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Spatial risk of pathogen transmission from cattle to vulnerable and endangered wild bovids in Thailand

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Abstract

The interaction between livestock and wildlife causes challenges for wildlife conservation and public health. Mapping interface areas is essential for prioritizing disease surveillance, implementing mitigation measures, and developing targeted control programs to protect threatened wildlife. We used spatial overlays of habitat suitability to predict interface areas with high risk of pathogen transmission for three Thai wild bovids (gaur [*Bos gaurus*], banteng [*Bos javanicus*] and wild water buffalo [*Bubalus arnee*]) and domestic cattle. We assumed that domestic cattle are the reservoir of important bovine infectious diseases and that high cattle density is a proxy for a higher transmission risk. We calculated the interface inside and outside Thai protected areas and classified these by land use types. Then, we counted the number of bovine infectious disease occurrences reported in high-risk areas. Our study indicated that the highest risk areas for these species are at the forest edges where high habitat suitability and cattle densities overlap. Suitable habitats for wild water buffalo had the largest proportion of high-risk areas (9%), while gaur and banteng had similar risk areas (4%). Kuiburi National Park had the largest risk area (274 km^2) for gaur and banteng, whereas the largest risk area for wild water buffalo overlapped with Huai Thabthan-Had Samran by 126 km^2. Cropland and unclassified forests had the highest percentage of interface areas, indicating a higher risk of pathogen transmission. Our results highlight how habitat suitability analyses could help infectious disease prevention and control strategies and may also support wild bovid conservation initiatives.

KEYWORDS

cattle, infectious disease, interface area, mapping, wildlife

1 | INTRODUCTION

Wild Bovidae (Mammalia: Artiodactyla) are distributed worldwide and play crucial ecosystem roles because they help determine forest and ecosystem structure, transport micronutrients, disperse plant seeds (Ripple et al., 2015, Romero et al., 2015) and are important prey species for predators (Simcharoen et al., 2018). In Asia, wild bovid populations are threatened by multiple factors, including habitat loss and hunting, especially in South and Southeast Asia (Tilker et al., 2019). Natural habitat loss often comes with increased free-grazing livestock encroachment into wildlife habitat, which can lead to problems including resource competition, reducing wildlife abundance (Bhandari et al., 2022), interbreeding between domestic and wild water buffalo (Bhattarai et al., 2023), and infectious disease transmission (Hassell et al., 2017).

Among the 27 recognized wild bovid species as of 2020 (IUCN, 2020), five species remain in Thailand, including gaur (*Bos gaurus*), banteng (*Bos javanicus*), wild water buffalo (*Bubalus arnee*), mainland serow (*Capricornis sumatraensis*) and Chinese goral (*Naemorhedus griseus*). Their habitat and populations have been threatened by human activities such as deforestation and hunting (Carr et al., 2023; Harrison et al., 2016; Nguyen, 2009). Wild bovids, especially large species of herbivores (e.g., gaur and banteng), adapt their distribution and foraging areas in response to human-driven ecosystem changes. For example, gaur have been found close to agricultural areas and forest edges where they forage on crop plantations (e.g., grass, cassava) (Chaiyarat et al., 2021). Banteng are also well adapted to secondary forests near villages and logging sites (Journeaux et al., 2018). These wild bovids are, therefore, able to use natural resources that overlap in space and time with free-grazing domestic bovids, which can potentially lead to pathogen transmission via direct contact, such as a physical contact with other animals, and indirect contact, such as contact with intermediate contaminated objects, surfaces acting as sources of infections, or via infected invertebrate vectors in the shared environment and water sources (Bacigalupo et al., 2020).

Interface areas can be defined as overlapping spaces where multiple species interact, increasing the probability of direct or indirect pathogen transmission, and potentially driving pathogen sharing through animal interactions (Barasona et al., 2014; Khanyari et al., 2021). These livestock-wildlife interfaces are important issues for wildlife conservation and global public health; multi-host pathogens are common among human (62%) and domestic mammal pathogens (livestock 77%, carnivores 90%) (Jones et al., 2008; Woolhouse et al., 2001). Multi-species interactions at interfaces between wildlife and livestock populations can be complex and involve numerous species (Cowie et al., 2016). Pathogens that cause bovine infectious diseases, such as bovine tuberculosis, brucellosis, and foot and mouth disease (FMD), can be transmitted and circulate in domestic and wild bovid populations (Caron et al., 2013). These diseases and their impact on wildlife and livestock population health have been studied in Europe (Martin et al., 2011), North America (Miller et al., 2013) and Africa (Garine-Wichatitsky et al., 2013), but less so in Asia, including Thailand.

Several factors can drive pathogen transmission between livestock and wildlife, such as expanding livestock production (Morand, 2020), shrinking and fragmented wildlife habitat (Wilkinson et al., 2018), and changes in wildlife distribution, demography, and behavior (Eby et al., 2023). Among these factors, high host density is a risk factor that can cause pathogen transmission, as it may translate to a higher probability of between- and among-host species interactions, contact, and pathogen exposure (Habib et al., 2011; Sirdar et al., 2021). The interspecies interactions between a new susceptible host and a reservoir in space and time may increase the chance of pathogen transmission by increasing the number and duration of direct and indirect contacts (Clifford et al., 2009). For wild and domesticated species, these areas are usually the transition areas between two or more land use types, such as the edges of forest and agricultural areas, which are likely to have more species activities leading to a greater chance of interaction and, thus, pathogen transmission among wildlife and livestock (Miguel et al., 2013). Previous studies in Thailand indicated the presence of some infectious diseases, such as babesiosis and leptospirosis (Simking et al., 2014; Yatbantoong & Chaiyarat, 2019) in domestic cattle at the edge of the forest, making these domestic animals a potential reservoir for pathogen transmission to the wild bovids.

Bovine infectious diseases can circulate between livestock and wild ungulates with varying levels of virulence (Caron et al., 2013). Certain pathogens can circulate within either livestock or wildlife populations without causing visible clinical signs but have a significant impact on other species. For example, FMD might not severely affect African buffalo (*Syncerus caffer*), but can cause mortality in gaur (Chandranaik et al., 2015). Similarly, *Pasteurella multocida* might be identified within farm environments as a non-pathogenic organism with limited haemorrhagic septicaemia mortality except under certain circumstances, but can cause mass mortality in saiga (*Saiga tatarica*) (Robinson et al., 2019). Chronic diseases, like bovine tuberculosis and brucellosis, with long incubation periods before symptoms could have long-term consequences by reducing populations due to disease (Gorsich et al., 2015; Jolles et al., 2005), whereas acute disease such as foot and mouth disease, which has higher transmission rates with short incubation periods but limited fatality or even acute but highly fatal infections such as anthrax (Dhollander et al., 2016; Yadav et al., 2019), may have lower impacts on the cattle populations because they do not cause severe mortality or they burn out too fast to kill many animals in a population (Horpiencharoen, Marshall, et al., 2024a).

The impact of transmitting bovine diseases from livestock to wildlife populations requires ongoing monitoring and preparation for long-term management. In the past 20 years, there have been numerous novel transboundary emerging disease outbreaks among domestic animals in Thailand, including lumpy skin disease (LSD) among cattle (Arjkumpa et al., 2022), African horse sickness among horses (King et al., 2020), and African swine fever among pigs (Thanapongtharm et al., 2022). Hence, it is crucial to investigate where there are high-risk areas to prevent disease transmission to wild populations, considering their susceptibility to similar pathogens shared by livestock. Identifying the potential risks of pathogen transmission in wildlife and livestock interface areas can support the implementation of disease surveillance and control measures that may help prevent cross-species transmission (Kelly et al., 2017).

Here, we aimed to (1) identify the spatial risk of infection transmission, reflecting potential exposure and cross-species transmission of pathogens, between wild bovids and cattle in Thailand and (2) provide suggestions for disease surveillance and conflict mitigation measures in the wildlife-livestock interface areas of Thailand. We defined potential high-risk areas as interface areas where wildlife and livestock distributions overlap, leading to potential resource sharing (e.g., water bodies, grassland, mineral lick) that might increase the opportunity for pathogen transmission from direct and indirect contact with infectious disease reservoirs and their environment (Barasona et al., 2014; Khanyari et al., 2021; Miguel et al., 2013).

2 | METHODS

2.1 | Study area

Thailand is located on the Indochina Peninsula, mainland Southeast Asia. The total country area is around 514,000 km^2, with agricultural land covering 41% and forested areas comprising around 32% of the country. Most agricultural areas consist of rice fields (51%) and crop plantations (34%; e.g., sugarcane, casava, corn), while livestock farming covers only around 0.6% of the total agricultural area or around 0.3% of the total country (MOAC & NECTEC, 2022). The predominant forest types are dry dipterocarp, mixed deciduous, and evergreen forest (Ishida et al., 2023). There is high cattle production in the central west, which includes free-range cattle and buffalo in some rural areas. These free-ranging livestock may share the same resources and habitats with wildlife.

2.2 | Study species

This study focused on wild bovid and domestic cattle. We selected gaur, banteng, and wild water buffalo because these large wild bovid species remain in Thailand's forests, are threatened, but are also widely distributed and likely able to share the same pathogens and resources as free-ranging cattle in agricultural areas (Prayoon et al., 2021; Suwanpakdee et al., 2024). We used cattle population estimates, rather than other livestock like sheep or domestic water buffalo, because cattle are widely farmed across Thailand, often raised free-range in various areas, and are more likely to have direct or indirect contact with wild bovids. Cattle production systems vary in scales and from intensive farming to free grazing. We focused on cattle acting as reservoirs of infection and transmitting bovine pathogens to wild bovids, without considering the reverse risk, to emphasize the threat to vulnerable species and identify spatial risk areas, though the reverse is possible. Therefore, for our analysis, a high cattle density is assumed to have a higher infection transmission risk, and a lower cattle density has a lower risk, as reported previously (Khanyari et al., 2021; Miguel et al., 2013).

2.3 | Identifying the potential risk

We identified the potential interface areas for wildlife and livestock, which reflect the potential of exposure and for cross-species transmission of pathogens, by calculating where high species' habitat suitability overlapped with high cattle density using two types of datasets: (1) wild bovid distribution and (2) cattle density. We overlaid the potential distribution of each wild bovid species separately with the cattle density and calculated the overlapping areas in 1-km^2 cells as a sampling unit.

2.3.1 | Wild bovid potential distribution

We assumed wild bovid distributions correlate with their suitable habitats, which we previously predicted using ecological niche models (Horpiencharoen, Muylaert, et al., 2024b). Our ecological niche models used 28 predictor environmental variables and 8 algorithms. We ran the ensemble models using the weighted mean method and used True Skill Statistics as a threshold to convert the ensemble models to binary values (1 = suitable and 0 = unsuitable habitat). We selected three wild bovid species for analysis: gaur (*B. gaurus*), banteng (*B. javanicus*), and wild water buffalo (*B. arnee*). Models for mainland serow (*C. sumatraensis*) or Chinese goral (*N. griseus*) did not perform well due to the limited occurrence records for both species. Full methods and model results can be found in Horpiencharoen, Muylaert, et al. (2024b).

2.3.2 | Cattle density

We downloaded cattle density data from the Global Livestock of the World 2015, GLW 4 dataset (Gilbert et al., 2022). This dataset gives cattle density at a 10 km^2 spatial resolution. We cropped the raster layer to Thailand and disaggregated the raster to 1 km^2 per cell to make it compatible with the habitat suitability raster using the disaggregate function from the *raster* package (Hijmans, 2023) in R. Then, we rescaled the density values to 0–1 using:

$$X_2 = \frac{X_1 - X_{\text{minimum}}}{X_{\text{maximum}} - X_{\text{mimimum}}}$$

where X is the value in the cattle density cell. Then, we used the mean of cattle density (0.14 cattle/km^2; median 0.08 cattle/km^2; IQR = 0.04–0.23) in Thailand calculated from the GLW 4 raster as a cut-off value for converting the cattle density raster into the binary values of high and low. Because the data were skewed, the mean includes fewer locations in the high category than the median, and those locations contain the greatest cattle numbers, allowing us to focus on those regions with the greatest potential pathogen transmission risk (see below). The raster cells containing values greater than the mean were converted to 1 (high density), and the values lower than the mean were converted to 0 (low density).

We assumed that higher cattle density correlates with a greater risk of infectious diseases for large wild bovids. Therefore, we counted the reported outbreaks in low- and high-cattle density areas to test this assumption. We divided the total number of outbreak events by the total area of cattle density for each category to check whether the higher number of outbreaks in high-density areas was not simply due to larger areas, as the following calculation:

$$\frac{\text{Number of outbreak in high (or low) cattle density}}{\text{Total area of high (or low) cattle density}}$$

The results indicated a higher incidence of outbreak events in high cattle density areas compared to low cattle density areas. Thus, we used cattle density as the major risk factor to identify the potential pathogen transmission areas (more details in the results Table 2).

2.3.3 | The potential risk areas

To define the risk areas, we overlapped the cattle density raster with the binary species' habitat suitability maps (1 = suitable and 0 = unsuitable habitat) and calculated the percentages of the potential risk areas, representing the interface areas between wild bovids and cattle, in Thailand. Then, we intersected the risk areas with the national protected areas (PA) (UNEP-WCMC and IUCN, 2021) to calculate the risk areas inside and outside PAs. We also classified the risk areas by land use types to prioritize where to implement disease surveillance. Lastly, we counted the occurrence of disease outbreaks reported by the Department of Livestock Development (DLD), Thailand, within the interface areas to explore the distribution of highly frequent diseases in the high-risk areas (see below).

2.3.4 | Disease occurrence data

We used the national database of livestock disease outbreak reports from 2013 to 2021 generated by the DLD, Thailand. Data collection starts when an outbreak in livestock is reported by local authorities or farm owners. Then, epidemiological data are recorded, including the date of the index case, animal type, clinical signs, and number of animals infected, followed by the submission of samples for laboratory diagnosis based on the diseases. If a diagnosis is confirmed and the causative pathogen identified, the authorities report this information in the database. Whenever the authorities could not diagnose the causative pathogen, they indicated a tentative diagnosis (either probable or suspected) based on the clinical signs. We only used laboratory-confirmed cases. The cause of outbreaks was often unidentified, though some occurred after cattle movement or the introduction of new animals into a herd. The coordinates of the outbreak (Figure 2) correspond to the centroid of the sub-district (average area of districts of Thailand = 87 km^2, range: 0.88–2387 km^2) where the laboratory-confirmed case was reported.

We selected five globally or regionally common bovine infectious diseases considered important for livestock health: (1) FMD (caused by Foot and mouth disease virus, FMDV), (2) haemorrhagic septicaemia (HS—*Pasteurella multocida*), (3) bovine tuberculosis (*Mycobacterium bovis*—bTB), (4) LSD (Lumpy skin disease virus) and (5) brucellosis (*Brucella abortus*) from the national database. These diseases have different transmission pathways. FMD is a viral disease primarily spread via direct contact with infected animals, aerosolized virus over typically short distances, contaminated feed, equipment, and clothing. Haemorrhagic septicaemia is a bacterial disease transmitted through direct contact with nasal secretions from infected animals or contaminated water and feed, especially in wet conditions. Bovine tuberculosis is a bacterial disease spread via respiratory droplets, direct contact, ingestion of contaminated milk, feed, or water. Lumpy skin disease is a viral vector-borne disease primarily transmitted by biting insects (mosquitoes, flies, ticks) and through direct contact with lesions or contaminated objects. Brucellosis is a bacterial disease mainly transmitted through ingestion of contaminated materials (aborted fetuses, placenta, milk), direct contact with infected secretions, or via venereal transmission.

We selected laboratory confirmed outbreaks from these five diseases in cattle, then cleaned the outbreak events by excluding incorrect coordinates falling outside Thailand and removing duplicates. Lastly, we counted the number of outbreaks within overlapping areas for each species and cattle population densities using the ‘extract’ function in the *raster* R package (Hijmans, 2023).

All spatial analyses were programmed in R 4.3.1 (R Core Team, 2023). The code is available at a public repository (https://github.com/Wantidah/BovidRiskMaps). Data are available upon reasonable request (dcontrol11@dld.go.th).

3 | RESULTS

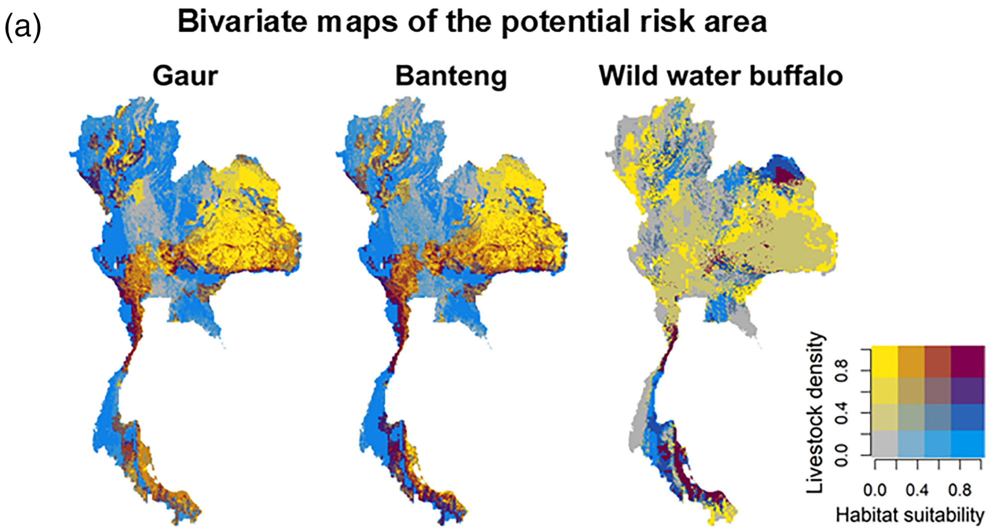
The high-risk areas with high wild bovid habitat suitability and high cattle density were mostly found in the central-western through the southern part of Thailand for the three species (Figure 1). The provinces that showed the highest percentages of the risk areas were Nakhon Si Thammarat (south), Ratchaburi, and Prachuap Khiri Khan for all three species. Wild water buffalo showed the largest of the total interface areas, covering ~44,000 km^2 (9% of Thailand), due to potentially suitable habitat predicted throughout the country. However, in the actual species distribution, only one population remains in the Huai Kha Khaeng Wildlife Sanctuary. Banteng and guar have similar distributions of potential habitat suitability, which resulted in both having ~22,000 km^2 (4% of Thailand) interface nationally (Table 1).

The highest percentage of risk areas inside PAs were identified in Namtok Sam Lan (also known as Phra Budda Chai) National Park (NP) (45 km^2) in Saraburi Province, covering approximately 89% for gaur, 83% for banteng, and 65% for buffalo. The second highest percentage for gaur and banteng was in Namtok Huai Yang NP (160 km^2) in Prachuap Khiri Khan, covering 60% (~100 km^2) of the total PA. For wild water buffalo, the highest percentage was identified in Huai Thabthan-Had Samran wildlife sanctuary (498 km^2), with approximately 25% (125 km^2) of the total PA being a high-risk area. For gaur and banteng, the largest risk area is located in the same PA—Kuiburi NP (970 km^2), representing 273 km^2 (28% of the PA). This is followed by the Kaengkrachan forest complex, representing 249 km^2 for gaur (8% of the PA) and 261 km^2 for banteng (9% of the PA). These two PAs are in close proximity, with high-risk areas situated along the western forest edge, connected to agricultural areas with high cattle density, while the western side is connected to the Myanmar forest (Figure 1). Moreover, large intact forests like the Western, Eastern, and Dong Payayen—Khoa Yai forest complex are areas with high habitat suitability with low cattle density within the PA, but had high-risk areas at the border of the forests, while the fragmented forests in the north illustrated the potential for there to be potentially high risk of pathogen transmission in regions with relatively low habitat suitability due to high cattle density and contact at the edge of fragmented suitable habitat.

According to the national disease surveillance, the total number of outbreak events was 7522 events for the five selected bovine infectious diseases from 2013 to 2021. Lumpy skin disease (6913) had the most reported outbreak events, followed by FMD (563) and brucellosis (39), while haemorrhagic septicaemia and bovine tuberculosis had only five and two reported events, respectively (Table 2 and Figure 2). This is because the first lumpy skin disease outbreak occurred in cattle herds in Thailand in 2021, leading to many events being reported across the country in a short period, while the other infections are endemic in the area and were reported less commonly.

Cattle density was correlated with the number of infectious disease outbreaks, and this correlation was proportional to the area size. In high density areas (190,076 km^2) there were more outbreak events, totaling around 6894 events (0.036 events per km^2), which is 18 times more than in low cattle density areas (324,335 km^2), where 640 events were reported (0.002 events per km^2; Table 2).

We found that the density of outbreak events in cattle within the potential high-risk area of gaur (0.01) and especially for wild water buffalo (0.015) were similar to the average density calculated for the country (0.0146) (Table 3). The number of events in suitable habitat for gaur (199) and banteng (162) were similar, whereas 647 events were reported within wild water buffalo habitat, likely because they have the largest area of potentially suitable habitat. The greatest numbers of disease events within high-risk areas was for lumpy skin



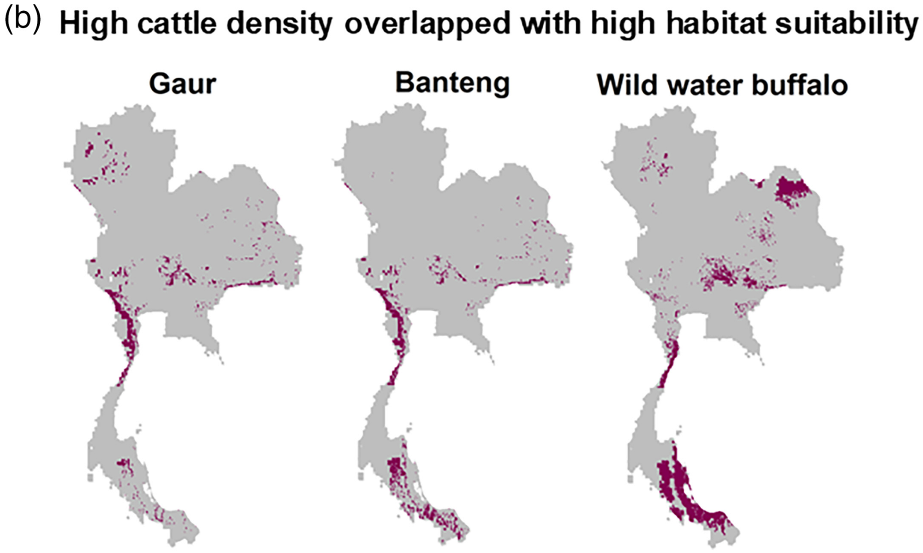


FIGURE 1 Maps of Thailand showing: (a) Bivariate maps of the overlap between wild bovid habitat suitability (blue) and cattle density (yellow) reveal the interface areas for pathogen transmission between three wild bovid species and domestic cattle populations. High-risk areas are represented in dark red, while low-risk areas are represented in gray. (b) Potential high-risk areas for pathogen transmission were identified based on the overlap between high habitat suitability for the three wild bovid species with high cattle density. High-risk areas are represented in dark red, extracted from the bivariate maps of the potential risk area in (a).

TABLE 1 The percentage of interface areas between wild bovid habitat suitability and high cattle density overlapped with protected areas (PA), and the percentage of the species distribution of the total country area for three wild bovid species. The interface areas are shown in Figure 1.

	Interface area with livestock (km^2)			Percentage of overlap area in Thailand	Percentage of species distribution in Thailand
Species	**Inside PA**	**Outside PA**	**Total**		
Gaur	2018	18,367	20,385	3.9	34.5
Banteng	2089	20,477	22,566	4.4	24.4
Wild water buffalo	747	43,642	44,389	8.7	26.4

disease and FMD in all species and the other diseases presented only small numbers.

Based on land use type, the most extensive interface areas were in closed unknown forests (meaning they did not match any of the other forest definitions), which may include mixed deciduous, dry dipterocarp, and secondary growth forest, and land types that could not be clearly classified, followed by cropland for three species. Closed evergreen forests also had risk areas for gaur and banteng. The open deciduous forest had no interface areas detected (Figure 3).

TABLE 2 The occurrence of outbreak events classified by infectious disease and cattle density from 2013 to 2021. Data are from the Department of Livestock Development, Thailand. High and low cattle densities are above and below the mean.

Infectious disease	Cattle density		
	Low	High	
	(<= mean; 0.14 cattle/km^2)	(> mean; 0.14 cattle/km^2)	Total
Bovine tuberculosis	2	0	2
Haemorrhagic septicaemia	3	2	5
Lumpy skin disease	445	6473	6918
Foot and mouth disease	175	395	563
Brucellosis	15	24	39
Total	640	6894	7534
Area of Thailand (km^2)	324,335	190,076	514,411
Total outbreak event per area (km^2)	0.0020	0.0363	0.0146

4 | DISCUSSION

We examined potential high-risk areas for pathogen transmission between wild bovids and domestic cattle to provide preliminary focus areas to be considered for disease surveillance and mitigation in Thailand for conservation purposes. Although this study did not include other domestic livestock such as water buffalo or small ruminants (e.g., sheep and goats) as proxy species, these livestock may also represent a risk for pathogen transmission to wild bovids. For example, from domestic to wild water buffalo or from small ruminants to serow or goral, as they also graze freely in some areas and are present in the forests. High-risk areas in Thailand ranged from 4% (gaur and banteng) to 9% (wild water buffalo) of the country, with most of the high-risk areas located in the central west (Ratchaburi) to the south (Nakhon Si Thammarat). The highest risk proportion inside PAs was at Namtok Sam Lan NP in central Thailand, and the largest risk areas were Kuiburi NP and Kaengkrachan NP in the western forest, which is related to the highest cattle density in Thailand. Strategic livestock grazing, such as managing grassland structure or nutritional hotspots, could be implemented inside or at the edges of protected areas as a conservation tool to increase habitat heterogeneity (Fynn et al., 2016). Gaur and banteng have similar risk areas mostly around the edge of forests, while habitat suitable for wild water buffalo has risk widely distributed

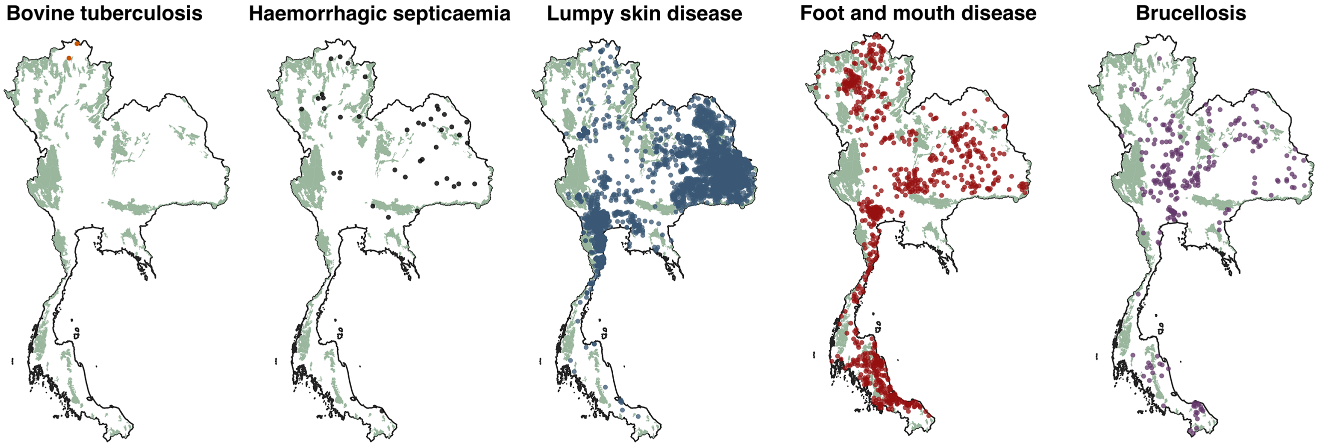


FIGURE 2 Occurrence of reported bovine disease outbreaks in Thailand from 2013 to 2021 and distribution of protected areas (green). The maps show outbreaks occurred across Thailand, particularly in proximity to protected and forest areas that overlap with suitable habitats for wild bovids. Infectious disease data are from the Department of Livestock Development, Thailand.

TABLE 3 Reported outbreak events of bovine infectious disease occurrences in the high-risk areas. Infectious disease data are from the Department of Livestock Development, Thailand.

		Within high cattle density—high habitat suitability		
Bovine infectious diseases	**All occurrences**	**Gaur**	**Banteng**	**Wild water buffalo**
Bovine tuberculosis	2	0	0	0
Haemorrhagic septicaemia	5	0	0	1
Lumpy skin disease	6918	166	108	442
Foot and mouth disease	563	32	51	190
Brucellosis	39	1	3	14
Total	7534	199	162	647
High risk areas (km^2)		20,385	22,566	44,389
Thailand	514,411			
Total outbreak event per risk area (km^2)	0.015	0.010	0.008	0.015

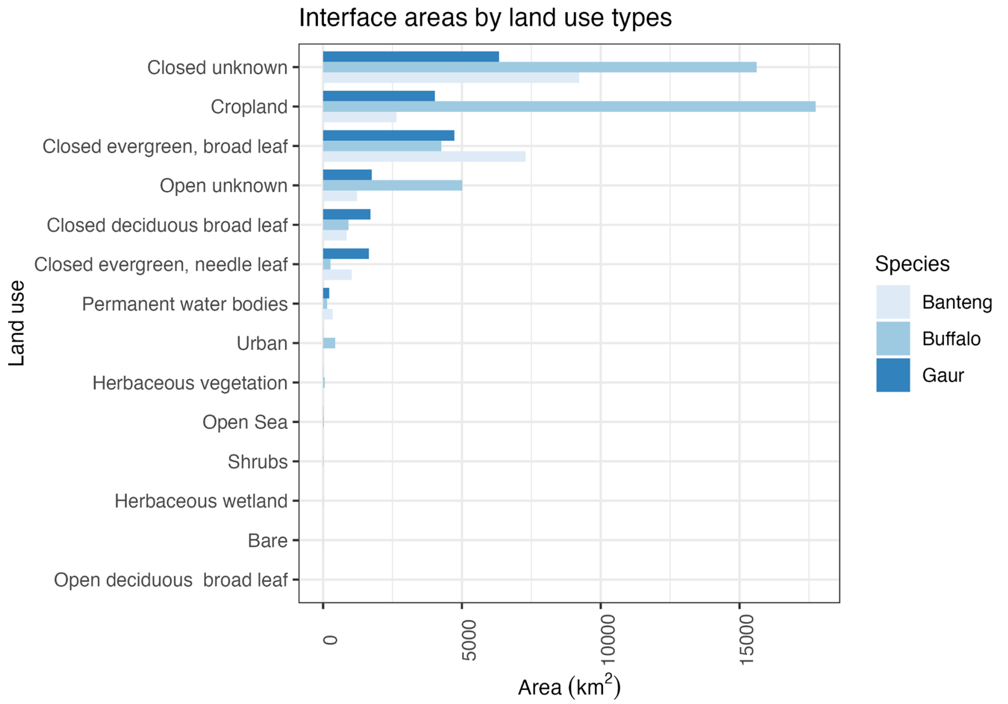


FIGURE 3 Interface areas of three wild bovid species and high domestic cattle density categorized based on land use types, from the land cover layers dataset (Buchhorn et al., 2019), https://zenodo.org/records/3243509). The term "Closed unknown" denotes a type of forest that does not match any of the other definitions. The interface areas are presented in Figure 1.

across the country because SDMs predicted extensive amounts of suitable areas in the central down to the southern parts of Thailand that coincide with high cattle density areas. These edge areas outside protected areas may lack formal management, increasing the likelihood of unregulated contact between livestock and endangered wild bovids.

Although the wild water buffalo had the largest areas of predicted suitable habitat among all three bovid species, it is also the most endangered. Its current known distribution is solely in the Huai Kha Khaeng Wildlife Sanctuary, with the population remaining stable and not exceeding 69 individuals for decades (Chaiyarat et al., 2004; Khiowsree et al., 2015). Thus, many areas identified as high risk for this species are unlikely to be current high-risk areas, but are important for future planning should wild buffalo ranges expand to these or they be relocated. This species is highly susceptible to endemic infectious diseases that could rapidly lead to serious decline or even local extinction. For instance, diseases like haemorrhagic septicaemia can cause a high fatality rate of up to 80% in domestic buffalo (Deepak & Aly, 2020). The highly contagious and fatal nature of diseases like rinderpest and FMD may have been contributing factors to population disappearances in Nepal and India (Choudhury, 2014). A disease outbreak could lead to local extinction in a single fragmented population (Horpiencharoen, Marshall, et al., 2024a), as the recovery process is prolonged and fragmentation potentially results in a lack of gene flow (McKnight et al., 2017; Sarataphan et al., 2017).

In contrast to wild water buffalo, gaur and banteng have more opportunities for contact with domestic cattle and humans due to their greater numbers and use of areas near human activity (Chaiyarat et al., 2023; Prayoon et al., 2024). Gaur and banteng can share habitats, making the interface areas similar to each other. However, gaur use a wider range of habitat types (e.g., evergreen, deciduous dipterocarp, mixed deciduous forests) than banteng, which is restricted to dry and open forests (e.g., dry dipterocarp, mixed deciduous forest) (Prayurasiddhi, 1997; Steinmetz, 2004). These two species show evidence of contact with livestock and humans due to their ability to adapt and tolerate human activities, resulting in conflicts in overlapping areas (Chaiyarat et al., 2021, 2023; Journeaux et al., 2018). However, their habitat suitability decreases with closer proximity to human settlement and the presence of domestic cattle grazing (Jornburom et al., 2020).

Our study identified potential high-risk areas in northeastern and southern Thailand, which had the highest cattle density but a low presence or even an absence of our three target wild bovids in some areas. This caveat is particularly evident in the ecological niche modeling of wild water buffalo, where high habitat suitability represents potential distribution and may not necessarily correspond to the actual species distribution. Nevertheless, this could be mitigated by collecting and regularly updating occurrences of these bovid species, as well as data on livestock density and distribution, or by restricting the analyses to areas with sufficient data. Future analyses could also include domestic buffalo, which are present at approximately one-fifth the density of domestic cattle in Thailand (DLD, 2024), but might be another important pathogen host.

Further studies may consider including other risk factors such as multi-species host distribution, the distance of risk factors, and contact patterns (Pepin et al., 2022; Sangrat et al., 2020). Additionally, improving the risk maps by using updated disease surveillance data and wild bovid species occurrences would enhance their accuracy, especially in areas with high model prediction uncertainty. Host density is one of the main risk factors in wildlife and livestock infectious disease transmission (Daszak et al., 2000; Smith et al., 2009). We used host density and distribution as the main risk factors to identify and prioritize the potential risk areas of wildlife and livestock pathogen transmission, as has been done in the other studies (Miller et al., 2017; Morgan et al., 2006; Yang et al., 2021). The advantage is knowing the target place for implementing the disease surveillance system, but disadvantages can arise from the complexity of pathogen transmission dynamics, which depend on factors such as host species movement (Morgan et al., 2006), contact patterns (Craft, 2015), high adaptability of wildlife behavior, transmission modes (e.g., density or frequency-dependent) (Pruvot et al., 2020; Smith et al., 2009) and population size (Lambert et al., 2018).

Urbanization and expansion of agricultural areas that encroach into forests increase opportunities for contact between domestic livestock and wildlife in Thailand. Thailand has experienced significant land cover changes (Wang et al., 2022), primarily driven by the increase of crop plantations and urbanization with concurrent population growth, which leads to changing wildlife and livestock interactions and risk of pathogen transmission (Shah et al., 2019). We found that the highest interface areas for our modeled species were in cropland and unclassified forests or unknown forest types, which may be unprotected or degraded habitats where surveillance and management are limited (Chaiyarat et al., 2021). Free-ranging livestock in Thailand, such as cattle and goats, are commonly part of the production system in rural areas. Depending on the practices, some farmers release animals during the day and confine them at night, while others tend to keep them free-ranging until they are sold, usually for meat consumption. These livestock can share forests and natural resources with wild ungulates, highlighting the need for improving foraging quality away from wildlife habitat, biosecurity for cattle farming, reducing the number of free-ranging livestock, and monitoring in interface areas regarding bovine infectious disease transmission (Yatbantoong & Chaiyarat, 2019), particularly in unprotected or peripheral zones where enforcement and surveillance may be limited.

Understanding the underlying factors is essential for planning effective disease mitigation and control strategies (see Tables S1 and S2). Prevention of transmission may need to be based on pathogen traits and modes of transmission. For example, FMDV is highly contagious and transmitted by aerosol, environmental contamination, and direct contact (Chanchaidechachai et al., 2023), while lumpy skin disease virus is vector-borne (Arjkumpa et al., 2022). This leads to different disease control measures on farms, such as vector control, movement restriction, and ring vaccination, if vaccines are available. One approach to prevent pathogen transmission between wildlife and livestock is to reduce direct and indirect contact rates between wildlife and livestock. Contact reduction might be through measures such as altering land use at the local level, or with “natural” (e.g., plant-based) or artificial (e.g., metal) fencing or barriers and zoning of forests, livestock, and human settlements to minimize the contact (Jori & Etter, 2016; Miller et al., 2013), which may reduce pathogen spillover (Plowright et al., 2021). Conserving intact forests with effective surveillance can mitigate the risk of pathogen transmission at the interface, especially in edge or transition areas. In contrast, fragmented forests increase the likelihood of wildlife being exposed to livestock and humans, leading to an elevated risk of pathogen transmission (Keesing et al., 2010; Muylaert et al., 2023; Wilkinson et al., 2018).

Livestock vaccination, when available, can be an effective tool for reducing disease. Often, however, this requires high (e.g., 80%) vaccination coverage to effectively prevent transmission, particularly in high-risk areas and populations (Hopker et al., 2021; Porco et al., 2023), though it can protect individuals from severe disease. However, capturing and delivering parenteral-route vaccinations to free-ranging wild bovids poses significant challenges, especially in tropical forests. Consequently, various aspects must be carefully considered in vaccination programs, including the target population, coverage, safety, and efficiency, to effectively reach herd immunity (Treanor et al., 2010). Non-invasive vaccination methods, like tuberculosis oral vaccination, have been tested in domestic cattle and some wildlife and are planned for use in wild cattle (Buddle et al., 2018). Culling livestock infected with zoonotic diseases (e.g., bovine tuberculosis, brucellosis) is implemented in Thailand (Peck et al., 2018; Singhla et al., 2017). However, infected animals often undergo illegal translocation, potentially spreading pathogens to other locations. To manage this issue, governments typically regulate animal movement, have guidelines for isolation of infectious animals during outbreaks, and provide appropriate compensation for culling cases.

Livestock and wildlife disease surveillance in Thailand is based on the DLD, Department of National Parks, Wildlife and Plant Conservation (DNP), Thailand, and World Organization for Animal Health (WOAH) guidelines (WOAH, 2024), which cover significant transboundary disease outbreaks in the country. Effective disease surveillance and control in the country is based on a multisectoral partnership, integrating livestock and wildlife health networks for rapid response, enhancing the surveillance system, and developing an outbreak control program (Suwanpakdee et al., 2024; Yano et al., 2018). The passive surveillance system relies on routine reporting of cases by healthcare providers, laboratories, or other institutions and is useful for recording the obvious clinical signs and emerging infectious diseases (like FMD and lumpy skin disease). However, there is a gap in collecting data relating to non-clinical to subclinical diseases due to these being challenging to detect. Moreover, passive surveillance leads to underreporting by farmers for some zoonoses like bovine tuberculosis and brucellosis, for which animals must be condemned due to the slow and partial (not less than 75% of the market price, but often not 100%) compensation from the government. Another drawback to passive surveillance is that animals may have moved from the area where infection occurred. Active surveillance such as sentinel or risk-based surveillance (Sansamur et al., 2020), outbreak investigations using a designed questionnaire (Arjkumpa et al., 2022), and screening programs (including seroprevalence studies) in hotspots or endemic areas are likely better able to find cases and potentially effectively allocate resources for disease mitigation and control strategies, though they are costlier to implement.

To sustainably manage data collection and surveillance systems, collaboration among government organizations and stakeholders is a key step in the process, involving considerations of political, ethical, administrative, regulatory, and legal (PEARL) aspects through all approaches (Hayman et al., 2023). An effective surveillance system, characterized by rapid detection and accurate results, not only monitors emerging diseases but also reduces the risk of pathogen transmission and minimizes the impact on lives, economies, and biodiversity during disease outbreaks (Ryser-Degiorgis, 2013). Also, the use of non-invasive data collection for wildlife disease surveillance and surveys, such as feces, urine, saliva, and environmental samples (e.g., soil, water) should be considered to avoid direct contact and reduce disturbing wildlife during capturing and data collection (Schilling et al., 2022).

5 | CONCLUSION

Our study predicted potential high-risk areas for infectious pathogen transmission by identifying interface areas between wildlife and domestic cattle, where livestock disease is frequently reported. High-risk areas for three large wild bovids in Thailand are most likely to occur with both high cattle density and high habitat suitability, particularly at the edges of forest-protected areas. Notably, small, fragmented forest areas with high cattle density had the highest proportion of the high-risk areas, with cropland and some closed forests exhibiting the largest interface areas. Our findings highlight the importance of conserving intact forests to mitigate contact between wild bovids and livestock to reduce pathogen transmission and vulnerability to extinction. This study not only supports disease surveillance but also facilitates the implementation of effective mitigation and control measures. Overall, we suggest prioritizing the conservation of intact forests and limiting livestock encroachment near fragmented forest edges to reduce wildlife–livestock disease risk and safeguard endangered wild bovids.

AUTHOR CONTRIBUTIONS

Wantida Horpiencharoen: Conceptualization, Methodology, Software, Formal analysis, Data Curation, Writing—Original Draft, Writing—review and Editing, Project administration, Funding acquisition. **Jonathan C. Marshall**: Methodology, Software, Validation, Formal analysis, Supervision, Writing—Original Draft, Review and Editing. **Renata L. Muylaert**: Methodology, Software, Validation, Formal analysis, Supervision, Writing—Original Draft, Review and Editing. Reju Sam John: Methodology, Software, Validation, Formal analysis, Supervision, Writing—Original Draft, Review and Editing. **David T. S. Hayman:** Conceptualization, Methodology, Validation, Supervision, Writing—Original Draft, Writing—Review and Editing, Project Administration, Funding Acquisition.

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DATA AVAILABILITY STATEMENT

The R code and supporting data can be found in GitHub Repository: https://github.com/Wantidah/BovidRiskMaps. Preprint: https://doi.org/10.1101/2024.05.04.592526.

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SUPPORTING INFORMATION

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