Double dengue serotypes in asymptomatic populations living in an area of Thailand endemic for dengue hemorrhagic fever

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ABSTRACT

Dengue virus infection remains a major health problem worldwide. Understanding dengue infections and characterizing circulating viruses are essential for disease prevention and control as well as vaccine development. In this study, we aimed to identify dengue virus in healthy people living in an area endemic for dengue disease. Blood samples were collected from 52 healthy local subjects living in a dengue-endemic area of Thailand. Viral RNA was detected using nested reverse transcription polymerase chain (RT-PCR) that amplified the E gene. Phylogenetic trees were constructed by neighbor-joining method using MEGA6.06. Dengue virus was detected in 5 of 52 samples (9.62%). Double virus serotypes were identified in two samples. Syltotic dengue serotype I genotypes were also observed. Serotype 4 belonged to genotype II. Interestingly, both genotypes I and II were found in one serotype 3 sample. These preliminary results may provide better understanding of dengue infections and viral transmission between populations and mosquitoes. Furthermore, these findings may be significant for epidemiological studies of dengue hemorrhagic fever.

INTRODUCTION

Dengue viruses (DENV-1 to DENV-4) are transmitted to human hosts through the bites of infected female Aedes aegypti and Ae. albopictus mosquitoes [1]. The disease is problematic worldwide, especially in tropical and subtropical areas. Of 390 million infected patients reported annually, 50-100 million dengue cases (10-15%) are symptomatic, approximately 500,000 develop DHF [2], and up to 300 million are asymptomatic or mild cases [3]. However, the relationship between asymptomatic and symptomatic infections and the role asymptomatic infections play in disease transmission remains unknown. Based on historical dengue incidence data during 2007 and 2012 obtained from the Department of Disease Control in Thailand’s Ministry of Public Health, provinces in the central region, such as Samut Sakhon, are at high risk for dengue outbreaks [4], therefore, this study tested for presence of the virus in local adult volunteers with no reported dengue signs, symptoms, or diagnoses. These findings could provide a better understanding of dengue pathogenesis and the relationship between the virus and its hosts in the mosquito-human-mosquito cycle within endemic areas. This information could be of interest to epidemiological studies and inform development of effective dengue control measures.

MATERIALS AND METHODS

Sample collection (Blood samples) → RNA extraction → Nested RT-PCR of the dengue virus envelope (E) gene → DNA Cloning and Sequencing → Phylogenetic tree construction

We identified asymptomatic dengue virus infections with both single and co-infections in a highly endemic area of Thailand. Study of subclinical infections could provide better understanding of disease pathogenesis in the human host. Moreover, basic knowledge of co-infection and concurrent transmission in endemic areas are key factors for epidemiological design of effective control programs. Additionally, data on variations in viral sequences could be used to support future development of diagnostic and treatment approaches as well as vaccine design.

CONCLUSIONS

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