Dengue virus (DENV) is composed of four distinct serotypes (DENV-1 to -4), which belong to the genus Flavivirus in the family Flaviviridae (1). DENV causes a wide range of clinical symptoms in humans, from acute febrile illness dengue fever to life-threatening dengue hemorrhagic fever/dengue shock syndrome (2). Dengue fever is considered a major public health problem in developing tropical countries, where the virus is endemic, and it is continuously spreading to new geographical areas around the world (3, 4). With increasing international travel to tropical regions where dengue is endemic or epidemic, the risk of DENV infection to travelers and expansion of its geographic distribution are continuously escalating (5, 6). The three clinical DENV-1 isolates used in this study were isolated from such imported cases (7). Based on the travel history, DenKor-01, DenKor-02, and DenKor-07 were isolated from travelers who returned from India-Singapore, Indonesia, and the Philippines, respectively.

Using a previously described protocol, the viruses were reverse-transcription PCR (RT-PCR) amplified in five overlapping fragments that covered the complete polyprotein (8). Both sense and antisense strands of each fragment were sequenced at a commercial sequencing facility (GenoTech, Daejeon, South Korea). The 5' and 3' terminal sequences of each viral genome were determined by rapid amplification of cDNA ends (RACE) using the FirstChoice RLM-RACE kit (Ambion, Austin, TX, USA), according to the manufacturer’s instructions. The sequencing results were assembled using CodonCode Aligner version 4.1.1 (CodonCode, Inc., Centerville, MA, USA) and further analyzed using the Geneious 6.1.8 (Biomatters Ltd., Auckland, New Zealand) software.

The complete genome sequences of the DenKor-01 (imported case in 2004), DenKor-02 (2005), and DenKor-07 (2006) isolates from the sera of travelers returning from Southeast Asia were 10,736, 10,735, and 10,734 nucleotides in length, respectively, and consisted of a single open reading frame (ORF), which encodes a 3,392-amino acid polyprotein. The nucleotide sequence identities for the complete genomes, including the 5' and 3' untranslated regions (UTR), ranged from 91.5 to 92.2%, while the amino acid sequence identities ranged from 97.5 to 97.9% among the three clinical isolates. The nucleotide sequence identities consisted of a single open reading frame (ORF), which encodes a 10,736, 10,735, and 10,734 nucleotides in length, respectively, and from the sera of travelers returning from Southeast Asia were case in 2004), DenKor-02 (2005), and DenKor-07 (2006) isolates from travelers who returned from India-Singapore, Indonesia, and the Philippines, respectively.

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Nucleotide sequence accession numbers. The assembled complete genome sequences of DenKor-01, DenKor-02, and DenKor-07 strains are deposited in GenBank under the accession numbers KP406801, KP406802, and KP406803, respectively.

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