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GENOME ANNOUNCEMENT

# Complete Genome Sequence of Dengue Virus Serotype 2 Cosmopolitan Genotype Strain in Guangdong, China

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**Here we report the complete genome sequence of a dengue virus serotype 2 (DENV-2) strain, GZ40, isolated in Guangdong, China, in 2010. A phylogenetic analysis classified GZ40 into the Cosmopolitan genotype, while previous Chinese DENV-2 isolates belong to the Asian I genotype. The reemergence of the Cosmopolitan genotype of DENV-2 in China deserves further investigation.**

Dengue has emerged as one of the most important arboviral infections during the last 3 decades and evoked international concern with health security due to its rapid epidemic spread beyond national borders (8). Dengue viruses (DENV) in nature contain four serotypes, and all of them are capable of causing a wide clinical spectrum (3). Laboratory and epidemiological data have indicated that it is DENV-2 that is frequently associated with severe disease accompanying secondary dengue infections (4).

All four serotypes of DNEV infections have been reported in mainland China (1, 2, 9). Of the four serotypes, DENV-1 has been recognized as the predominant serotype circulating in Guangdong Province for the past 3 decades (10). The dengue epidemic caused by DENV-2 was only reported four times (9). During the autumn of 2010, DENV-2 reemerged in Guangdong, China, and several DENV-2 strains were isolated and sequenced. To date, only a few complete genome sequences of the Chinese DENV-2 strain have been ever reported.

In this study, a DENV-2 strain, GZ40, was isolated from the acute-phase serum of a 40-year-old female patient, who was diagnosed with dengue fever on 31 October 2010. Total RNA was extracted using the RNeasy minikit (Qiagen) from infected C6/36 cells. Then cDNA was produced by using Moloney murine leukemia virus (MMLV) reverse transcriptase (TaKaRa, Japan) with a specific 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 identified using rapid amplification of cDNA ends as described previously (11). 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 the newly isolated strain GZ40 is 10,723 nucleotides (nt) in length. The length of the 5′ and 3′ untranslated regions are 96 and 451 nt, respectively. A phylogenetic analysis based on the complete envelope gene was conducted using the neighbor-joining method. DENV-2 strains fall into five genotypes, and GZ40 belongs to the Cosmopolitan genotype together with most Southeast Asian strains (6, 7), including strain SG/07K3608DK1/2008 from Singapore and strain 98900666 from Indonesia. The amino acid homologies to these two strains are 97.6% and 97.2%, respectively. GZ40 is most closely related to ZH1340, which was previously isolated in Guangdong Province in 2007, and the amino acid homology is 97.8%. Our findings implied that these DENV-2 strains were possibly imported from Southeast Asia.

In this decade, DENV-2 was only occasionally reported in China, and the reemergence of DENV-2 in Guangdong Province increases the risk of severe secondary dengue infection (5). Previously, large outbreaks of dengue caused by DENV-2 have been reported in Hainan, China (9), and all these isolates belong to the Asian I genotype. The introduction and circulation of a novel DENV-2 genotype strain in Guangdong deserves further study. Overall, the complete genome sequence of a DENV-2 Cosmopolitan genotype strain described here will help to understand the molecular epidemiology and evolution of DENV-2 in mainland China.

**Nucleotide sequence accession number.** The complete genome sequence of the dengue virus serotype 2 strain GZ40 was submitted in GenBank under the accession number JX470186.

## ACKNOWLEDGMENTS

This work was supported in part by the National Basic Research Program of China (grant 2012CB518904) and the National Natural Science Foundation of China (grants 31270196 and 31270974). C.-F.Q. was supported by the Beijing Nova Program of Science and Technology (grant 2010B041).

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Received 18 September 2012 Accepted 19 September 2012

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doi:10.1128/JVI.02562-12

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