

# **Analysis on the Epidemiology and Etiologic Characteristics of First Imported Dengue Fever Disease Case in Shenzhen in 2015**

Fan Yang<sup>1\*</sup>, Renli Zhang<sup>1</sup>, Chunli Wu<sup>1</sup>, Dana Huang<sup>1</sup>, Yue Li<sup>1</sup>, Yijun Tang<sup>1</sup>

<sup>1</sup>Shenzhen Center for Disease Prevention and Control

## **Background/Objective**

To study the epidemiology and the etiology characteristics of first imported Dengue fever case reported in Shenzhen city in 2015.

## **Method**

Data on descriptive epidemiology was collected to study the characteristics to the epidemic. The serum sample collected from the suspect dengue fever case was detected for IgM, IgG, NS1 antigen by ELISA, immunochromatography and dengue virus nucleic acid by real-time RT-PCR. The samples were further inoculated in C6/36 cells for virus isolation. E gene of isolated virus strain was amplified by RT-PCR and sequenced to construct homology comparison and phylogenetic tree of E gene with the strains isolated from other areas.

## **Result**

The case was laboratory confirmed imported Dengue fever disease cases in Shenzhen on January 2015. IgM, NS1 antigen and RNA of type 2 dengue virus were detected, and dengue virus named DEN2-SZ1503 was successfully isolated from the serum sample. The homology of nucleotide sequence and the deduced amino acid sequence of E gene of SZ1503 with standard type 2 dengue virus NGC strain were 93.8% and 97.8%, but the homology with standard dengue virus 1,3,4 in the same fragment were 67.1%,66.5%,65.8% and 67.7%,66.7%,63.0%, respectively. The phylogenetic tree indicated that SZ1503 had the greatest similarity with the SG(EHI)D2/06572Y13 strain (Malaysia 2013) and they lied in the same branch of the phylogenetic tree. The isolated dengue virus type 2 belonged to genotype IV with 1051 strain (Indonesia 76), 10 strain (Somalia 84) and 271-206 strain (Sri Lanka 90).

## **Conclusion**

The virological, serological and molecular features showed that the imported case of dengue fever was caused by type 2 dengue virus and genetic characteristics of the SZ1503 virus strain are consistent with Dengue virus popular in Malaysia. This imported case did not cause the secondary cases.