

Complete Genome Sequence of a Dengue Virus Serotype 4 Strain Isolated in Guangdong, China

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Here we report the first complete genome sequence of a dengue virus serotype 4 genotype II strain, GZ30, isolated in Guangzhou, Guangdong Province, China, in 2010. The sequence information provided herein will help us to understand the molecular epidemiology of dengue virus and predict the risk of severe diseases in mainland China.

The global emergence of dengue virus (DENV) infections poses a great public health and economic burden worldwide, especially in tropical and subtropical regions (1). DENV contains four serotypes, and each of them can cause mild dengue fever (DF), severe dengue hemorrhagic fever, and deadly dengue shock syndrome (2). Although the pathogenesis of severe diseases remains poorly understood, secondary infection with another DENV serotype is believed to increase the risk of severe diseases via the mechanism of antibody-dependent enhancement (5).

In mainland China, DF is listed as a notifiable infectious disease by the Chinese Ministry of Health. Guangdong Province in Southern China is one of the major DENV-affected areas (7). During autumn 2010, a local outbreak of DF was confirmed in Guangzhou City, Guangdong Province, and the causative agent was identified as DENV serotype 4 (DENV-4). To date, no complete genome sequence of the Chinese DENV-4 strain has been reported, except for strain Guangzhou B5 (GenBank accession no. AF289029), which was isolated about 20 years ago (8).

Here we report the complete genome sequence of a DENV-4 strain, GZ30, which was isolated from the serum of a 54-year-old female DF patient on 20 October 2010, 3 days after the onset of symptoms. Total RNA was extracted from viral culture in C6/36 cells using the Purelink RNA minikit (Life Technology). Next, cDNA was produced by using Moloney murine leukemia virus (Mo-MLV) reverse transcriptase (TaKaRa, Japan) with a reverse primer, and 13 primer pairs were used to generate overlapping amplicons spanning the entire genome accordingly. The 5' and 3' ends of the viral genome were determined using rapid amplification of cDNA ends. All sequencing was carried out using an ABI 3730 Sanger-based genetic analyzer, and the genome was assembled using DNASTAR version 7.0.

The complete genome sequence of this new isolate, GZ30, is 10,653 nucleotides (nt) in length. The lengths of the 5'- and 3'-untranslated regions are 102 and 387 nt, respectively. Phylogenetic analysis based on the nucleic acid sequence of the complete envelope gene was conducted using the neighbor-joining method. DENV-4 falls into four genotypes, and GZ30 belongs to genotype II together with most Southeast Asian strains (4, 6). However, another Chinese DENV-4 strain, Guangzhou B5, isolated in 1990, belongs to genotype I (8). GZ30 has a close relationship with DENV-4 isolates from

Southeast Asia, including SW38i from Indonesia, SG(EHI)D4/2641Y08 from Singapore, and ThD4_0734_00 from Thailand. The amino acid homologies to these strains are 99.6%, 99.4%, and 99.4%, respectively. This outbreak of DF in Guangzhou 2010 was possibly initiated by the introduction of DENV-4 from Southeast Asia.

Previously, DENV-1, which has circulated in Guangzhou for decades, was the only known DENV serotype in this region (9). The sudden introduction of DENV-4 increased the risk of secondary infection (3), and intensive surveillance and vector control should be warranted in the future. The complete genome sequence of the Chinese DENV-4 strain described here will help us to understand the molecular epidemiology and contribute to disease control of DENV infections in mainland China.

Nucleotide sequence accession number. The complete genome sequence of dengue virus serotype 4 strain GZ30 has been submitted to GenBank under accession no. JQ822247.

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