

Chikungunya Virus in Thailand; An Update

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Chikungunya virus (CHIKV) is an emerging or re-emerging mosquito borne virus that can be found in several countries in Africa and Asia. Belonging to *Alphavirus* genus of the *Togaviridae* family, CHIKV is an enveloped, single-stranded, positive-sense RNA virus. It was first discovered in Tanzania, east Africa in 1952 and was identified in Thailand in 1958. There are four distinct lineages of CHIKV based on the E1 envelope glycoprotein sequences: the West African lineage, the East Central and South African (ECSA) lineage, the Asian lineage, and the Indian Ocean lineage (IOL). IOL is a new lineage that evolved from the ECSA lineage, which first emerged in Kenya in 2004 and spread to Indian Ocean Islands, India, and Southeast Asia (Parola et al., 2006). However, no evidence indicates the virulence difference among CHIKV lineages. Transmission cycle of CHIKV involves *Aedes* mosquito vectors, humans, and possibly mammal reservoir hosts (Jupp and McIntosh, 1990; Turell et al., 1992). Transovarial transmission of CHIKV was also indicated in *Aedes* mosquitoes (Thavara et al., 2009).

CHIKV causes low mortality, but high morbidity in humans. Most of the infected patients have rash, fever, and painful peripheral polyarthritides which affect their life quality. Viremia in infected patients can only be found during the first week of infection with the viral load between 10^7 and 10^9 copies/ml of the serum (Parola et al., 2006). During this period, the patient can be diagnosed by virus isolation and confirmed by reverse transcription polymerase chain reaction (RT-PCR) (CV et al., 2007; Theamboonlers et al., 2009). After the viremia period, patient diagnosis has to be performed based on the clinical signs and serology (IgM and IgG) profiles (Grivard et al., 2007). However, misdiagnosis can be found in the area that also has the outbreak of Dengue virus. The patient can sometimes be infected with both viruses which health care professionals need to be concerned about and aware of (Thaung et al., 1975; Chahar et al., 2009; Leroy et al., 2009; Theamboonlers et al., 2009).

Levels of the viral load in patients indicated above are very high and sufficient for infecting the

blood-fed mosquitoes and causing them to become potential vectors for this virus. Even though CHIKV has long been neglected, the outbreak of this virus has occurred again in several countries since 2000. The change in the virus properties and mosquito ecology might cause the outbreak of CHIKV during this decade. CHIKV re-emerged and caused the outbreak in the Southern part of Thailand in September 2008, and it was spread nationwide. According to the Bureau of Epidemiology, Department of Disease Control, Ministry of Public Health, Thailand, there were 2,433, 49,069 (7.41/100,000) and 1,533 (2.41/100,000) human cases in 2008, 2009, and 2010, respectively.

The present study indicated an alanine-to-valine substitution at the position 226 of the E1 envelope glycoprotein (E1-A226V) on an IOL. This substitution causes the virus to lose cholesterol dependence for growth and increases its replication and infectivity, and leads to the adaptation to different mosquito species which make *Aedes albopictus* more potential vectors than *Aedes aegypti* (Tsetsarkin et al., 2007). It is very important to realize the ability of RNA viruses to evolve rapidly which might increase their host or vector range (Tsetsarkin et al., 2007). In the past, CHIKV isolated from Thailand was in the Asian lineage and the competent vector was *Aedes aegypti*; however, CHIKV that was responsible for the outbreak in Thailand during 2008-2010 was the IOL with E1-A226V and the majority of the vector was *Aedes albopictus* (de Lamballerie et al., 2008; Thavara et al., 2009). The 2008 CHIKV isolated from Thailand was also closely related to a virus that caused the outbreak in India in 2007 and in Singapore in 2008 (Theamboonlers et al., 2009).

Besides human patients, other mammals might play important roles in the ecology of this virus. Viremia has been indicated in monkeys whereas antibodies have been demonstrated in chimpanzees, monkeys, horses, pigs, water buffaloes, cattle, dogs, rabbits, and bats (Weinbren et al., 1958; Osterrieth and Blanes-Ridaura, 1960; Halstead and Udomsakdi, 1966). The animal infection study in laboratory also indicated that young mice can be

infected with CHIKV (Couderc et al., 2008; Ziegler et al., 2008). To document the possibility of each animal to act as an amplifying host in the ecology of CHIKV, virus isolation needs to be performed in field or experiment animals. Since traveling within or between country can occur within one day, the spread of CHIKV or other pathogens takes place very quickly. This point needs to be taken into consideration when the outbreak of any pathogen occurs. Even though the situation of CHIKV outbreak in Thailand has ameliorated, people and health care professionals are still required to become aware of this virus, which the outbreak potentially occurs again any time in the future.

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