**11TH ASIAN SOCIETY OF VETERINARY PATHOLOGY (ASVP) &**

**16TH MALAYSIAN ASSOCIATION OF VETERINARY PATHOLOGY (MAVP) SCIENTIFIC CONFERENCE**

**25 – 27 JULY 2025**

**INSTRUCTIONS TO AUTHORS**

1. All papers (oral and poster) are to be submitted in **ABSTRACT** with the general format requirements are as follows:
2. **Paper Size:** A4 size paper (21 x 29.7cm).
3. **Margins**: 1 inch top and bottom; 1.25 inches on sides.
4. **Title:** 12 pt bold Tahoma, centered, and in capital letters.
5. **Author(s)/Affiliation/E-mail:**One blank line after the title, names of authors should be written in full, 10 pt bold Tahoma, centered and in capital letters. The name and address of the institution where the work was done shall be 10 pt Tahoma, centered and in italics. The corresponding author's email shall be indicated with the asterisk symbol (\*).
6. **Abstract Header:** 11 pt bold Tahoma and centered, with one blank line above and below.
7. **Abstract:** 11 pt Tahoma, single spacing, justified on both margins, **MUST NOT EXCEED 350 WORDS**.
8. **Keywords:** Include a maximum of 5 keywords below the abstract.
9. Please 'save as' the abstract with your full name in Word Document format **(e.g., Sarahabdullah.doc.)**
10. All papers must be submitted electronically to **confmavpreg@gmail.com** by **15th June 2025** for inclusion in the Conference Proceedings. Authors are responsible for obtaining permission for reprinting any material included in their papers that is already copyrighted elsewhere.
11. The Committee will review all submitted abstracts. Notification regarding abstract acceptance and scheduling will be sent to the submitting author.
12. The Conference Committee will organise:
13. **POSTER PRESENTATION:** The Best Poster Presentation Award (student and researcher categories).
14. **ORAL PRESENTATION:** The Best Oral Presentation Award (student and researcher categories).
15. If you have any inquiries, please contact the Scientific Committee via email at **confmavpreg@gmail.com** or visit the **Malaysian Association of Veterinary Pathology (MAVP) Facebook** page**.**

**POSITIVE WEST NILE VIRUS (WNV) DETECTION VIA PCR AND ELISA AMONG EQUINE IN CENTRAL PART OF MALAYSIA**

**1NOOR SIFA SHAIDA ABD HAMID,1\*NOR YASMIN ABD RAHAMAN,**

**2NORANIZA MOHD ADZAHAN, 7HUSSNI O MOHAMMED, 3,6ABDUL RAHMAN OMAR, 4SITI SURI ARSHAD, 5JALILA ABU AND**

**8NUR AIN NAJWA MOHD YUSERI**

*1,8Department of Veterinary Laboratory Diagnostics*

*2Department of Farm and Exotic Animal Medicine and Surgery*

*3,4Department of Veterinary Pathology and Microbiology*

*5Department of Veterinary Clinical Studies*

*Faculty of Veterinary Medicine*

*Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia*

*6Institute of Bioscience*

*Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia*

*7Department of Population Medicine and Diagnostic Sciences*

*Cornell University College of Veterinary Medicine
Ithaca, NY 14853*

\*Corresponding author: noryasmin@upm.edu.my

**Abstract**

West Nile virus (WNV) is a zoonotic and arthropod-borne flavivirus that can be transmitted by biting infected mosquitoes. The horse is a dead-end host that is highly susceptible to the disease, which may develop nervous signs. A previous orang asli and companion birds report revealed seropositivity against WNV in Malaysia. However, thus far, there is no data reported on the status of WNV infection in a horse in Malaysia which makes this study serve as preliminary research. Although WNV is not endemic in Malaysia yet, most breeds imported to Malaysia were derived from WNV endemic countries. By considering these facts, this study aims to detect the presence of WNV in horses via serological and molecular methods by using competitive ELISA (ID Screen ® West Nile Competitive Multi-species) and rt-PCR, respectively. Convenient sampling was performed by obtaining serum and oropharyngeal swabs from 20 horses in 3 different states: Selangor, Putrajaya, and Kuala Lumpur. By using ELISA, 19/20 samples were positive against WNV anti-prE antibodies. One step rt-PCR targeting the highly conserved gene between capsid and pre-membrane revealed that seven samples were positive (Gender: Mare=2, Gelding=5; Location: Putrajaya=3, Kuala Lumpur=4, Selangor=0 and Breed: Thoroughbred=3, Warmblood=4). The positive bands were submitted to First Base Laboratory for sequencing analysis and revealed 98-99% homologous to WNV strain from South Africa, the USA, Hungary, Italy and North Europe. The phylogenetic tree revealed that the positive samples aligned with strains found in USA and Austria, Central Europe. In conclusion, this study confirmed that WNV was successfully being detected and this proved that there was exposure to WNV among equine populations in the central part of Malaysia.

**Keywords***: West Nile virus, equine, flavivirus, ELISA, PCR, central Malaysia*