory ungulates for sustaining healthy populations: Application to critically-endangered saiga antelopes *Saiga tatarica*. *Biological Conservation* 266:109465.
- Khanyari M, Robinson S, Milner-Gulland EJ *et al.*, 2022b. Pastoralism in the high Himalayas: Understanding changing practices and their implications for parasite transmission between livestock and wildlife. *Pastoralism* 12(1):44.
- Khanyari M, Robinson S, Morgan ER *et al.*, 2022c. Identifying relationships between multi-scale social–ecological factors to explore ungulate health in a western Kazakhstan rangeland. *People and Nature* 4(2):382-399.
- Kiyan V, Smagulova A, Uakhit R *et al.*, 2025. Molecular identification of cryptic cysticercosis: *Taenia* spp. in wild and domestic intermediate hosts in Kazakhstan. *Diversity* 17(9):655.
- Kock RA, Woodford MH and Rossiter PB, 2010. Disease risks associated with the translocation of wildlife. *Revue Scientifique et Technique* 29(2):329.
- Kozhayeva A, Kereyev A, Shevtsov A *et al.*, 2025. Molecular prevalence of *Coenurus cerebralis* in sheep exhibiting neurological symptoms in Kazakhstan. *Frontiers in Veterinary Science* 12:1620425.
- Kushaliyev K, Shamshidin A, Kozhayeva A *et al.*, 2024. Creation of nurseries and veterinary preventive measures for saigas of Betpakdala and Ural populations in Kazakhstan. *Scientific Horizons* 27(1):41-53.
- Kushaliyev K, Ussenov Z, Alimbekov S *et al.*, 2023. Study of the saiga helminth fauna and Ural sheep in the western region of Kazakhstan. *Open Veterinary Journal* 13(4):485-494.
- Lane JK, Kelly T, Bird B *et al.*, 2025. A one health approach to reducing livestock disease prevalence in developing countries: advances, challenges, and prospects. *Annual Review of Animal Biosciences* 13(1):277-302.
- Libera K, Konieczny K, Grabska J *et al.*, 2022. Selected livestock-associated zoonoses as a growing challenge for public health. *Infectious Disease Reports* 14(1):63-81.
- Makovska I, Dhaka P, Chantzias I *et al.*, 2023. The role of wildlife and pests in the transmission of pathogenic agents to domestic pigs: A systematic review. *Animals* 13(11):1830.
- Malhi Y, Lander T, le Roux E *et al.*, 2022. The role of large wild animals in climate change mitigation and adaptation. *Current Biology* 32(4):R181-R196.
- Marzouk E and Alajaji AI, 2025. Preventive Immunology for Livestock and Zoonotic Infectious Diseases in the One Health Era: From Mechanistic Insights to Innovative Interventions. *Veterinary Sciences* 12(10):1014.
- Miller M, Gómez MA, Tanner R *et al.*, 2025. Workshop report: One Health challenges and knowledge gaps in the control of intracellular infections with a focus on tuberculosis and leishmaniasis. *Vaccine* 53:126929.
- Newsome T, Cairncross R, Cunningham CX *et al.*, 2024. Scavenging with invasive species. *Biological Reviews* 99(2):562-581.
- Nikolaenko D, 2024. An ecotoxicological research of the mass mortality of Saiga antelope (*S. tatarica*) and consideration the notion of "hyper-virulence" as an explanation for catastrophic viral occurrences. *Environmental Epidemiology* 18(2).
- Nuvey FS, Arkoazi J, Hattendorf J *et al.*, 2022. Effectiveness and profitability of preventive veterinary interventions in controlling infectious diseases of ruminant livestock in sub-Saharan Africa: a scoping review. *BMC Veterinary Research* 18(1):332.
- Orkara S, Khamzina A, Sandybayev N *et al.*, 2025. Epidemiological landscape and genetic prospects for marker-assisted selection in Kazakh sheep. *Frontiers in Veterinary Science* 12:1647959.
- Panwar S, Duggirala KS, Yadav P *et al.*, 2023. Advanced diagnostic methods for identification of bacterial foodborne pathogens: contemporary and upcoming challenges. *Critical Reviews in Biotechnology* 43(7):982-1000.
- Piorunek M, Brajer-Luftmann B and Walkowiak J, 2023. *Pasteurella multocida* infection in humans. *Pathogens* 12(10):1210.
- Pruvot M, Fine AE, Hollinger C *et al.*, 2020. Outbreak of peste des petits ruminants among critically endangered Mongolian saiga and other wild ungulates, Mongolia, 2016–2017. *Emerging Infectious Diseases* 26(1):51.
- Robinson NA, Robledo D, Sveen L *et al.*, 2023. Applying genetic technologies to combat infectious diseases in aquaculture. *Reviews in Aquaculture* 15(2):491-535.
- Rojas A, Germitsch N, Oren S *et al.*, 2024. Wildlife parasitology: sample collection and processing, diagnostic constraints, and methodological challenges in terrestrial carnivores. *Parasites & Vectors* 17(1):127.
- Rulli MC, D'Odorico P, Galli N *et al.*, 2025. Land use change and infectious disease emergence. *Reviews of Geophysics* 63(2):e2022RG000785.
- Schlecht E, Turner MD, Hülsebusch CG *et al.*, 2020. Managing rangelands without herding? Insights from Africa and beyond. *Frontiers in Sustainable Food Systems* 4:549954.
- Schmitz JE, Stratton CW, Persing DH *et al.*, 2022. Forty years of molecular diagnostics for infectious diseases. *Journal of Clinical Microbiology* 60(10):e02446-02421.
- Serikbayeva AT, Akimzhanov DS, Iskakova ZA *et al.*, 2023. Saiga (*Saiga tatarica*) conservation strategy in Kazakhstan. *Brazilian Journal of Biology* 83:e275397.
- Shahzad MN, Zafar MA, Tahir AH *et al.*, 2024. Effects of Tyloxapol in the Amelioration of Endotoxemic Effects of *Pasteurella multocida* During Hemorrhagic Septicemia in Water Buffaloes. *Pakistan Veterinary Journal* 44(3):675.
- Sharifian A, Fernández-Llamazares Á, Wario HT *et al.*, 2022. Dynamics of pastoral traditional ecological knowledge: a global state-of-the-art review. *Ecology and Society* 27(1):14.
- Stavi I, Roque de Pinho J, Paschalidou AK *et al.*, 2022. Food security among dryland pastoralists and agropastoralists: The climate, land-use change, and population dynamics nexus. *The Anthropocene Review* 9(3):299-323.
- Struelens MJ, Ludden C, Werner G *et al.*, 2024. Real-time genomic surveillance for enhanced control of infectious diseases and antimicrobial resistance. *Frontiers in Science* 2:1298248.
- Taubae U, Ichshanova A, Kirkimbaeva Z *et al.*, 2024. Properties of *Pasteurella multocida* isolated from animals during the seasonal migration of saigas. *Brazilian Journal of Biology* 84:e280780.
- Teague R, 2023. Livestock interactions in regenerative soil systems. *Biological Approaches to Regenerative Soil Systems*:239-248.
- Thompson L, Cayol C, Awada L *et al.*, 2024. Role of the World Organisation for Animal Health in global wildlife disease surveillance. *Frontiers in Veterinary Science* 11:1269530.
- Tigistu-Sahle F, Mekuria ZH, Satoskar AR *et al.*, 2023. Challenges and opportunities of molecular epidemiology: using omics to address complex One Health issues in tropical settings. *Frontiers in Tropical Diseases* 4:1151336.
- Timsina J, 2024. Agriculture-livestock-forestry Nexus in Asia: Potential for improving farmers' livelihoods and soil health, and adapting to and mitigating climate change. *Agricultural Systems* 218:104012.
- Tomori O and Oluwayelu DO, 2023. Domestic animals as potential reservoirs of zoonotic viral diseases. *Annual Review of Animal Biosciences* 11(1):33-55.
- Usmani MW, Rizvi F, Shakir MZ *et al.*, 2023. Factors influencing the emergence and re-emergence of zoonotic infectious diseases in livestock and human populations. *Zoonosis. Faisalabad: Unique Scientific Publishers*:316-326.
- Varcasia A, Tamponi C, Ahmed F *et al.*, 2022. *Taenia multiceps* coenurosis: a review. *Parasites & Vectors* 15(1):84.
- Vashisht V, Vashisht A, Mondal AK *et al.*, 2023. Genomics for emerging pathogen identification and monitoring: prospects and obstacles. *BioMedInformatics* 3(4):1145-1177.
- Velado-Alonso E, Morales-Castilla I and Gomez-Sal A, 2022. The landscapes of livestock diversity: grazing local breeds as a proxy for domesticated species adaptation to the environment. *Landscape Ecology* 37(4):1035-1048.
- Woelfel S, Silva MS and Stecher B, 2024. Intestinal colonization resistance in the context of environmental, host, and microbial determinants. *Cell Host & Microbe* 32(6):820-836.
- Yeshey, Keenan RJ, Ford RM *et al.*, 2023. Sustainable development implications of human wildlife conflict: an analysis of subsistence farmers in Bhutan. *International Journal of Sustainable Development & World Ecology* 30(5):548-563.
- Zhang N, Huang D, Wu W *et al.*, 2018. Animal brucellosis control or eradication programs worldwide: A systematic review of experiences and lessons learned. *Preventive Veterinary Medicine* 160:105-115.
- Zinsstag J, Kaiser-Grolimund A, Heitz-Tokpa K *et al.*, 2023. Advancing one human–animal–environment health for global health security: what does the evidence say? *The Lancet* 401(10376):591-604.