

The First Outbreak of Autochthonous Zika Virus in Sabah, Malaysian Borneo

ABSTRACT

Background: Zika virus (ZIKV) infection is a public health concern. The first ZIKV outside Africa was detected in mosquito in Malaysia. More than six decades ago, serological surveys indicated the presence of human infection with ZIKV in the Malaysian Borneo state of Sabah. It has also been demonstrated that orangutans in Sabah have antibodies against ZIKV. Several years ago, a case of human ZIKV infection was reported in a traveler who visited Sabah. Therefore, it is thought that ZIKV is endogenous to Sabah and is widely distributed. During the recent global epidemic of ZIKV, the first autochthonous case and two subsequent autochthonous cases were detected in Sabah. Because ZIKV infection is mainly asymptomatic or mildly symptomatic, the extent of ZIKV infection in the population of Sabah is not known. Furthermore, the presence of ZIKV in vector mosquitoes and animals has not been investigated. Therefore, the present study was performed to analyze the outbreak cases of ZIKV infection and to determine their relationship with the burden of ZIKV infection in the local population, mosquitoes, and wild nonhuman primates in Sabah.

Methods: Serum and urine samples were collected from two local patients with ZIKV infection, their household members, and those who resided within 400m of the patients' residences. Serum samples were also collected from four wild *Maca fascicularis*. Mosquito samples, mostly female *Aedes albopictus*, were collected from 30 sites in Kota Kinabalu. The presence of ZIKV was assessed by RT-qPCR and RT-PCR. Phylogenetic analysis was performed using the neighbor-joining method.

Results: Two cases of ZIKV infection were identified by reverse-transcription quantitative PCR (RT-qPCR) in residents of Kota Kinabalu, and the Taiwanese health authorities reported one case in an individual who visited Kota Kinabalu during the study period. All household members of both local patients and people living within a 400 m radius of the patients were negative for ZIKV. Furthermore, mosquitoes collected from the surroundings of the residences and places visited by the patients and four serum samples

from *M. fascicularis* were also negative for ZIKV. A phylogenetic tree constructed using the nucleotide sequences of the envelope genes of ZIKV showed that the strains from Sabah formed a cluster with strains from Thailand and Cambodia, and belong to the Asian lineage.

Conclusions: Our study revealed that ZIKVs in Sabah is of Asian lineage and are not related to the recent outbreak strains in the Americas and Singapore. ZIKV infection in Sabah is sporadic, possibly because of limited transmission of the virus. Further studies are needed to characterize the evolutionary history of ZIKV in Sabah to understand the epidemiology of this infection in Borneo.