

Complete Genome Sequence of a Chikungunya Virus Isolated in Guangdong, China

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Chikungunya virus belongs to the genus *Alphavirus* in the family *Togaviridae*. Here we report the complete genome sequence of a chikungunya virus strain, GD05/2010, isolated in 2010 from a patient with chikungunya fever in Guangdong, China. The sequence information is important for surveillance of this emerging arboviral infection in China.

Chikungunya virus (CHIKV), a member of the genus *Alphavirus* and the family *Togaviridae*, is the causative agent of chikungunya fever, which is characterized by fever, rash, myalgia, and arthralgia (7). CHIKV is transmitted to humans by infected mosquitoes, and it has emerged and reemerged in Africa, South America, and Southern and Southeastern Asia, with a potential global threat to public health (1–3, 8). No licensed vaccine or antiviral is now available for CHIKV infection.

Although several imported cases of Chikungunya fever have been documented in China (12), no outbreak has ever been reported. However, a sudden chikungunya outbreak with 173 patients was reported in Guangdong, China, in October 2010 (11).

To date, no complete genome sequence of a Chinese CHIKV isolate has ever been reported. Here we report the complete genome of CHIKV strain GD05/2010 isolated from the acute-phase serum from a chikungunya patient in Guangdong, China. The genome RNA of CHIKV was extracted from viral culture in BHK-21 cells, and cDNA was produced by using Moloney murine leukemia virus (M-MLV) reverse transcriptase with a random primer. Sixteen primer pairs were used to generate the amplicons that spanned the entire viral genome. The 5' and 3' terminals of the viral genome were determined using 5' and 3' rapid amplification of cDNA ends (RACE). All sequencing was carried out using an ABI 3730 Sanger-based genetic analyzer, and one contig containing high-quality trace files was assembled using DNASTAR version 7.0.

The genome of CHIKV strain GD05/2010 is a positive single strand of RNA of 11,811 nucleotides (nt), and it contains two open reading frames (ORFs) embedded between the 5' and 3' untranslated regions. The first ORF, of 7,422 nt, encodes the nonstructural polyprotein (consisting of nsP1, 2, 3, and 4), and the second ORF, of 3,744 nt, encodes the structural proteins (consisting of C, E2, E3, and E1). The untranslated junction region between the two ORFs is 65 nt in length.

Three phylogenetically distinct groups of CHIKV with distinct antigenic properties have been identified, namely the Asian genotype, the West African genotype, and the East, Central, and Southern African (ECSA) genotype (1, 5, 6). Genome-scale phylogenetic analysis was performed by using MEGA5.0 with the neighbor-joining method, and the results demonstrated that strain GD05/2010 belonged to the homogeneous Indian Ocean clade of the ECSA genotype. Phylogenetic analysis based on the E1 sequence also supported this conclusion. Sequence analysis of the

E1 gene shows that GD05/2010 has 99.5%, 99.4%, and 97.1% nucleotide identities to SGEHICHS277108 isolated in Singapore (FJ445510), LR2006_OPY1 isolated in Reunion (DQ443544), and the S27-African prototype (AF369024), respectively. Recombination analyses within CHIKV strains were performed with SimPlot software (4), and no obvious recombinant event was observed. Notably, the single-amino-acid mutation (A226V) in the E1 protein that determined infectivity and vector specificity (9, 10) was present in this Chinese strain.

The first outbreak of chikungunya fever in China has aroused wide public concerns. The complete genome of a Chinese CHIKV strain is important for future surveillance and research for this emerging arboviral infection in China.

Nucleotide sequence accession number. The complete genome sequence of CHIKV strain GD05/2010 was submitted to GenBank under accession no. [JX088705](https://www.ncbi.nlm.nih.gov/nuclotide/JX088705).

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