Spatial Circulation of Dengue Serotypes in Eastern Thailand during 2012-2015

Salakchit Chutipongvivate1* and Youngyut Prompunjai2

1Department of Medical Sciences, Medical Sciences Technical Office, Ministry of Public Health, Thailand.
2Department of Medical Sciences, Regional Medical Sciences Center 6, Ministry of Public Health, Thailand.

Authors’ contributions

This work was carried out in collaboration between both authors. Author SC designed the study and wrote the protocol. Authors SC and YP did the statistical analysis and literature searches while analyses of study was done by author SC. Both authors read and approved the final manuscript.

Article Information

DOI: 10.9734/IJTDDH/2016/30034

(1) Viroj Wiwanitkit, Department of Laboratory Medicine, Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand.
(2) Pablo A. Méndez-Lázaro, University of Puerto Rico, USA.
(2) Raul H. Morales-Borges, Ashford Institute of Hematology & Oncology, USA.
Complete Peer review History: http://www.sciencedomain.org/review-history/17025

Received 13th October 2016
Accepted 22nd November 2016
Published 25th November 2016

Original Research Article

ABSTRACT

Dengue virus infection is an epidemic infectious disease and currently a major public health problem in Thailand. The epidemiology of dengue is characterized by cyclic epidemic activity alternating between years of relatively low and high dengue incidence. The annual change of predominant serotypes was the cause of severity of the disease. This study was to determine the circulating dengue serotype by reverse transcription polymerase chain reaction (RT-PCR) during January 2012 to December 2015. A total of 527 seropositive acute samples were analyzed from dengue fever patients in eight provinces in eastern Thailand. Two hundred and forty five samples were found positive, of which 39.2%, 35.5%, 14.3% and 11.0% were affected with DENV-1, DENV-3, DENV-4 and DENV-2 respectively. From 2012 to 2013, the predominant dengue serotype was DENV-1 whereas DENV-3 and DENV-4 were predominant in 2014. There was an apparent increase in the percentage of DENV-4 from 2014 to 2015 and DENV-4 was predominant in 2015, DENV-2 was the least dengue serotype in this region. The study indicated that all four dengue

*Corresponding author: Email: salakchit.c@dmsc.mail.go.th;
serotypes were circulating in eastern Thailand and the predominant serotypes were dynamic. The identification of dengue viruses infecting the human population provides an important means of early detection of any change in the prevalence of dengue virus serology. Our study has shown the pattern of dengue virus in eight provinces of eastern Thailand from year to year and provided some insight into the dengue epidemic situation in this region. This information should be beneficial to dengue surveillance and prevention and control programs in Thailand.

Keywords: Dengue serotype; epidemiology; eastern Thailand.

1. INTRODUCTION

Dengue is a global mosquito-borne viral disease affecting humans. The primary vector is the Aedes aegypti mosquito. Before 1970, dengue was present in the tropical and subtropical regions of the Americas, Africa, Mediterranean, Western Pacific region and Southeast Asia regions [1]. The incidence of dengue has grown dramatically around the world in recent decades. In 2012, imported cases were detected in mainland Portugal and 10 other countries in Europe. Many cases occurred in China, Costa Rica, Honduras and Mexico in 2013. The year 2015 was characterized by large dengue outbreaks worldwide, with the Philippines reporting more than 169,000 cases and Malaysia exceeding 111,000 cases, representing a 59.5% and 16.0% increase in case numbers to the previous year, respectively. Moreover, dengue continues to affect India, the Island of Hawaii of United States of America, Brazil, the Pacific land countries of Fiji, Tonga and French Polynesia [2]. Dengue disease is a public health priority in Southeast Asia, and Thailand contributes substantially to the regional disease burden [3].

The first dengue outbreak occurred in Bangkok in 1958, initially in a pattern with a 2-year cycle, and subsequently in irregular cycles, as the disease spread throughout the country. The largest outbreak was reported in 1987, with an incidence rate of 325 cases/100,000 population. In 1999, the Ministry of Public Health, Thailand initiated a dengue control program to reduce the incidence rate to less than 50 cases/100,000 population [4]. Over the review period wide yearly variations in incidence occurred, with regular epidemics in 2001, 2002, 2010 and 2013 with dengue disease remaining a highly seasonal disease. The data showed a seasonal peak of dengue disease in the numbers of cases and deaths between May and September annually. The pattern coincides with the rainy season in Thailand. In addition, the age group shifted during the review period from younger towards older, although dengue disease in Thailand remains a childhood disease predominately with higher severity reported in young children [3,5-6]. In recent years, increasingly larger dengue outbreaks have occurred. There were 139,355 114,800, 116,497, 108,728 cases of dengue reported to the Bureau of Epidemiology in 2001, 2002, 2010 and 2013 respectively [6].

Dengue infections are caused by four closely related viruses named DENV-1, DENV-2, DENV-3, and DENV-4. These four viruses are called serotypes because each has different interactions with the antibodies in human blood serum. The four dengue viruses are similar — they share approximately 65% of their genomes — but even within a single serotype, there is some genetic variation. Despite these variations, infection with each of the dengue serotypes results in the same disease and range of clinical symptoms [7]. Dengue virus causes varying clinical symptoms ranging from dengue fever (DF) and dengue haemorrhagic fever (DHF) to dengue shock syndrome (DSS) according to the World Health Organization criteria [8]. Recovery from infection by one serotype provides lifelong immunity against that particular serotype [7]. However, cross-immunity to the other serotypes after recovery is only partial and temporary. Subsequent infections by other serotypes increase the risk of developing dengue haemorrhagic fever [9-10]. Gubler et al. [11] and Lam et al. [12] reported that virological surveillance, which involves monitoring of dengue virus infection in humans, has been used as an early warning system to predict outbreaks. Such surveillance, based on the isolation and identification of dengue viruses infecting the human population, provides an important means of early detection of any change in the prevalence of dengue virus serotypes. Nisalak et al. [13] reported that the predominant dengue serotype in the outbreaks in Bangkok during 1997–1998 was DENV-3. Anantapreecha et al. [14] detected the predominant serotypes DENV-1 and DENV2 in six provinces across Thailand during 2001–2002. Veeraseatakul et al. [15] reported the predominant serotypes DENV-2 in four provinces of northern Thailand during