Veterinary Integrative Sciences 2026; 24(1): e2026022-1-11. DOI: 10.12982/VIS.2026.022

Veterinary Integrative Sciences
ISSN; 2629-9968 (online)

**Research article**

# Geographical distribution and spatiotemporal clusters of African horse sickness outbreaks in Thailand

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## Abstract

African horse sickness (AHS) is a deadly infectious vector-borne disease affecting equine species. Outbreaks of the disease can cause substantial economic loss due to its high mortality rate and the virus's ability to extend beyond endemic areas. In March 2020, Thailand experienced the first confirmed AHS case, resulting in more than 600 horses dying and the mortality rate exceeding 90%. This study aims to determine the spatial distribution of AHS in Thailand. Initially, records on the first outbreak of AHS in 2020 were used for geoprocessing and visualized distribution. Subsequently, spatial and spatial-temporal statistical analyses were performed using QGIS and SaTScan 10.1 software. The results reveal the occurrence of AHS incidents in the central, lower northeastern, eastern, and western regions of Thailand at a total of 131 locations. The spatial analysis demonstrates significant clustering of AHS in 2020. Additionally, the Getis-Ord statistic reveals a high-density (hotspot) of AHS at the central plane, encompassing the central, lower northeastern, and eastern regions of Thailand. The space-time permutation model depicts the spatiotemporal pattern of AHS. The output identifies two significant clusters in the central part of the country, covering the central, eastern, and western regions (P-value 0.000028) and another cluster in the lower northeastern region (P-value 0.012) between February and September 2020. These findings provide crucial insights into the spatial and spatiotemporal distribution of AHS in Thailand, which is necessary for improving disease management and prevention strategies.

**Keywords**: African horse sickness, Hotspot, Outbreak, Spatial analysis.

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***Funding:*** *The Geo-Informatics and Space Technology Development Agency (GISTDA) and the Ministry of Higher Education, Science, Research, and Innovation, Thailand.*

***Article history;*** *received manuscript: 24 February 2025,*
*revised manuscript: 31 March 2025,*
*accepted manuscript: 16 May 2025,*
*published online: 13 June 2025,*
***Academic editor;*** *Korakot Nganvongpanit*

# INTRODUCTION

African horse sickness (AHS) is a deadly infectious vector-borne disease affecting equine species, including horses, donkeys, and mules. It is caused by the African horse sickness virus (AHSV), a double-stranded RNA virus belonging to the Reoviridae family, Orbivirus genus (Toh et al., 2022). AHS is primarily transmitted by *Culicoides spp*. biting midges (Robin et al., 2016) and is characterized by severe alterations in respiratory and circulatory function, with case mortality rates reaching up to 95% in unimmunized horse populations (Carpenter et al., 2017). Due to its high mortality and potential for rapid transboundary spread, the World Organization for Animal Health (OIE) classifies AHS as a listed disease, necessitating strict surveillance and control measures to prevent outbreaks (OIE, 2020).

AHS is currently endemic in sub-Saharan Africa, where it poses persistent challenges to equine health and industry (Dennis et al., 2019). However, global changes, including climate variations, increased trade, and the movement of animals, have facilitated the expansion of the disease beyond its traditionally endemic regions. In previous decades, outbreaks have been reported in Europe (Rodriguez et al., 1992) and Asia (Howell, 1960), highlighting the virus's ability to emerge in non-endemic regions. Thailand experienced the first documented outbreak of AHS in March 2020, when veterinary authorities confirmed a case in Pak Chong, Nakhon Ratchasima. The disease subsequently spread to other areas of the country, resulting in over 500 horse deaths across 15 outbreaks, with a mortality rate exceeding 90%. Prior to this outbreak, AHS had never been reported in Thailand. The equine population, totaling 7,960 horses across more than 3,000 farming locations, had no previous exposure to the virus, lacking prior immunity, thus making them highly susceptible to severe clinical manifestations of the disease. Despite Thailand's established animal health surveillance systems, the outbreak highlighted potential gaps in biosecurity measures and vector control strategies. The ability to prevent future outbreaks requires a comprehensive understanding of AHS transmission dynamics, the identification of potential hotspots, and the assessment of the spatiotemporal patterns of disease spread.

Spatial analysis tools, statistical modeling, and geographical information systems (GIS) have demonstrated significant value in understanding disease transmission processes, particularly for vector-borne diseases (Palaniyandi et al., 2014). The application of GIS in epidemiological studies has increased significantly since the 1990s (Koch, 2012), facilitating the integration of spatial data from diverse sources, disease mapping, and cluster detection (Graham et al., 2004). Previous studies have utilized spatial analytical techniques such as the SaTScan to detect clusters of disease outbreaks such as lumpy skin disease (Punyapornwithaya et al., 2022). Numerous studies have examined the spatial distribution of vector-borne diseases (López et al., 2018; Chimera et al., 2022; Li et al., 2023), including AHS in endemic regions (Fairbanks et al., 2022). However, no such research has been conducted in Thailand.

This study aims to analyze the spatial patterns of AHS distribution, identify hotspot areas, and conduct spatiotemporal analysis to evaluate the AHS clusters associated with the first documented outbreak in Thailand by employing GIS applications and epidemiological modeling approaches. The findings are expected to be valuable for public health policymakers, epidemiologists, and equine industry stakeholders by providing critical insights into AHS outbreaks in Thailand, leading to the development of targeted control measures.

# MATERIALS AND METHODS

## Data Collection

The datasets comprise demographic data and disease outbreak reports collected by the Department of Livestock Development (DLD). The data include information on the horse population, the number of infected cases, and geographical locations of reported outbreaks in 2020. The data on horse population were derived from the annual census conducted by local DLD officials and livestock volunteers through house-to-house surveys, with the results submitted via a web-based reporting system, which can be accessed at https://eregist.dld.go.th/eregist-portal/. Following data collection, the datasets were structured, verified, and prepared in shapefile format for analysis. The spatial distribution of disease was subsequently analyzed and visualized using spatial and spatial-temporal statistical approaches to identify the overall disease spatial patterns, spatial correlation, disease clustering, and hot spot detection. A summary of the data used in this study is presented in Table 1.

**Table 1** Data and data type from Department of Livestock Development in year 2020 used in this study

| Data | Data type |
|---|---|
| Horse population | Number |
| Location of cases reported | Coordinates |
| Infected cases | Number |

## Spatial Analysis

This study applies geoprocessing and statistical tools in spatial and spatiotemporal analysis, conducted using QGIS 3.18 and SaTScan 10.1 software. Spatial visualization of AHS is performed to illustrate the distribution of the disease and related information geographically. Disease clustering is then investigated by identifying the location, generating a hotspot map, and finally, assessing the spatiotemporal distribution to evaluate the pattern, intensity, and area of the disease cluster.

### Spatial Autocorrelation and Cluster Analysis

The records on the first AHS outbreak in Thailand are geographically processed using QGIS software to visualize the overall pattern of disease distribution. For the initial analysis, a shapefile format containing 3,462 farm location points is utilized, comprising 131 locations with reported cases and 3,331 locations without reported cases or no incidence of AHS. This dataset is used to assess spatial autocorrelation as a preliminary step prior to conducting hotspot detection. The Global Moran's I index is used to evaluate the spatial autocorrelation in the dataset (Waldhör, 1996). The Getis-Ord statistics are applied in this study to identify local disease clustering patterns or detect hotspots, with the selection based on data type and nature of the disease being assessed. The non-case points are incorporated into the cluster analysis as part of the spatial dataset to allow the Getis-Ord Gi* statistic to identify significant hotspots and cold spots based on the overall distribution of both cases and non-cases. Hotspot analysis, a key component of spatial mapping and analysis, aims to identify the spatial phenomena occurring in clusters. These phenomena are visually represented on a geographical map as points indicating the locations of specific objects or occurrences (Mclafferty, 2015). In this step, the farm-level AHS infection rate per 100 individuals is analyzed. The infection rate at the farm level is calculated using the following formula.

$$Infection\ rate = Number\ of\ Sick\ horse\ /\ Total\ population \times 100$$

### Spatiotemporal Analysis

Spatiotemporal analysis is conducted to examine the AHS clustering pattern in Thailand according to space and time. This process is performed using SaTScan

10.1 software and the space-time permutation model. This approach allows the statistical significance of a significant cluster to be identified by creating a window across space and time, allowing the number of observed and expected examples to be calculated. The SaTScan™ determines space-time clusters using circular geographical windows and time intervals given as the height of a cylinder with the window base (Kulldorff, 2018). The dataset used for analysis includes file reports with details of the case and time (date of confirmed cases) and a location file with coordinates of disease occurrence with the same location ID as the case file prepared in CSV file format. The study period and time precision are then defined. A precision unit of the day is selected. The spatial window size is 50%, and the temporal window size is also 50%. After the parameter setting, the software is assigned to conduct a space-time retrospective analysis using the space-time permutation probability model scan statistics.

# RESULTS

The clustering and spatiotemporal analysis results were achieved using the previously mentioned space-time permutation model. The data used for the analysis consisted of the horse population, locations of cases reported, and number of infected cases as the farm-level AHS infection rate.

## Spatial Analysis (Global Moran's I and the Getis-Ord statistic)

Global Moran's I test and the Getis-Ord statistic were used to analyze the clustering or hotspots of AHS occurrence in Thailand along with global spatial autocorrelation. Table 2 summarizes the results of Global Moran's I analysis. According to the findings of Global Moran's test for AHS occurrence, the Moran's I value was 0.048844, and the corresponding P-value was 0.0095. This indicates that during 2020, there was a significant cluster of AHS in Thailand. The associated z-score of 2.591515 reveals that the likelihood of clustered patterns being the consequence of random events is less than 1%.

**Table 2** Summary of Global Moran's I result

| Index | Result |
|---|---|
| Moran's Index | 0.048844 |
| z-score | 2.591515 |
| P-value | 0.009555 |

The statistical analysis using the Getis-Ord method identified significant spatial clustering of AHS infection rates across different regions, with high-incidence areas concentrated in the central and northern parts of the southern regions of Thailand.

A statistically significant hotspot (P-value <0.01) was identified in the central area of the country, involving three major regions: central, northeastern, and eastern Thailand. Another cluster (marked red in Figure 1) with a P-value <0.05 was detected in the western region. The analysis revealed that hot spots, representing areas with significantly higher infection rates, were most prominent at the 99% confidence level (667 locations), followed by the 95% (25 locations) and 90% (20 locations) confidence levels.

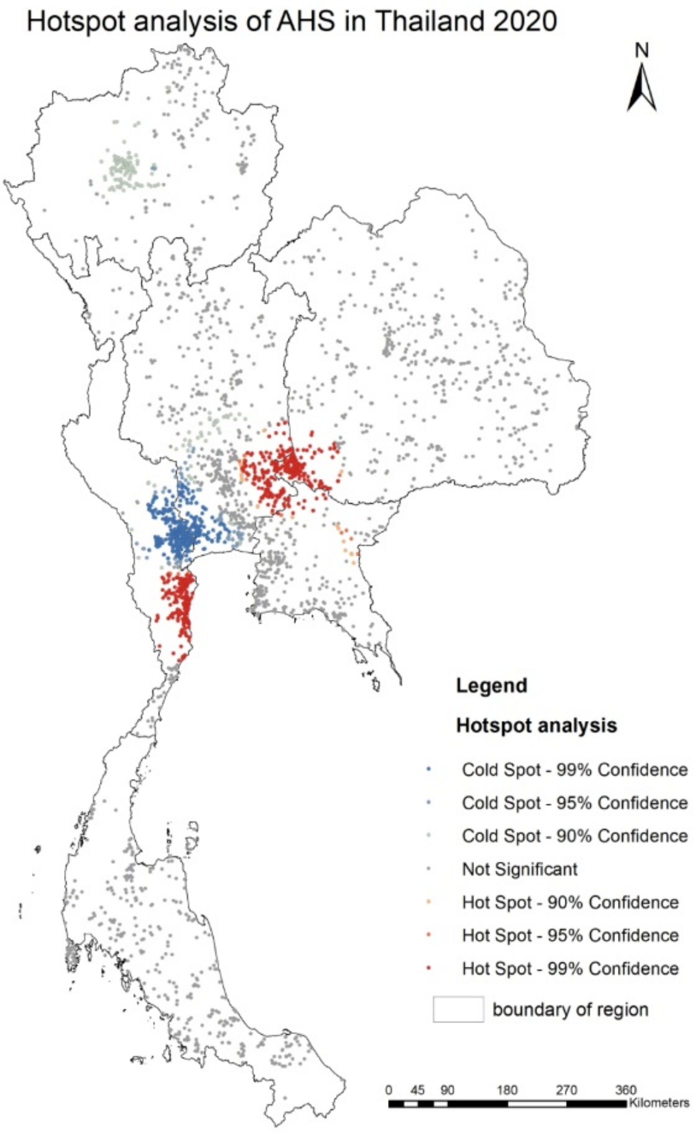

**Figure 1** Hotspot analysis results of AHS outbreaks in Thailand (2020)

**Table 3** Summary of the Getis-Ord statistical analysis results

| z-score | P-value | % Confidence level | Number of locations |
|---|---|---|---|
| < -1.65 | <0.01 | Cold spot 99% | 532 |
| < -1.96 | <0.05 | Cold spot 95% | 77 |
| < -2.58 | <0.10 | Clod spot 90% | 201 |
| | | Not significant | 1,940 |
| > +1.65 | <0.10 | Hot spot 90% | 20 |
| > +1.96 | <0.05 | Hot spot 95% | 25 |
| > +2.58 | <0.01 | Hot spot 99% | 667 |

In contrast, cold spots (represented in blue in Figure 1) indicate areas with lower infection rates, primarily located in the lower part of the central region, extending into the midsection of the western region. Cold spots were detected at the 99% confidence level (532 locations), with fewer locations at the 95% (77 locations) and 90% (201 locations) confidence levels. A substantial number of locations (1,940) were not statistically significant. These findings highlight the presence of distinct geographical variations in disease prevalence, emphasizing the need for targeted intervention strategies to control the spread of AHS in high-risk areas while maintaining surveillance in low-risk regions.

## Spatiotemporal Analysis

The space-time permutation model was employed to analyze the spatiotemporal distribution of AHS outbreaks in Thailand. The results, illustrated in Figure 2, identify clusters of infection, with red and green circles indicating detected cluster areas and red dots representing the location of reported AHS cases. The findings of the study reveal the occurrence of AHS outbreaks between February and September 2020, with a total of 131 locations reporting cases and 610 confirmed infections. Two significant clusters cover the central part of the country, involving a total of 59 locations. Statistical significance was determined using a P-value threshold of <0.05.

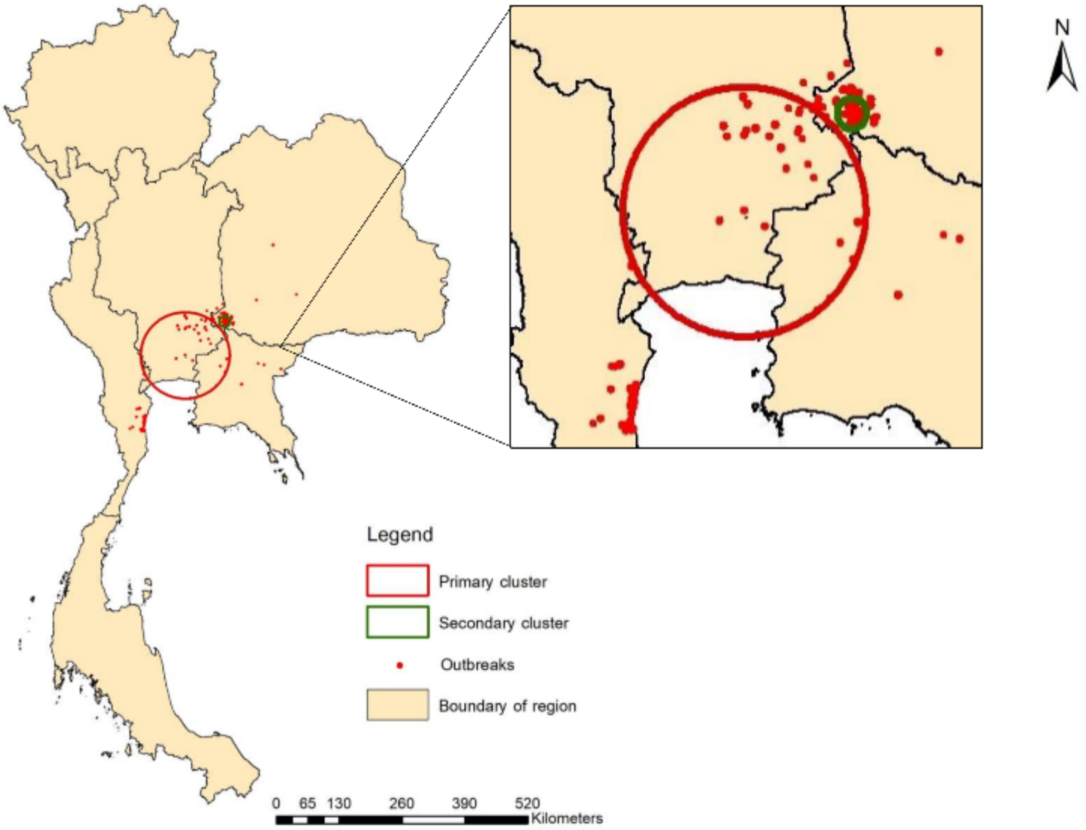

**Figure 2** Space-time permutation analysis results

The primary cluster, emerging between May 2 and August 1, was the most statistically significant (P-value 0.000028). This cluster had a radius of 89.28 km, covering the central region, the northern part of the eastern region, and some parts of the western region, with cases reported in 23 locations. The second cluster, observed between February 24 and April 1 in the lower northeastern region of Thailand, encompassed 22 cases within a 10.9 km radius and a statistically significant P-value of 0.012, as shown in Figure 2 and Table 4. These findings highlight the spatial and temporal patterns of AHS outbreaks, emphasizing the need for targeted surveillance and intervention strategies in high-risk areas.

**Table 4** Spatiotemporal analysis results of AHS outbreaks in Thailand 2020 using the space-time permutation model

| Cluster | Cluster time | Centroid/ Radius(km) | O | E | O/E ratio | LLR | P-value |
|---|---|---|---|---|---|---|---|
| 1 | May 2 and August 1, 2020 | 13.952900 N, 100.712200 E/ 89.28 km | 2.99 | 7.69 | 0.3888 | 10.871 | <0.001 |
| 2 | February 24 and April 1, 2020 | 14.583700 N, 101.445700 E/ 10.9 km | 2.32 | 9.47 | 0.2449 | 6.689 | 0.011 |

O=observed case; E=expected case; O/E ratio=ratio of observed cases/expected cases; LLR=log-likelihood ratio.

# DISCUSSION

AHS is considered to be a highly fatal, vector-borne viral disease. It has a severe economic impact on the equine industry as well as equine health and welfare. Given its devastating effects, studying the epidemiology and spatial distribution of AHS is crucial for a better understanding of disease patterns for occurrence, leading to effective prevention and outbreak control. During the 2020 outbreak of AHS in Thailand, hundreds of horses were affected, with a case-fatality rate exceeding 90%. This is consistent with the previous outbreak in Africa in 2011 (Grewar et al., 2013). Whereas during the 1989 outbreak in Portugal, a mortality rate of 62.2% was reported in the vaccinated population (Portas et al., 1999).

Hotspot analysis is a spatial analysis technique used to identify statistically significant clusters of high and low disease occurrences, providing insights into the geographical distribution of outbreaks. This approach offers the visualization of high-risk areas, enabling researchers and policymakers to implement targeted control measures, while spatiotemporal analysis extends this understanding by incorporating the temporal dimension, allowing for the detection of patterns over time and identifying trends in disease spread. Together, these methods enhance epidemiological surveillance, facilitating more effective prevention and intervention strategies.

The spatial analysis of past AHS outbreaks reveals distinct geographical clustering, with cases often concentrated, and a greater risk of disease occurrence in areas where vector populations are abundant, climatic conditions favorable, equine density high, or a large amount of horse movement exists (Faverjon et al., 2015; Kim et al., 2024). Similarly, in Thailand, cases were reported predominantly in central and northeastern regions, suggesting a spatially structured disease distribution influenced by environmental and epidemiological factors.

The results of Global Moran's I test and the Getis-Ord statistical analysis provide strong evidence of significant spatial clustering in the occurrence of AHS in Thailand during 2020. The results confirm that the observed clustering is unlikely to be due to random chance, indicating a structured spatial distribution of the disease. In contrast, in a recent study conducted in Indonesia between 2018 and 2022 on bovine anaplasmosis (a vector-borne disease with different vector and ecological contexts), the results of Global Moran's I indicate a random pattern of disease prevalence throughout the study period (Wibowo et al., 2024). According to the study, the Getis-Ord analysis further refines this observation by identifying high-incidence hotspots predominantly in the central, northeastern, and eastern regions, with the most significant clustering occurring at a 99% confidence level in 667 locations. Conversely, cold spots, representing areas of lower infection rates, are concentrated in the lower central and mid-western regions. The presence of both hot and cold spots highlights the heterogeneous nature of AHS distribution, reinforcing the necessity for spatially targeted intervention strategies. High-risk areas require immediate control measures, including enhanced surveillance, vaccination programs, and vector management, while sustained monitoring in low-risk regions remains essential to prevent potential outbreaks.

Although this study primarily focuses on the spatial and spatiotemporal analysis of African Horse Sickness (AHS) outbreaks in Thailand and does not directly include an analysis of environmental factors, certain distinct spatial characteristics may plausibly facilitate the occurrence and transmission of the disease. For instance, the hot spot areas identified in the central and lower northeastern regions of Thailand are characterized by abundant natural water sources, extensive irrigation systems, and predominantly agricultural land use. These environmental features create favorable conditions for vector development and may serve as potential breeding sites. Furthermore, horse management practices in these areas, such as open grazing or housing horses near water bodies, can increase the likelihood of exposure to insect vectors. The density and movement pattern of the horse population in these regions may also play a role in enhancing the risk of disease transmission.

On the other hand, the cold spot areas may reflect not only spatial and climatic conditions less conducive to vector proliferation but also the presence of effective disease control measures and robust veterinary public health systems, potentially contributing to the lower incidence of AHS observed in those regions.

The clusters of AHS outbreaks identified in this study, in practical terms, could assist authorities in focusing their attention on located outbreak farms in order to obtain further information on risks and dissemination of the disease. Comparing farms located in and outside of clusters would allow researchers to examine management strategies and other possible causes of AHS outbreaks. Official authorities could additionally assign priority to regions with a large number of cases while allocating resources and enforcing stringent surveillance and control measures.

Although there are currently no ongoing outbreaks of AHS in Thailand, and the World Organization for Animal Health (WOAH) has officially reinstated Thailand’s status as an AHS-free country effective March 10, 2023, the risk of re-emergence remains a concern. Despite this achievement, continuous surveillance, preventive measures, and effective control strategies are essential for preventing future outbreaks and maintaining the country’s disease-free status.

Several studies have explored various AHS control measures, including the use of live attenuated vaccines, vector control strategies, and movement restrictions to mitigate disease transmission (Diouf et al., 2013; Castillo-Olivares, 2020). Vector management, particularly targeting *Culicoides midges*, has been identified as a critical component of disease control since these insects serve as the primary transmission vectors. However, there is currently a significant lack of data on vector abundance in Thailand, highlighting the need for further research on potential vectors. Additionally, Thailand has developed a comprehensive contingency plan, which includes enhanced surveillance, early detection systems, vaccination protocols, and outbreak response strategies to ensure rapid containment in the event of reintroduction. These proactive measures are vital for reducing the risk of future outbreaks and protecting equine health at both national and regional levels.

The findings of this study underscore the importance of integrating spatial epidemiological approaches into national disease control policies to ensure efficient resource allocation for preventing, controlling, and mitigating the risk of AHS spread. Understanding these spatial patterns is critical for predicting future outbreaks and developing targeted control strategies, such as vector management, movement restrictions, and vaccination programs. By leveraging spatial analysis, policymakers and veterinary authorities can implement proactive and evidence-based interventions, ultimately strengthening disease surveillance and protecting equine health in Thailand.

# CONCLUSIONS

In 2020, there a notable clustering of AHS cases was detected in Thailand, according to the results of the Global Moran's I test and spatial evaluation. Considering a Moran's I value of 0.048844, a P-value of 0.0095, and a z-score of 2.591515, the study suggests that the disease possessed a structured geographical distribution, and the observed spatial clustering was unlikely to be due to random events. Furthermore, the Getis-Ord Gi* statistics identified high-incidence hotspots, primarily located in the central area of the country covering the central, lower northeastern, and eastern regions, characterized by a high equine population density. Two significant clusters were identified in the central region, the northern part of the eastern region, and some parts of the western region (P-value 0.000028), with another cluster in the lower northeastern region (P-value 0.012) between February and September 2020, according to the space-time permutation analysis, which examined the spatiotemporal pattern of AHS. This implies that the clustering of AHS may have been associated with common factors that possessed similar characteristics spatially.

These findings offer critical insights into the spatial and spatiotemporal distribution of AHS in Thailand, which are essential for enhancing disease management and prevention strategies. By integrating GIS applications with epidemiological modeling methodologies, this study provides a comprehensive understanding of AHS outbreaks in horses. Such an approach enables risk-based surveillance and supports evidence-based decision-making for disease control, aligning with national and area-specific policies to mitigate the impact of AHS.

# ACKNOWLEDGEMENTS

I would like to express my sincere gratitude to the Department of Livestock Development for providing essential material support for this research. My deepest appreciation goes to Dr. Kitsanai Charoenjit and Dr. Pattama Phodee for their invaluable guidance and insightful instruction throughout this study. I am also grateful for the financial support provided by the Geo-Informatics and Space Technology Development Agency (GISTDA) and the Ministry of Higher Education, Science, Research, and Innovation, Thailand, which made this research possible.

# AUTHOR CONTRIBUTIONS

**Maytawee Tamprateep**: Conceptualization and writing - original draft preparation. **Phattraporn Soytong**: Methodology and supervision. **Piyanart Lekcharoensook**: Resource and project administration. **Weerapong Thanapongtharm**: Validation and supervision. **Jianzhong Lu**: Writing – Review & Editing.

# CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

# REFERENCES

Carpenter, S., Mellor, P.S., Fall, A.G., Garros, C., Venter, G.J., 2017. African horse sickness virus: history, transmission, and current status. Annu. Rev. Entomol. 62, 343-358.

Castillo-Olivares, J., 2020. African horse sickness in Thailand: challenges of controlling an outbreak by vaccination. Equine Vet. J. 53(1), 9.

Chimera, E.T., Fosgate, G.T., Etter, E.M.C., Jemberu, W.T., Kamwendo, G., Njoka, P., 2022. Spatio-temporal patterns and risk factors of foot-and-mouth disease in malawi between 1957 and 2019. Prev. Vet. Med. 204, 105639.

Dennis, S.J., Meyers, A.E., Hitzeroth, II, Rybicki, E.P., 2019. African horse sickness: a review of current understanding and vaccine development. Viruses. 11(9), 844.

Diouf, N.D., Etter, E., Lo, M.M., Lo, M., Akakpo, A.J., 2013. Outbreaks of african horse sickness in senegal, and methods of control of the 2007 epidemic. Vet. Rec. 172(6), 152-152.

Fairbanks, E.L., Baylis, M., Daly, J.M., Tildesley, M.J., 2022. Inference for a spatio-temporal model with partial spatial data: African horse sickness virus in Morocco. Epidemics. 39, 100566.

Faverjon, C., Leblond, A., Hendrikx, P., Balenghien, T., de Vos, C.J., Fischer, E.A.J., de Koeijer, A.A., 2015. A spatiotemporal model to assess the introduction risk of african horse sickness by import of animals and vectors in france. BMC Vet. Res. 11(1), 127.

Graham, A.J., Peter, M.A., Danson, F.M., 2004. Spatial analysis for epidemiology. Acta. Trop. 91(3), 219-225.

Grewar, J.D., Koen, P., Davey, S., Visser, D., Russouw, E., Buhrmann, G., Weyer, C.T., Guthrie, A.J., Quan, M., 2013. The 2011 outbreak of African horse sickness in the African horse sickness controlled area in South Africa: Original research. J. S. Afr. Vet. Assoc. 84(1), 1-7.

Howell, P.G., 1960. The 1960 epizootic of African horse sickness in the middle east and S.W. Asia. J. S. Afr. Vet. Assoc. 31(3), 329-334.

Kim, K., Xu, T., Kannan Villalan, A., Chi, T., Yu, X., Jin, M., Wu, R., Ni, G., Sui, S., Wang, Z., Wang, X., 2024. Environmental and historical determinants of African horse sickness: Insights from predictive modeling. Transbound. Emerg. Dis. 2024, 5586647.

Koch, T., 2012. Knowing its place: mapping as medical investigation. Lancet. 379(9819), 887-888.

Kulldorff, M., 2018. Satscantm user guide. Available online: https://www.satscan.org/

Li, Y., An, Q., Sun, Z., Gao, X., Wang, H., 2023. Risk factors and spatiotemporal distribution of lumpy skin disease occurrence in the asian continent during 2012–2022: an ecological niche model. Transbound. Emerg. Dis. 2023(1), 6207149.

López, M.S., Müller, G.V., Sione, W.F., 2018. Analysis of the spatial distribution of scientific publications regarding vector-borne diseases related to climate variability in South America. Spat. Spatio-Temporal Epidemiol. 26, 35-93.

Mclafferty, S., 2015. Disease cluster detection methods: recent developments and public health implications. Ann. GIS. 21(2), 127-133.

Palaniyandi, M., Anand, P., Maniyosai, R., 2014. Spatial cognition: a geospatial analysis of vector borne disease transmission and the environment, using remote sensing and GIS. Int. J. Mosq. 1(3), 39-54.

Portas, M., Boinas, F., Sousa, J.O.E., Rawlings, P., 1999. African horse sickness in portugal: a successful eradication programme. Epidemiol. Infect. 123(2), 337-346.

Punyapornwithaya, V., Seesupa, S., Phuykhamsingha, S., Arjkumpa, O., Sansamur, C., Jarassaeng, C., 2022. Spatio-temporal patterns of lumpy skin disease outbreaks in dairy farms in Northeastern Thailand. Front. Vet. Sci. 9, 957306.

Robin, M., Page, P., Archer, D., Baylis, M., 2016. African horse sickness: the potential for an outbreak in disease-free regions and current disease control and elimination techniques. Equine Vet. J. 48(5), 659-669.

Rodriguez, M., Hooghuis, H., Castaño, M., 1992. African horse sickness in Spain. Vet. Microbiol. 33(1), 129-142.

Toh, X., Wang, Y., Rajapakse, M.P., Lee, B., Songkasupa, T., Suwankitwat, N., Kamlangdee, A., Judith Fernandez, C., Huangfu, T., 2022. Use of nanopore sequencing to characterize African horse sickness virus (AHSV) from the African horse sickness outbreak in Thailand in 2020. Transbound. Emerg. Dis. 69(3), 1010-1019.

Waldhör, T., 1996. The spatial autocorrelation coefficient moran's i under heteroscedasticity. Stat. Med. 15(7-9), 887-892.

Wibowo, S.E., Andityas, M., Nuraini, D.M., Zurbein, Nugraheni, Y.R., Awaludin, A., Rahayu, P., Insulistyowati, A., 2024. Spatial analysis of bovine anaplasmosis in Jambi province, Indonesia: 2018-2022. Vet. Integr. Sci. 22(3), 857–869.

World Organisation for Animal Health (OIE), 2020. Guidelines on preparedness and implementation of emergency vaccination in the asian region. Paris, France, OIE.

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How to cite this article;

Maytawee Tamprateep, Jianzhong Lu, Phattraporn Soytong, Piyanart Lekcharoensook and Weerapong Thanapongtharm. Geographical distribution and spatiotemporal clusters of African horse sickness outbreaks in Thailand. Veterinary Integrative Sciences. 2026; 24(1): e2026022-1-11.

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