Distribution of dengue cases in the state of Oaxaca, Mexico, during the period 2004–2006

Jeannette Günthera, Luis Román Ramírez-Palaciob, David Guillermo Pérez-Ishiwaraa, Juan Santiago Salas-Benitob,∗

a Programa Institucional de Biomedicina Molecular, Escuela Nacional de Medicina y Homeopatía del Instituto Politécnico Nacional, México, Mexico
b Laboratorio Estatal de Salud Pública del estado de Oaxaca, México, Mexico

A R T I C L E  I N F O

Article history:
Received 13 January 2009
Received in revised form 5 May 2009
Accepted 6 May 2009

Keywords:
Dengue
Mexico
Gender
Co-infection
RT-PCR
Epidemiology

A B S T R A C T

Background: Dengue virus infection is an emergent viral disease and the most important transmitted by a vector worldwide. In Mexico it has been an important public health problem since 1995 and Oaxaca is one of the most affected states in the country.

Objective: To determine the geographic distribution of confirmed dengue cases in the state of Oaxaca, Mexico, the serotypes circulating, and the main gender and age groups affected.

Study design: Information about confirmed dengue cases obtained by LESPO during the period 2004–2006 was classified, sorted, and analysed. A RT-PCR technique was used to determine the serotype of the virus in serum samples.

Results: A substantial increment in the number of dengue cases was noticed during the period of this study. The most affected sanitary jurisdiction was located on the coast where the climatic conditions were ideal for vector development and where there is significant migratory activity. The most affected group was the 11–15-year-old group. Dengue haemorrhagic fever was more frequent in men than in women over 16 years old, with a significant difference evaluated by χ2-test (p < 0.001). Four serotypes of the virus were detected in the state and two co-infections with DEN2–3 and DEN3–4 were identified.

Conclusions: The increment in the number of dengue cases in the state of Oaxaca could be explained by several factors such as the presence of the four serotypes of the virus, the migratory phenomenon, the climatic conditions and the socioeconomic level of the population.

© 2009 Elsevier B.V. All rights reserved.

1. Background

The four dengue (DEN) virus serotypes are the infectious agents responsible for the most important mosquito–borne viral disease in the world, affecting more than 100 countries including America, Africa and South East Asia. Approximately 50–100 million cases are reported annually, of which 250,000–500,000 require hospitalization and 24,000 are fatal.

DEN virus is a member of the Flaviviridae family, Flavivirus genus and is transmitted to humans mainly by the mosquito Aedes aegypti, which is distributed worldwide between latitudes 35° North and 35° South. The infection caused by the four serotypes of DEN virus may be asymptomatic or displays symptoms of a mild disease named dengue fever (DF), which is characterized by fever, headache with retro-orbital pain, arthralgia, myalgia, anorexia and occasionally a rash. Secondary infections are more likely to be associated with a more serious illness known as dengue haemorrhagic fever (DHF), which is characterized by bleeding that usually requires hospitalization. DHF can evolve to a dengue shock syndrome (DSS) that might be fatal.

The number of cases of DEN has increased worldwide since the seventies, as a consequence of several factors such as invasion of virulent genotypes of the virus to new geographic areas, and increased vector distribution as a result of unplanned and uncontrolled urbanization, migration of the rural population to the cities, inadequate wastewater management, and failure of the vector control programmes. The first DHF outbreak in Mexico occurred in 1995 and at the present time, DEN is an important public health problem in the country where Oaxaca is one of the most endemic states.