Complete Coding Sequence of Zika Virus from a French Polynesia Outbreak in 2013

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Zika virus is an arthropod-borne Flavivirus member of the Spondweni serocomplex, transmitted by Aedes mosquitoes. We report here the complete coding sequence of a Zika virus strain belonging to the Asian lineage, isolated from an infected patient returning from French Polynesia, an epidemic area in 2013/2014.

The virus genome is 10,617 nucleotide-long, including the virus complete open reading frame (ORF) sequence (10,272 nt). The ORF encodes a polyprotein with three structural proteins, capsid (105 amino acids [aa]), premembrane/membrane (187 aa), and envelope (505 aa, including the envelope-154 glycosylation motif previously associated with virulence [3]), and seven nonstructural proteins, NS1 (352 aa), NS2A (217 aa), NS2B (139 aa), NS3 (619 aa), NS4A (127 aa), NS4B (255 aa), and NS5 (904 aa). The cleavage sites are identical to those reported previously. Partial 5′ and 3′ noncoding region (NCR) sequences were obtained (46/107 and 297/428 nt long, respectively, with reference to previous sequences of ZIKV isolates).

Maximum likelihood phylogenetic reconstruction (GTR + G + I model, determined from the data set using the MEGA6 program) indicated that it belonged to the Asian lineage, sharing common ancestorship and ca. 99.9% nt and aa identities with isolates circulating in southern Asia and the Pacific islands in the late 2000s (accession no. JN860885 in Cambodia, 2010, and accession no. EU545988 in Micronesia, 2007). This points to the spread of the Asian lineage, which has been suggested to originate from the introduction of ZIKV in Southeast Asia around 1945 (3, 6).

In silico analysis predicted efficient detection of the FP strain genome by previously published RT-PCR systems, with no mismatch for systems 835-911c (5), 9271-9373 (7), and ZIKVF9027-ZIKVR9197c (8) and one mismatch for systems ZIKVENVF-ZIKVENVR in the reverse primer (residue 16/20) (9) and 1086-1162c in probe ZIKV_1107 (residue 19/31) (5).

Nucleotide sequence accession number. The virus genome sequence described here has been deposited in the GenBank database under the accession no. KJ776791.

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