

ISWAVLD 2Ö23

International Symposium of the World Association of Veterinary Laboratory Diagnosticians 29 JUNE-1 JULY 2023 Congress Centre Lyon

Towards
the veterinary
diagnostics
of the
future

Main topic: Surveillance and control of emerging diseases

Seasonal abundance, diversity, and role of Culicoides spp. in African Horse Sickness transmission in horse, Thailand

 $\underline{\textit{UNJIT K.}}^1, \, \textit{SAIYASOMBAT R.}^1, \, \textit{WATTANAMETHANONT J.}^1, \, \textit{TATTIYAPONG M.}^1, \, \textit{AMORNCHAISUWAN T.}^1, \, \textit{JIRATHANH M.}^1, \, \textit{PREMASHTHIRA S.}^2, \, \\ \textit{THEPPARAT A.}^3$

National Institute of Animal Health, Department of Livestock Development, 50/2 Kaset-Klang, Chatuchak, Bangkok, Thailand; ² Bureau of Disease Control and Veterinary Services, Department of Livestock Development, 69/1 Ratchathewi, Bangkok, Thailand; ³ Department of Agricultural Technology, Faculty of Science, Ramkhamhaeng University, Hua Mak, Bang Kapi, Bangkok, Thailand

Introduction

African Horse Sickness (AHS) is a non-contagious, infectious disease that affects equids. It was first reported in Thailand in March 2020. AHS is not directly transmissible, but it is known to be spread by insect vectors, which are usually related to species of *Culicoides* biting midges. Therefore, the aim of this study is to investigate abundance of *Culicoides* in each season, their diversity and role in AHS transmission in Thailand.

Material and Methods

Vector surveillance for AHS was launched after the last clinical case, both in infected and non-infected areas, across Thailand during October 2021 to September 2022. The study area was divided into Northern, Northeastern, Central, Upper-southern and Lower-southern regions, plus two locations in the Eastern area where zebras are kept. In each area, three horse farms were chosen from one province with the highest population of horses. Sample collections were carried out three times a year according to the three seasons of Thailand: winter, summer, and rainy season. Five UV light traps were placed at horse-raising areas from dusk to dawn. Adult *Culicoides* were identified using wing morphology, and the representative of each species was confirmed using cytochrome c oxidase subunit I (COI) mtDNA molecular marker [1]. *Culicoides* taken from the infected area were examined by real-time PCR to detect RNA of AHS virus. *Culicoides* midges were pooled with up to 25 midges of the same species for AHS RNA detection [2].

Results and Discussion

The result revealed that a total of 63,858 *Culicoides* samples were identified, with 30 species of *Culicoides* spp. found, and it appears that *C. oxystoma* showed the most abundant species. The highest diversity of *Culicoides* species was found in the northern region, with 26 *Culicoides* species identified. However, there was less diversity of *Culicoides* collected from zebra farms than horse farms. In term of seasonal abundance, summer revealed the highest abundance of *Culicoides* followed by rainy and winter, respectively. *C. imicola*, a proven species that can transmit AHS virus, was found in all seasons in horse farms located in 4 regions and in two zebra farms, except for the lower-southern region where only one *C. imicola* was found in summer. This suggests that lower-southern region is a low-risk area for AHS. All 754 pools of 8,217 Culicoides midges collected in all seasons from areas that were previously affected by AHS outbreak tested negative by real-time PCR, which has proven the absence of virus circulation during vector surveillance. These results show *Culicoides* vector data in horse and zebra farms in Thailand and will contribute to further study in a particular area and perform strategic control.

Acknowledgements

The study was granted by the National Research Council of Thailand.