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Evidence of West Nile virus infection in migratory and resident wild birds in west coast of peninsular Malaysia

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ABSTRACT

West Nile virus (WNV) is a zoonotic mosquito-borne flavivirus that is harbored and amplified by wild birds via the enzootic transmission cycle. Wide range of hosts are found to be susceptible to WNV infection including mammals, amphibians and reptiles across the world. Several studies have demonstrated that WNV was present in the Malaysian *Orang Asli* and captive birds. However, no data are available on the WNV prevalence in wild birds found in Malaysia. Therefore this study was conducted to determine the serological and molecular prevalence of WNV in wild birds in selected areas in the West Coast of Peninsular Malaysia. Two types of wild birds were screened, namely migratory and resident birds in order to explore any possibility of WNV transmission from the migratory birds to the resident birds. Thus, a cross-sectional study was conducted at the migratory birds sanctuary located in Kuala Gula, Perak and Kapar, Selangor by catching 163 migratory birds, and 97 resident birds from Kuala Gula and Parit Buntar, Perak at different time between 2016 and 2017 (Total, $n = 260$). Blood and oropharyngeal swabs were collected for serological and molecular analysis, respectively. Serum were screened for WNV antibodies using a commercial competitive ELISA (c-ELISA) (ID Screen® West Nile Competition Multi-species ELISA, ID VET, Montpellier, France) and cross-reactivity towards Japanese Encephalitis virus (JEV) was also carried out using the JEV-double antigen sandwich (DAS) ELISA. Oropharyngeal swabs were subjected to one-step RT-PCR to detect WNV RNA, in which positive reactions were subsequently sequenced. WNV seropositive rate of 18.71% (29/155) at 95% CI (0.131 to 0.260) and molecular prevalence of 15.2% (16/105) at 95% CI (0.092 to 0.239) were demonstrated in migratory and resident wild birds found in West Coast Malaysia. Phylogenetic analyses of the 16 WNV isolates found in this study revealed that the local strains have 99% similarity to the strains from South Africa and were clustered under lineage 2. Evidence of WNV infection in resident and migratory birds were demonstrated in this study. As a summary, intervention between migratory birds, resident birds and mosquitoes might cause the introduction and maintenance of WNV in Malaysia, however the assumption could be further proven by studying the infection dynamics in the mosquitoes present in the studied areas.

1. Introduction

West Nile virus (WNV) infection can cause significant morbidity and mortality in humans and animals worldwide, as were seen in the outbreaks in New York and India [4,23]. WNV was first reported in a

woman from Uganda in 1937 [36]. Since then, the virus has spread globally and caused epidemic outbreaks on all continents except for Antarctica [31,36]. Transmission of the virus occurs in an enzootic cycle between wild birds and mosquitoes, in which wild birds serve as reservoirs and amplifiers, while mosquitoes such as *Culex* spp. and

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