

## Isolation and genomic characterization of *Culex* flaviviruses from mosquitoes in Myanmar

Aung Kyaw Kyaw<sup>a,b</sup>, Mya Myat Ngwe Tun<sup>a</sup>, Corazon C. Buerano<sup>a,c</sup>, Takeshi Nabeshima<sup>a</sup>,  
Miako Sakaguchi<sup>d</sup>, Tsuyoshi Ando<sup>a</sup>, Shingo Inoue<sup>a</sup>, Yi Yi Mya<sup>b</sup>, Daisuke Hayasaka<sup>a</sup>,  
Hlaing Myat Thu<sup>b</sup>, Kyaw Zin Thant<sup>b</sup>, Kouichi Morita<sup>a</sup>

<sup>a</sup> Department of Virology, Institute of Tropical Medicine, Nagasaki University, Nagasaki, Japan

<sup>b</sup> Department of Medical Research (Pyin Oo Lwin Branch), Ministry of Health and Sports, Myanmar

<sup>c</sup> Research and Biotechnology, St. Luke's Medical Center, Quezon City, Philippines

<sup>d</sup> Central Laboratory, Institute of Tropical Medicine, Nagasaki University, Nagasaki, Japan

Abstract Book, 59<sup>th</sup> Japanese Society of Tropical Medicine, Nagasaki, Japan, 2018.

An entomological surveillance of arboviruses was conducted in Myanmar in 2014. A total of 8357 *Culex* mosquito vectors were collected in the Mandalay area and virus isolation was done by using the mosquito cell line C6/36 E2. A total of eighteen strains of *Culex* flavivirus (CxFV) were isolated from *Cx. tritaeniorhynchus*, *Cx. vishnui* and *Cx. fuscocephala*. Like other insect-specific flaviviruses, CxFV can replicate only in mosquito cells but not in mammalian cells. These CxFV strains that were isolated in Japan from mosquitoes collected in Myanmar were closely related to the Wang Thong virus detected from *Cx. fuscocephalus* in Thailand and *Cx. theileri* flavivirus (CTFV) isolated from *Cx. theileri* mosquitoes in Portugal and Turkey. They encode a single open reading frame with 3357 amino acid residues. They have the characteristics of flaviviruses and have 95.62% amino acid identity with CTFV. This is the first report of CxFV in Myanmar with the characterized viral genome. This study illustrated that CxFV was circulating among the vectors of human pathogenic arboviruses in Myanmar but the impact of CxFV on other flaviviruses which are endemic in the study area still remains to be explored.