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Complete coding sequence of Zika virus from Martinique outbreak in 2015

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Abstract

Zika virus is an *Aedes*-borne *Flavivirus* causing fever, arthralgia, myalgia rash, associated with Guillain–Barré syndrome and suspected to induce microcephaly in the fetus. We report here the complete coding sequence of the first characterized Caribbean Zika virus strain, isolated from a patient from Martinique in December, 2015.

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Keywords: *Aedes*, Americas, microcephaly, outbreak, Zika virus

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Zika virus (ZIKAV) (Family *Flaviviridae*, genus *Flavivirus*) is an *Aedes*-borne virus, phylogenetically and antigenically related to Spondweni virus. It is associated to dengue-like symptoms and to Guillain–Barré syndrome [1]. Moreover, a potential link between ZIKAV infection in early pregnancy and fetal microcephaly has been suspected, first in French Polynesia and currently in Brazil [1,2]. (From October 2015 to January 2016, 3500 suspected cases have been detected; the usual rate would be 100 cases per year.)

ZIKAV was first identified in 1947 in rhesus monkeys in Uganda [3]. The first human case was reported in 1952 [3]. Sporadic human infections were reported until a massive outbreak in Yap Island in 2007 [4]. Two main lineages were then defined: the African and the Asian. In 2013, a large ZIKAV outbreak occurred in French Polynesia [5]. Autochthonous cases were then reported in 2013 in French Guyana, in 2014 in New Caledonia and since 2015 on the South American continent [6]. As of January 2016, 26 countries in the Americas have reported ZIKAV cases [1].

In December 2015, a 54-year-old woman was hospitalized in Martinique with mild presentation, fever, rash, conjunctival

injection, arthralgia, oedema and proteinuria. ZIKAV infection was detected using specific real-time RT-PCR (French Reference Center for Arboviruses). ZIKAV strain MRS_OPY_Martinique_PaRi_2015 was isolated after cytopathic effect (passage 1, day 3) on Vero cells (ATCC-CCL 81) from the patient's serum (available from the global European Virus Archive—<http://global.european-virus-archive.com/>). Viral RNA was subsequently extracted from the primary culture supernatant, amplified with specific and random primers and sequenced using New Generation Sequencing (Ion Torrent, Life Technologies; CLC Genomics Workbench software, CLC Bio). A 10 617-nucleotide (nt) consensus sequence including the complete open reading frame (10 272 nt) was obtained from 455 095 reads. Partial 5' and 3' non coding region sequences were obtained (47/107 and 298/428 nt long, respectively, with reference to published sequences of ZIKAV).

The open reading frame encodes a polyprotein with three structural proteins, capsid (105 amino acids (aa)), pre-membrane/membrane (187 aa), and envelope (505 aa), and seven non-structural 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 [1].

Maximum likelihood phylogenetic reconstruction (GTR+G+I model, determined from the data set using the MEGA6 program)

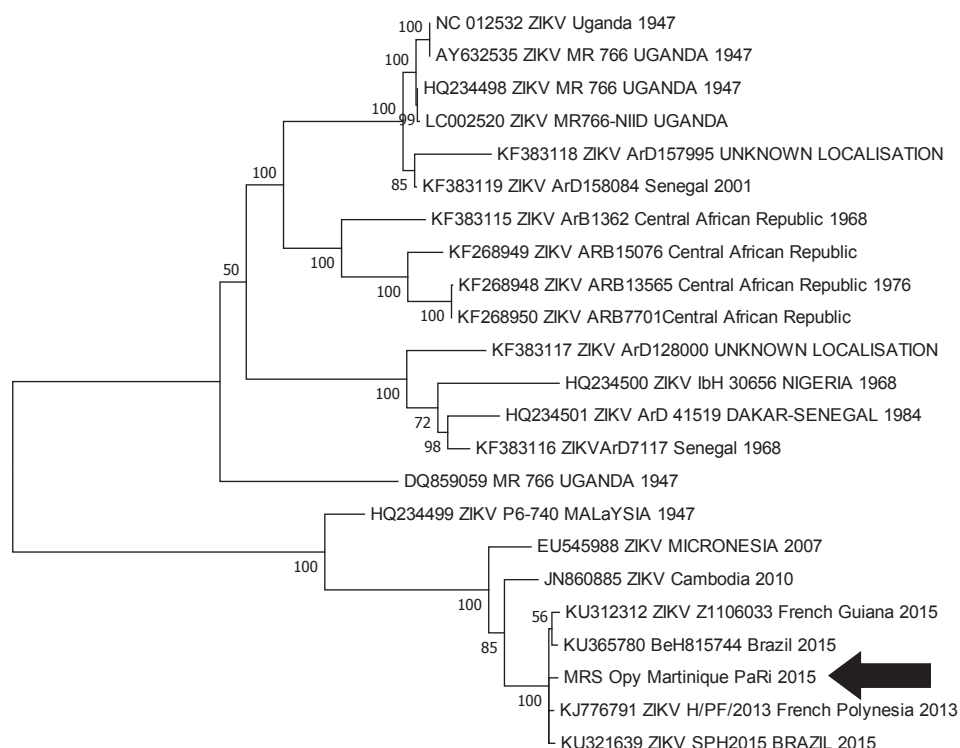


FIG. 1. Phylogenetic tree constructed from nucleic acid data from Zika virus coding sequences by maximum likelihood algorithm in MEGA.

indicates that it belongs to the Asian lineage (Fig. 1), sharing common ancestorship and c.99.9% nucleotide and amino acid identities with isolates circulating previously in French Polynesia and currently in South America (accession no. KJ776791 in French Polynesia, 2013, and accession no. KU321639 in Brazil, 2015). The membrane gene is the most divergent with reference to the French Polynesia 2013 and Brazil 2015 isolates.

In silico analysis predicted efficient detection of the Martinique strain genome by previously published RT-PCR systems, with no mismatch for systems 835-911c [7] 9271-9373 [8], ZIKVF9027-ZIKVR9197c [9] and ZIK-VENVF-ZIKVENVR [10] and one mismatch for 1086-1162c in probe ZIKV_1107 (residue 19/31) [7].

Nucleotide Sequence Accession Number

The virus genome sequence described here has been deposited in the GenBank database under the accession no KU647676.

Conflict of interest

None declared.

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