

# Mapping the risk of disease transmission between wild bovids and domestic livestock in Thailand

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**Abstract:** The livestock-wildlife interface is one of the most important issues threatening wildlife conservation and public health. Habitat fragmentation, overlapping areas, expansion of livestock farming and lack of efficient disease control can lead to an infectious disease transmission between these populations (Wilkinson et al., 2018). To support disease surveillance and control programs targeting threatened wild bovids, we predicted areas at risk of infectious disease transmission based on the spatial overlap between Thai's wild bovids (including gaur, banteng, wild buffalo mainland serow and Chinese goral) and domestic livestock. Our preliminary study informs disease monitoring and surveillance planning, especially in limited resource scenarios. We assume that domestic cattle may act as the main sources of bovine infectious diseases. Therefore, high livestock density areas with high habitat suitability for wild bovids will be those with the highest risk disease transmission. First, we predicted suitable habitats for wild bovids using climate and land use as predictors and individual species occurrences from camera traps and animal sign data as response variables. We built a weighted mean ensemble of ecological niche models from eight algorithms. Then, to predict the potential risk areas, we multiplied the suitable habitat outputs for each species, ranging from 0 – 1, by cattle and buffalo density (Gilbert et al., 2018). Our results indicate that gaur has the largest suitable area across the country and Chinese goral has the smallest suitable area, only in the northern forests. We found forest protected areas in the western and central parts of Thailand (e.g., Huai Kha Khaeng, Khao Yai, Thap Lan yen and Kui buri) show high risk with suitable areas for all wild bovids except Chinese goral, and they are surrounded by livestock farming (high cattle and buffalo density). Our work highlights how habitat suitability might be helpful for infectious disease control planning and may also support the conservation of wild bovids through informing decision-making about protecting their habitats and preventing disease transmission between wild and domestic bovids. For further studies, we suggest improving the model by training with updated disease outbreak locations allowing for more disease-specific risk forecasting.

## REFERENCES

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