1 **Spatial risk of disease transmission between wild bovids and livestock in Thailand**

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8 **Abstract**

9 　　The livestock-wildlife interface is one of the most essential issues threatening wildlife
10 conservation and public health. Identifying interface areas can help to prioritise disease
11 surveillance and implement mitigation measures and control programs for targeting
12 threatened wildlife. We predicted interface areas which were assumed to be areas at risk of
13 infectious disease transmission based on the spatial overlap between three Thai wild bovids
14 (including gaur, banteng and wild water buffalo) habitat suitability and domestic cattle. We
15 assumed that domestic cattle are the reservoir of bovine infectious disease, and that high
16 cattle density is a proxy for a higher risk of disease transmission. Our study indicated that the
17 highest risk areas for the native species are at the forest edges where overlap exists between
18 high habitat suitability and high cattle density. Wild water buffalo showed the largest
19 proportion of high-risk areas (8%), while gaur and banteng showed similar risk areas (4%) in
20 Thailand. The largest proportion of risk areas overlapping with protected areas was Namtok
21 Sam Lan PAs at 89% for gaur, 84% for banteng and 65% for wild water buffalo. Kuiburi NP has
22 the largest risk area around 274 km^2 (around 28% of the total protected area) for gaur and
23 banteng, whereas wild water buffalo has the largest risk area overlapping with Huai
24 Thabthan-Had Samran around 126 km^2 (10% of the PA). Kaengkrachan Forest Complex
25 showed the second largest risk area from 249 km^2 for gaur and 273 km^2 for banteng (8-9% of
26 the PA). Our results address how habitat suitability might be helpful for infectious disease
27 prevention and control strategies focused on native fauna and One Health. Furthermore, this
28 work may also support the wild bovid habitat conservation initiatives and land use planning
29 by informing decision-making about balancing wildlife habitats and livestock farming.

30 　　Keywords: Cattle, infectious disease, interface area, mapping, wildlife

31 **Introduction**

32 　　Wild Bovidae (Mammalia: Artiodactyla) are distributed worldwide and play crucial
33 ecosystem roles, because they determine the forest and ecosystem structure, transport
34 micronutrients, and disperse plant seeds (1, 2) and are also important prey species of
35 predators (3). In Asia, wild bovid populations are threatened by multiple factors, including
36 habitat loss and hunting, especially in South to Southeast Asia (4). Natural habitat loss often

37   comes with increased free-grazing livestock interaction, which can lead to problems as varied
38   as resource competition, reducing wildlife population abundance (5), interbreeding between
39   domestic and wild water buffalo (6), and infectious disease transmission (7).

40   Among the twenty-seven recognized wild bovid species as of 2020 (IUCN), five species
41   remain in Thailand, including gaur (*Bos gaurus*), banteng (*Bos javanicus*), wild water buffalo
42   (*Bubalus arnee*), mainland serow (*Capricornis sumatraensis*) and Chinese goral (*Naemorhedus*
43   *griseus*). Their habitat and populations have been threatened by human activities such as
44   deforestation and hunting (8-10). Wild bovids, especially the large herbivores (e.g. gaur,
45   banteng and wild water buffalo), gradually adapt their distribution and behaviour to land use
46   change. For example, gaur has been found close to agricultural areas and forest edges where
47   they forage on crop plantations (e.g. grass, cassava) (11). Banteng is also well-adapted to
48   secondary forests near villages and logging sites (12). These wild bovids are, therefore, able
49   to share natural resources with free-grazing domestic bovids, which can potentially cause
50   disease transmission via direct and indirect contact with the sources of infections (e.g.
51   infectious cattle, host, environmental reservoirs (13).

52   The livestock-wildlife interface is one important issue threatening wildlife
53   conservation and global public health because 72% of reported emerging diseases originate
54   from wildlife to humans and/or livestock (14). Bovine infectious diseases, such as bovine
55   tuberculosis, brucellosis and foot and mouth disease, can be transmitted and circulate in
56   domestic and wild bovid populations (15). These diseases and their impact on wildlife and
57   livestock population health have been studied in Europe (16), North America (17) and Africa
58   (18), but less so in Asia, including Thailand.

59   Several factors can drive disease transmission between livestock and wildlife
60   populations, such as the expanding livestock production (19), the shrinking of wildlife habitat
61   (20) and changes in wildlife distribution, demography and behaviour (21). Among these
62   factors, high host density is potentially a determinant risk factor that can lead to successful
63   disease transmission as it may translate to a higher probability of between- and among-host
64   species interactions, contact and pathogen exposure (22, 23). The movement and spatial
65   overlap of wildlife and livestock can lead to increased infectious disease transmission risk.
66   Areas where there is potential for interaction between a new susceptible host and a reservoir
67   can increase the chance of disease transmission through increasing contact rates and time
68   (24). For wild and domesticated species, these areas are usually the transition areas between
69   two or more land use types, such as the edges of forest and agricultural areas, which are likely
70   to have more species activities leading to a greater chance of interaction and so disease
71   transmission among wildlife and livestock (25). Previous studies indicated the presence of
72   some infectious diseases, such as babesiosis and leptospirosis (26, 27) in domestic cattle at
73   the edge of forest, making these domestic animals a potential reservoir of disease
74   transmission to the wild bovids.

75   Bovine infectious diseases can circulate between livestock and wild ungulates with
76   varying levels of virulence (15). Certain pathogens can circulate within either livestock or
77   wildlife populations without causing visible clinical signs but have a significant impact on other
78   species. For example, foot and mouth disease (FMD) might not affect African buffalo, but can
79   lead to mortality in gaur (28). Similarly, haemorrhagic septicaemia (*Pasteurella multocida*)
80   might be identified within the farm environment as non-pathogenic with limited mortality
81   except under certain circumstances but can cause mass mortality in saiga (29). Chronic
82   diseases like bovine tuberculosis and brucellosis with long incubation and relatively low
83   fatality rates could potentially have long-term consequences by reducing populations due to
84   disease, while FMD, which has a higher transmission rate with short incubation periods or
85   even highly fatal infections such as anthrax, may have lower impacts on populations (30)

86   Moreover, in the past twenty years, there have been numerous transboundary
87   emerging disease outbreaks among domestic animals in Thailand. For example, there have
88   been outbreaks of lumpy skin disease among cattle (31), African horse sickness among horses
89   (32), and African swine fever among pigs (33). Hence, it is crucial to investigate where there
90   are high risk areas to prevent disease transmission to wild populations, considering their
91   susceptibility to similar pathogens shared by livestock. Targeting the potential risks of disease
92   transmission in wildlife and livestock interface areas can support the implementation of
93   surveillance and control measures that may help prevent cross-species transmission (34).

94   In this study, we aim to 1) identify the potential risk of disease transmission of wild
95   bovids and livestock in Thailand and 2) provide suggestions for disease surveillance and
96   conflict mitigation measures in the wildlife-livestock interface areas of Thailand. The outputs
97   could be used to prioritise local surveillance and mitigation measures for optimising resource
98   allocation.

99   **Methods**

100   **Study area**

101   Thailand is located on the Indochina Peninsula, part of mainland Southeast Asia.
102   Thailand borders four countries, Myanmar, Laos, Cambodia and Malaysia, with the Gulf of
103   Thailand on the southeast connected to the Pacific Ocean and the southwest connected to
104   the Andaman Sea. The total country area is around 514,000 km², with agricultural land
105   covering 41% and forested areas comprising around 32% of the country area. Most
106   agricultural areas consist of rice fields (51%) and crop plantations (34%), while livestock
107   farming covers only around 0.6% of the total agricultural area or around 0.3% of the total
108   country (land use data source: https://agri-map-online.moac.go.th/). There is high cattle
109   production in the central west, which includes free-range cattle and buffalo in some rural
110   areas. These free-ranging livestock have encroached into wildlife habitats and share the same
111   resources. Moreover, there is shared land use, for example, domestic buffalo may use rice
112   fields.

Populations

This study focuses on wildlife and livestock populations, and we calculate the largest potential for wildlife-livestock interface areas. We selected the remaining wild bovid species in Thailand because they are widely distributed and likely to share the same resources and pathogens as livestock, especially the large bovids (gaur, banteng and wild water buffalo) distribution, which tends to overlap with free-ranging cattle and agricultural areas. For the livestock population, we used the cattle population estimates as cattle production is all over the country, with varied production scales and systems from intensive farming to free grazing. We assume that domestic cattle can be a pathogen reservoir and transmit diseases to the wild bovid population, and our focus is on livestock transmitting infection to wild species, though the alternative is possible. Therefore, for our analysis, a high cattle density is assumed to have a higher risk transmission risk and a lower cattle density have a lower risk, as reported in previous studies (25, 35).

Identifying the potential risk

Briefly, we identified the risk area using two types of datasets: 1) wild bovid distribution and 2) cattle density. Then, we overlaid these together and calculated the overlapping areas in 1-km^2 cells as a sampling unit.

Wild bovid potential distribution

We assumed wild bovid distributions correlate with their suitable habitat we previously predicted by ecological niche models (36). Ecological niche models used 28 as predictor environmental variables using 8 algorithms. We conducted 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 areas and 0 = unsuitable). We selected three wild bovid species for further analysis: gaur (*B. gaurus*), banteng (*B. javanicus*), and wild water buffalo (*B. arnee*), and excluded Mainland serow (*C. sumatraensis*) or Chinese goral (*N. griseus*) from the analyses because the ecological niche models did not perform well. Full methods and model results can be found in Horpiencharoen et al. (2023) (36).

Cattle density

We downloaded cattle density data from Global Livestock of the World 2015, GLW 4 (link). This data gives values of cattle density at an original spatial resolution of 10 km^2. We cropped the raster layer to Thailand limits and disaggregated the raster to 1 km^2 per cell to make it compatible with the habitat suitability raster using the raster package (37). Then, we rescaled the density values to 0 - 1 using this equation:

$$X_2 = (X_1 - X_{minimum})/(X_{maximum} - X_{minimum})$$

Where X is the value in the cattle density cell. Then, we used the mean of cattle density (0.14 cattle/km^2) 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. The raster cells containing

150 values greater than the mean were converted to 1 (high density), and the values lower than
151 the mean were converted to 0 (low density).

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

157
$$\frac{Number\ of\ outbreak\ in\ high\ (or\ low)\ cattle\ density}{Total\ area\ of\ high\ (or\ low)\ cattle\ density}$$

158   The results found a higher incidence of outbreak events in high cattle density areas
159 compared to low cattle density areas. Thus, we used cattle density as the major risk factor to
160 identify the potential disease transmission areas (more details in the resultsTable 2**Error!**
161 **Reference source not found.**).

162 *The potential risk areas*

163   In this study, the potential high risk areas refer to the interface areas between wildlife
164 and livestock that potentially share the resources (e.g. water bodies, grassland, mineral lick)
165 and have a higher risk of disease transmission due to the increased opportunity of direct and
166 indirect contact with disease reservoirs and environment, compared to other areas (25, 35,
167 38).

168   To define the risk areas, we overlapped the cattle density raster with the species'
169 binary maps and calculated the percentages of the potential risk areas in Thailand. Then, we
170 intersected the risk areas with the national protected areas (PA) (39) to calculate the risk
171 areas inside and outside PAs and also classified the risk areas by land use types to prioritise
172 where to implement the disease surveillance. Lastly, we counted the occurrence of disease
173 outbreaks reported by the Department of Livestock Development, Thailand, within the
174 interface areas to explore the distribution of highly frequent diseases in the high risk areas
175 (see below). All spatial analyses were programmed in R 4.3.1 (40). The code is available at a
176 public repository (https://github.com/Wantidah/BovidRiskMaps). Data is available upon
177 reasonable request.

178 *Disease occurrence data*

179   We used the national database of livestock disease outbreak reports from 2013 to 2021
180 generated by the Department of Livestock Development, Thailand. The data collection starts
181 when an outbreak in livestock is reported by local authorities or farm owners. Then
182 epidemiological data are recorded, including the date of the index case, animal type, clinical
183 signs, and number of animals infected, followed by collecting the samples for laboratory
184 diagnosis. If a diagnosis is made and the causative pathogen and disease known, the
185 authorities will record this in the database. If the authorities cannot find the causing
186 pathogen, they will add the tentative diagnosis from the clinical signs. Each outbreak will be

187 reported as confirmed if the causative pathogen is identified by laboratory diagnostics.
188 However, if there is no laboratory result, the authority will fill in the tentative diagnosis
189 according to animal clinical signs. The GPS location of the outbreak refers to the centroid of
190 the sub-district (average area of districts of Thailand = 87 km^2, range: 0.88 - 2,387 km^2) where
191 the outbreak occurred.

192 Here we selected five globally or regionally common bovine infectious diseases
193 considered important for livestock health: 1) foot and mouth disease (FMD), 2) haemorrhagic
194 septicaemia (HS - *Pasteurella multocida*), 3) bovine Tuberculosis (*Mycobacterium bovis* - bTB),
195 4) lumpy skin disease (LSD) and 5) brucellosis (*Brucella abortus*) from the national database.
196 We selected outbreaks from these five diseases in cattle, then cleaned the outbreak events
197 by excluding incorrect coordinates falling outside Thailand using R. Lastly, we counted the
198 number of outbreaks within overlapping areas for each species and cattle population
199 densities using the 'extract' function in the raster R package (37).

Results

201 The high-risk areas with high wild bovid habitat suitability and high cattle density are
202 mostly found in the central-western through the southern part of Thailand for the three
203 species (Figure 1). The districts that showed the highest percentages of the risk areas are
204 Nakhon Si Thammarat (south), Ratchaburi and Prachuap Khiri Khan) for all three species. Wild
205 water buffalo showed the largest of the total interface areas, covering ~44,000 km^2 (8% of
206 Thailand), due to their potential habitat suitability predicted across the country. However, in
207 the actual species distribution, only one population remains in the Huai Kha Khaeng Wildlife
208 Sanctuary. Banteng and Guar showed similar potential habitat suitability species, which also
209 resulted in the closest number of interface areas, ~22,000 km^2 (4% of Thailand) (Table 1).

210 The highest percentage of risk areas inside the PA were identified in Namtok Sam Lan
211 (also known as Phra Budda Chai) National Park (NP) (45 km^2) in Saraburi Province, covering
212 approximately 89% for gaur, 83% for banteng and 65% for buffalo. The second highest
213 percentage for gaur and banteng is Namtok Huai Yang (160 km^2) NP in Prachuap Khiri Khan,
214 covering 60% (~100 km^2) of the total PA, and for wild water buffalo is Huai Thabthan-Had
215 Samran (498 km^2) representing 25% (125 km^2) of the total PA. However, for gaur and banteng,
216 the largest risk area is located in the same PA—Kuiburi NP (970 km^2), representing 273 km^2
217 (28% of the PA). This is followed by the Kaengkrachan forest complex, representing 249 km^2
218 for gaur (8% of the PA) and 261 km^2 for banteng (9% of the PA). These two protected areas
219 are in close proximity, with high-risk areas situated along the western forest edge, connected
220 to agricultural areas with high cattle density, while the western side is connected to the
221 Myanmar forest (Figure 1). Moreover, the large intact forests like the Western, Eastern and
222 Dong Payayen - Khoa Yai forest complex illustrated high habitat suitability with low cattle
223 density within the PA, but showed high risk at the border of the forests, while the fragmented
224 forests in the north illustrated the potential high risk of disease transmission with high cattle
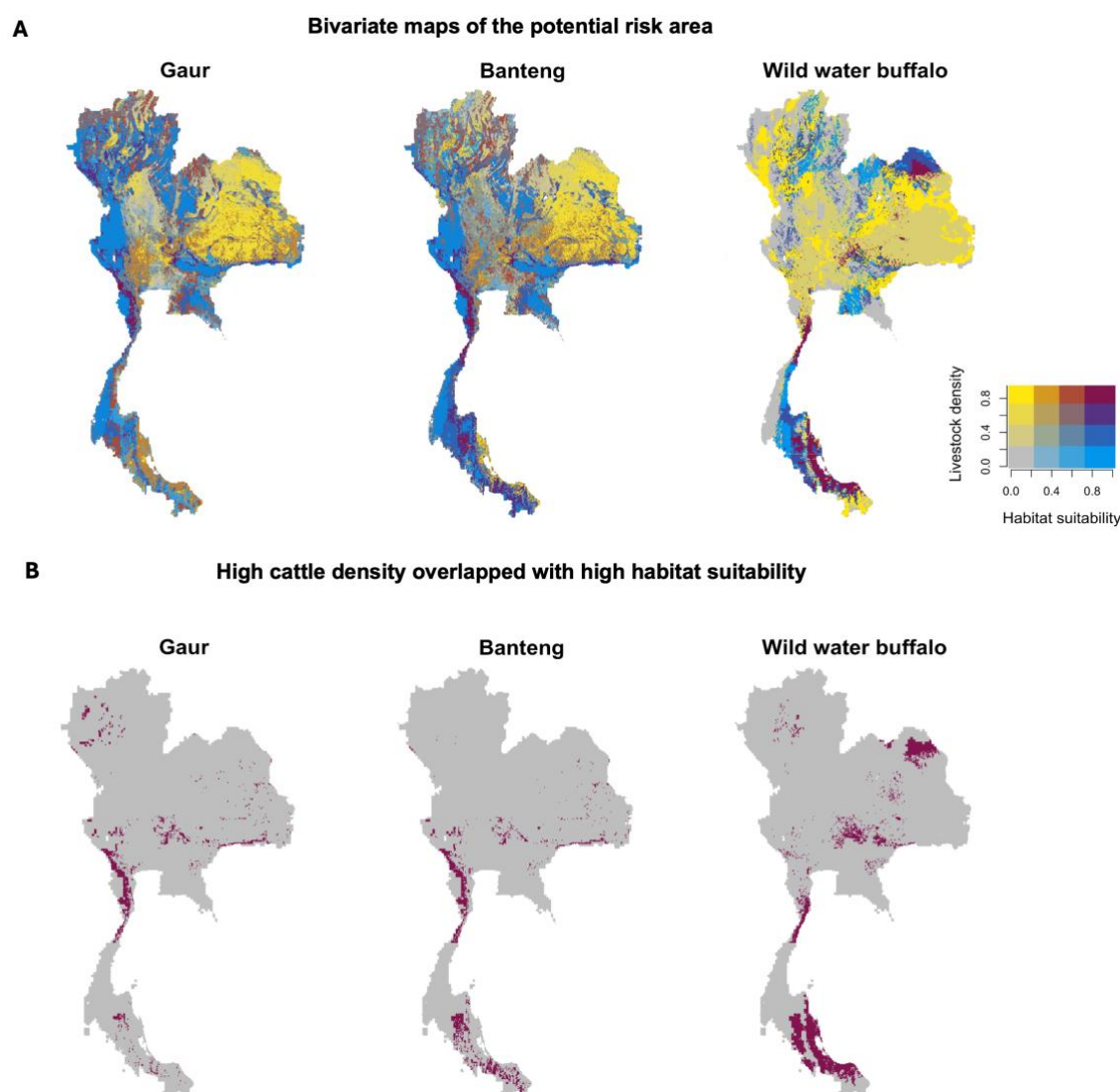225 density and low habitat suitability.

226

Figure 1 Bivariate maps of the potential risk area (A) between the habitat suitability (blue) and cattle density (yellow) reveal the interface areas between three wild bovid species and domestic cattle populations in Thailand. High-risk areas are represented in dark red, while low-risk areas are represented in grey.The potential high risk areas for disease transmission between three wild bovid species and cattle populations in Thailand (B). High-risk areas are represented in dark red, extracted from the interface areas in (A).

235　Table 1 The percentage of interface areas overlapped with protected areas by three wild
236　bovid species.

Species	Interface area with livestock (km^2)			Percentage (%) of overlap area in Thailand
	inside PA	outside PA	total	
Gaur	2,018	18,367	20,385	3.9
Banteng	2,089	20,477	22,566	4.4
Wild water buffalo	747	43,642	44,389	8.7

237　　　　According to the national disease surveillance, the total number of outbreak events is
238　7,522 events for the five selected bovine infectious diseases from 2013 to 2021. LSD (6,913)
239　has the most recorded outbreak events among the others, followed by FMD (563) and
240　brucellosis (39), while HS and bTB have only 5 and 2 events, respectively (Table 2 and Figure
241　2). This is because the first LSD outbreak occurred in cattle herds in Thailand in 2021, leading
242　to a large number of events reported across the country in a short period, while the other
243　infections, which have lower records, are endemic in this area.

244　　　　The cattle density demonstrated correlations with the number of infectious disease
245　outbreaks, and this correlation is proportional to the area size. We observed that in high cattle
246　density areas (190,076 km^2), there were higher outbreak events, totalling around 6,894
247　events (0.036 events per km^2), 18 times more than low cattle density areas (324,335 km^2),
248　which had 640 events (0.002 events per km^2). The results of outbreak events by cattle density
249　areas are presented in Table 2

250　Table 2 The occurrence of outbreak events classified by infectious disease and cattle density
251　from 2013 to 2021.

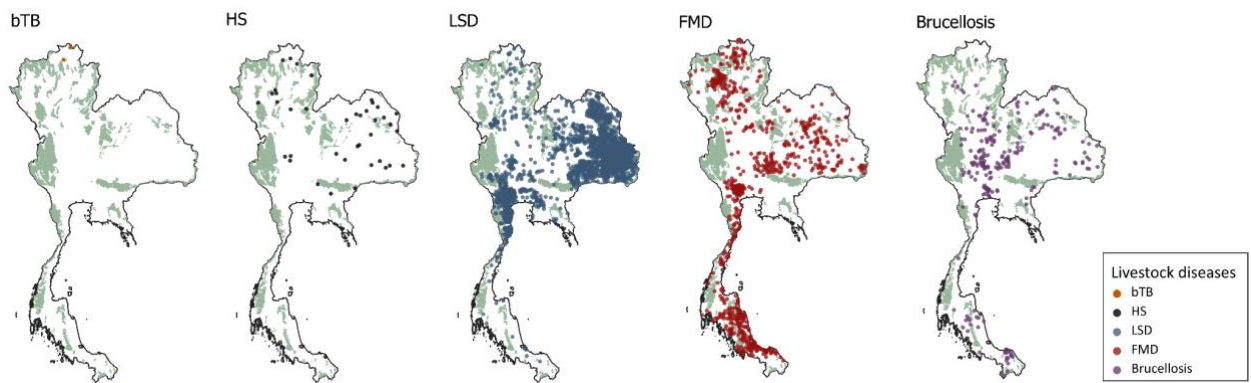| Infectious disease	Cattle density		Total
	Low (<=mean)	High (>mean)	
bTB	2	0	2
HS	3	2	5
LSD	445	6,473	6,918
FMD	175	395	563
Brucellosis	15	24	39
Total	640	6,894	7,534
Area of Thailand (km^2)	324,335	190,076	514,411
Total outbreak event per area (km^2)	0.0020	0.0363	0.0146

252

253

254 Figure 2 Occurrence of recorded bovine infectious disease outbreaks in Thailand from 2013
255 to 2021 and protected area distribution (PA; green). The maps show that the outbreaks
256 occurred across Thailand, particularly in proximity to protected and forest areas that overlap
257 with suitable habitats for wild bovids.

258 Table 3 The reported outbreak events of bovine infectious disease occurrences in the high
259 risk areas.

Bovine Infectious Diseases	All occurrences	Within high cattle density - high habitat suitability		
		Gaur	Banteng	Wild water buffalo
Tuberculosis	2	0	0	0
HS	5	0	0	1
LSD	6,918	166	108	442
FMD	563	32	51	190
Brucellosis	39	1	3	14
Total	7,534	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

260 We found that the density of outbreak events in cattle within the potential high risk
261 area of gaur (0.01) and especially for wild water buffalo (0.015) were similar to the average
262 density calculated for the country (0.0146) (Table 3). Wild water buffalo showed the highest
263 events (647) within the risk areas as they have the largest potential habitat areas across the
264 country while gaur (199) and banteng (162) show close results to each other. Similar to Table

265   2, the greatest numbers of disease events within high risk areas was for LSD and FMD in all
266   species and the other diseases presented only small numbers.

267   Moreover, according to the land use types, the most extensive interface areas were
268   found in close unknown forests (meaning they did not match any of the other forest
269   definitions), followed by cropland for three species. Closed evergreen forests also contain risk
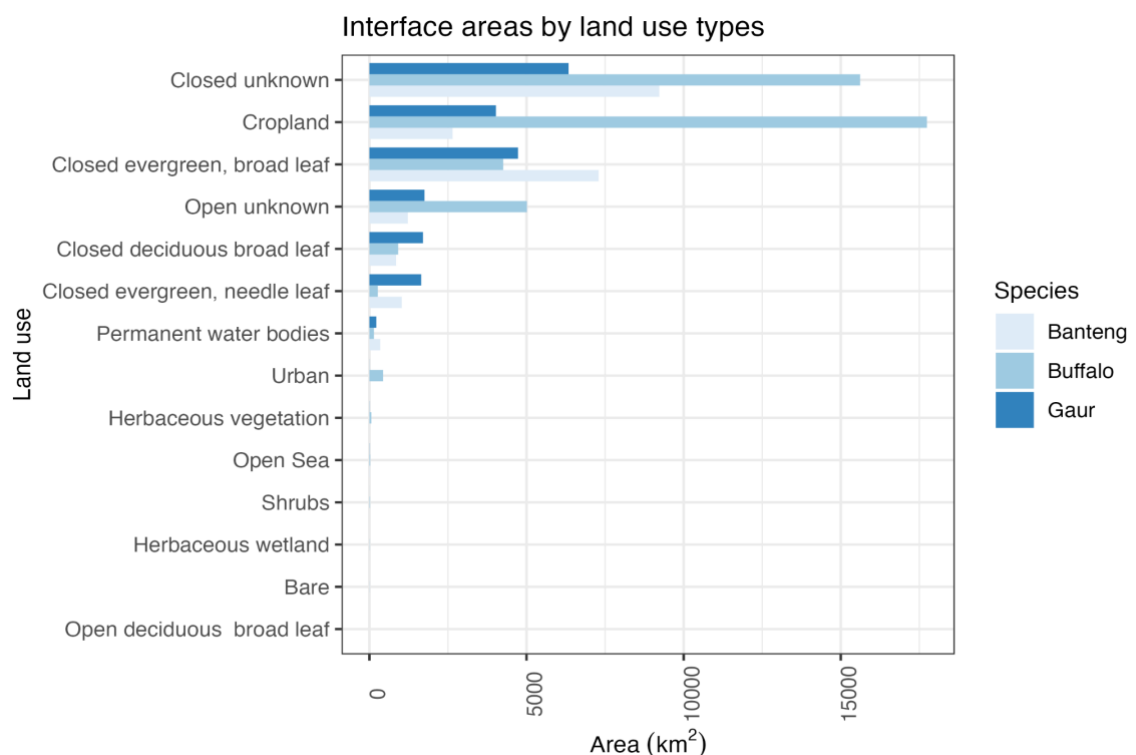270   areas for gaur and banteng. The open deciduous forest had no interface areas detected
271   (Figure 3).

272

273   Figure 3 Interface areas of three wild bovid species are categorised based on land use types,
274   from the land cover layers dataset ((41), https://zenodo.org/records/3243509). The term
275   closed unknown forest denotes a type of forest that does not match any of the other
276   definitions.

Discussion

278   We examined potential risk areas of disease transmission between wild bovids and
279   livestock and provided the preliminary focus area that should be considered for disease
280   surveillance and mitigation in Thailand. Total risk areas in Thailand are between 4% (gaur and
281   banteng) to 9% (wild water buffalo) of the country, with the most high risk areas being from
282   the central west (Ratchaburi) to the south (Nakhon Si Thammarat). The highest risk
283   proportion inside PAs was at Namtok Sam Lan National Park (NP) in the central, and the
284   largest risk areas were Kuiburi NP and Kaengkrachan NP in the western forest, related to the
285   highest cattle density in Thailand. Gaur and banteng have similar risk areas mostly around the

286 edge of forests, while wild water buffalo have risk widely across the country because models
287 predicted extensive amounts of suitable areas in the central down to the southern part that
288 coincide with the high cattle density areas.

289 Although the wild water buffalo showed the largest areas of predicted suitable habitat
290 among all three bovid species, it is also the most endangered. This is due to its current
291 distribution being confined solely to the Huai Kha Khaeng Wildlife Sanctuary, with the
292 population remaining stable and not exceeding 69 individuals for decades (42, 43). Thus,
293 many areas identified as high risk are unlikely to be current high risk areas but are important
294 for future planning should wild buffalo ranges expand to these or they be relocated. This
295 species is highly susceptible to endemic infectious diseases that could rapidly lead to serious
296 decline or even local extinction. For instance, diseases like HS can cause a high fatality rate of
297 up to 80% in domestic buffalo (44). The highly contagious and fatal nature of diseases like
298 rinderpest and FMD may be contributing factors to population disappearances in Nepal and
299 India (45). An outbreak could also lead to local extinction in a single fragmented population,
300 as the recovery process is prolonged and potentially results in a lack of gene flow (46),
301 especially with the independent mother origin of Thai wild water buffalo (47).

302 In contrast to wild water buffalo, gaur and banteng have more opportunities for contact
303 with domestic cattle and humans, while wild water buffalo may encounter livestock and
304 humans encroaching into the protected areas and suitable habitat. Gaur and banteng can
305 share habitats, making the interface areas similar to each other. However, gaur uses a wider
306 range of habitat types (e.g., evergreen, deciduous dipterocarp, mixed deciduous forests) than
307 banteng, which is restricted to dry and open forests (e.g., dry dipterocarp, mixed deciduous
308 forest) (48, 49). These two species show evidence of contact with livestock and humans due
309 to their ability to adapt and tolerate human activities, resulting in conflicts in overlapping
310 areas (11, 12, 50). However, their habitat suitability decreases when the distance is closer to
311 human settlement and the presence of domestic cattle grazing (51).

312 Our study identified the potential high-risk areas in the northeastern and southern
313 parts, which have the highest cattle density but low or even an absence of the actual species
314 distribution in some areas. This caveat is observed in the ecological niche modelling of wild
315 water buffalo, where high habitat suitability represents potential distribution and may not
316 necessarily correspond to the actual species distribution. Nevertheless, this caveat could be
317 mitigated by collecting and regularly updating occurrences of these bovid species, as well as
318 data on livestock density and distribution, or by restricting the analyses to areas with
319 sufficient data.

320 Urbanisation and expansion of agricultural areas increase the opportunity for contact
321 between domestic livestock and wildlife. Contact rate, the probability of transmission and the
322 location shifts of animals at each time step, are the major factors that need to be considered
323 for the spatial disease transmission model (52). The direct contact between wildlife and
324 livestock is unlikely but indirect contact in the same space at different times via shared

325 resources (e.g. water, grassland, supplement) with domestic animals potentially causes a
326 chance of wildlife exposure to pathogens and disease transmission (13, 53). However, to
327 succeed in cross-species infection, several factors should converge to drive pathogens
328 through the natural barriers before having a pathogenic infection into a new host (54). We
329 found that the highest interfaced areas were identified in cropland and unclassified forests,
330 which potentially can be shared by free-ranging livestock and wild bovids. Thailand also
331 experienced significant land cover changes (55) primarily driven by the increase of crop
332 plantations and urbanisation with concurrent population growth, which leads to changing
333 wildlife and livestock interactions and risk of disease transmission as per the previous studies
334 (56).

335 Host density is one of the main risk factors in wildlife and livestock disease transmission
336 (57, 58). We used host density and distribution as the main risk factors to identify and
337 prioritise the potential risk areas of wildlife and livestock disease transmission, as has been
338 used in the other studies (53, 59, 60). The advantage is knowing the target place for
339 implementing the disease surveillance system, but the disadvantages can arise from the
340 complexity of disease transmission dynamics, which depend on factors such as host species
341 movement (60), contact pattern (61), high adaptability of wildlife behaviour, transmission
342 modes (e.g. density or frequency-dependent) (58, 62) and population size (63).

343 Understanding the underlying factors that contribute to disease outbreaks in a specific
344 potential risk area is essential for planning effective disease mitigation and control strategies.
345 Multidisciplinary approaches incorporating key elements like pathogens, hosts, and
346 environmental factors (supplementary materials Table S1-S2, describe the generic risk factors
347 for disease transmission and mitigation methods between wildlife and livestock) also help
348 policymakers develop disease control and mitigation measures. Pathogen spillover events are
349 complicated, with a convergence of risk factors, which are difficult to approach. Integrating a
350 complex system of human, animal and environmental will benefit prevention efforts or at
351 least mitigate the impact of the next spill-over event (64).

352 Mitigation strategies will likely vary according to local socioeconomic conditions, but
353 among the preventive actions are using vaccination of livestock or even wild species, targeted
354 reduction of infected individual animals, herds or farms (ideally with compensation), along
355 with reducing livestock herd sizes and densities, transport of livestock among farms, and
356 contacts between farmed animals and wild species (65, 66). Contact reduction might be
357 through measures such as altering land use at the local level, or with "natural" (e.g. plant-
358 based) or artificial (e.g. metal) fencing or barriers and zoning of forests, livestock and human
359 settlements to minimise the contact (17, 67), which may lead to reduce pathogen spillover
360 (68). Longer term strategies might include societal transitions to lower meat-based, more
361 plant-based proteins to reduce demand for meat and dairy products. Conserving intact forests
362 with effective surveillance can mitigate the risk of disease transmission at the interface,
363 especially in edge or transition areas. In contrast, fragmented forests increase the likelihood

364   of wildlife being exposed to livestock and humans, leading to an elevated risk of disease
365   transmission (20, 69, 70).

366   Livestock vaccination is crucial for reducing outbreak incidences of endemic diseases,
367   requiring approximately 80% coverage to effectively prevent disease transmission for many
368   pathogens based on pathogen specific, particularly in high-risk areas and populations, as part
369   of routine practice (71, 72). However, capturing and delivering parenteral-route vaccinations
370   to free-ranging wild bovids pose significant challenges, especially in tropical forests where
371   animals might be hidden. Consequently, various aspects must be carefully considered in the
372   vaccination plan, including the target population, coverage, safety, and efficiency, to
373   effectively stimulate herd immunity (73). Non-invasive vaccination methods, like tuberculosis
374   oral vaccination, have been tested in domestic cattle and some wildlife and are planned for
375   use in wild cattle (74). Research and development for other endemic diseases like FMD, HS,
376   and brucellosis is still ongoing (75-77). Culling livestock infected with zoonotic diseases (e.g.,
377   bTB, brucellosis) is commonly implemented in Thailand (78, 79). However, infected animals
378   often undergo illegal translocation, potentially spreading the disease to other locations. To
379   manage this issue, the government should rigorously regulate animal movement, regulating
380   the guidelines for isolation of infectious animals during outbreaks, and providing appropriate
381   compensation for culling cases. The effectiveness of these mitigation actions is influenced by
382   the presence and use of effective infection and disease surveillance, as discussed below.

383   Livestock and, likely, wildlife disease surveillance in Thailand is based on the DLD, DNP
384   (Thailand) and WOAH guidelines (80), which cover significant transboundary disease
385   outbreaks in the country. Even though the passive surveillance system is useful for recording
386   the obvious clinical signs and emerging infectious diseases (like FMD and LSD), there is a gap
387   in collecting non-clinical to subclinical signs of disease due to these being challenging to
388   detect. Moreover, passive surveillance leads to underreporting by the farmers for some
389   zoonoses like bovine tuberculosis and brucellosis, for which animals must be condemned due
390   to the slow and partial (not less than 75% of the market price, but often not 100%)
391   compensation from the government. Another drawback is the clinical signs reported from
392   passive surveillance may not refer to the place where the animal got infected if those are
393   moved from the original area. Therefore, active surveillance such as risk-based (81), disease
394   surveys (Arjkumpa et al., 2020) screening or detecting seroprevalence are necessary in
395   hotspots or endemic areas to effectively allocate resources for disease mitigation and control
396   strategies. Furthermore, even when reported, further work must be undertaken to
397   understand the disease risk in depth. Reported data might refer to one event being a single
398   case or multiple cases, and infectious diseases are, by default, dynamic in their nature.
399   Without significant further work, passive surveillance data may offer a limited and biased
400   understanding of the true disease risk in a location at a particular time. The impact of the
401   detection of some infections on trade must be addressed, as this might be a barrier to
402   effective surveillance and reporting (82, 83). The involvement of field authorities is another
403   crucial aspect of data collection, indispensable for obtaining real-time information. Modern

404 technologies or data sharing can help identify risk areas and plan preparedness
405 implementations (62, 84, 85). Therefore, one should consider investing more in field data
406 collection and incorporating field practitioners or epidemiologists into the team before
407 formulating policies (86).

408   Using a One Health approach, a framework for disease surveillance has been developed,
409 incorporating essential considerations of spillover events into the processes. To sustainably
410 manage data collection and surveillance systems, collaboration among government
411 organisations and stakeholders is a key step in the process, involving considerations of
412 political, ethical, administrative, regulatory, and legal (PEARL) aspects through all approaches
413 (87). An effective surveillance system, characterised by rapid detection and accurate results,
414 not only monitors emerging diseases but also reduces the risk of disease transmission and
415 minimizes the impact on lives, economies, and biodiversity during disease outbreaks (88).
416 Also, the use of non-invasive data collection for willdife disease surveillance and surveys, such
417 as faces, urine, saliva and environmental samples (e.g. soil, water) should be considered to
418 avoid direct contact and reduce disturbing wildlife during capturing and data collection (89).
419 Further studies may consider including other risk factors such as multi-species host
420 distribution, the distance of risk factors and contact pattern (90, 91), as well as improving the
421 model by using updated disease surveillance data and wild bovid species occurrences,
422 especially for areas where the uncertainty of model predictions is high.

Conclusion

424   Our study predicted the potential risk areas by using the interface areas between
425 wildlife and domestic cattle, where livestock disease is frequently reported. We overlaid
426 suitable habitats of three large wild bovids in Thailand with cattle density to create potential
427 risk maps. High-risk areas were identified in locations with both high cattle density and high
428 habitat suitability, particularly at the edges of forest-protected areas. Notably, small,
429 fragmented forest areas with high cattle density presented the highest proportion of the high-
430 risk areas. Among various land-use types, cropped land and some closed forests exhibited the
431 largest interface areas. Our findings highlight the importance of wildlife habitat and intact
432 forest conservation to mitigate contact and reduce vulnerability to extinction, reduce shared
433 areas and address the potential risk areas for disease transmission between wild bovids and
434 livestock. This methodology not only supports disease surveillance but also facilitates the
435 implementation of effective mitigation and control measures.

Acknowledgements

Supplementary Materials

Table S1: Generic risk factors for disease transmission in wildlife and livestock interface areas, including studies and perspectives in Thailand and internationally. Table S2: Mitigation methods for infectious disease transmission.

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