

Complete Genome Sequence of a Dengue Virus Serotype 4 Strain Isolated in Roraima, Brazil

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Dengue is the most important arboviral disease worldwide. We report the complete genome sequence of a dengue virus serotype 4, genotype II strain isolated in 2010 from a patient with classical dengue fever in Boa Vista, Roraima, Brazil.

Dengue virus (DENV) infections are the most important cause of arthropod-borne viral diseases worldwide (7). DENVs are single-stranded RNA viruses which belong to the *Flavivirus* genus of the *Flaviviridae* family; four immunologically related types, also known as serotypes, are recognized (DENV-1 to DENV-4) (5). Phylogenetic analyses have shown that each serotype may be further separated into different genotypes, and four DENV-4 genotypes have been described (13).

DENV-4 and DENV-1 were first recorded in Brazil during an outbreak in 1981 and 1982 in Boa Vista, the capital of Roraima State (11). Unlike the other serotypes, DENV-4 was not detected again in Brazil until 2008, when it was reported in autochthonous cases occurring in Manaus, the capital of Amazonas State (3). In 2010, DENV-4 reemerged in Roraima (1), this time spreading to several Brazilian states. To date, no complete Brazilian DENV-4 genome sequence has been reported, although this is an important issue that can contribute to our understanding of DENV-4 epidemiology.

Here we report the complete genome sequencing of a DENV-4 strain, Br246RR/10, which was isolated from a male patient presenting with classical dengue fever in Boa Vista, Roraima, Brazil, on 8 September 2010, 4 days after the onset of symptoms. His serum was NS1 enzyme-linked immunosorbent assay (Bio-Rad) positive and was therefore inoculated onto *Aedes albopictus* C6/36 monolayers for an indirect immunofluorescence assay for viral typing (8). Cell supernatants were used for a seminested reverse transcription-PCR protocol (9) to confirm the DENV-4 serotype. A second reverse transcription reaction was conducted using a reverse primer, D4AS1, which was designed to recognize the last 21 nucleotides (nt) in the 3' region common to all DENV-4 genotypes. DENV-4 strain Br246RR/10 was further amplified using eight primer pairs to generate overlapping amplicons spanning the entire viral genome. All sequencing was carried out using an ABI 3130 Sanger-based genetic analyzer (primer sequences are available upon request). One contig containing high-quality trace files was assembled using Geneious Pro 5.5.3 (2) and a single reference sequence (GenBank accession no. NC_002640).

The complete genome sequence of Br246RR/10 is 10,649 nt long, with a 5' untranslated region (UTR) of 101 nt, followed by a polyprotein precursor coding sequence of 10,164 nt and a 3' UTR of 384 nt. A full-genome MegaBLAST search with Br246RR/10 returned Colombian (2005) and Venezuelan (2007) DENV-4 strains as the closest matches. A phylogenetic analysis based on the 1,485-nt region (positions 939 to 2423), which encodes the envelope protein, was conducted using the maximum-likelihood

method with the PhyML (6) plugin for Geneious and nucleotide sequences encompassing the four known DENV-4 genotypes (13). Results showed that strain Br246RR/10 is a representative of DENV-4 genotype II, which has a well-known history of circulation in the Caribbean and South America (4, 10, 12, 14).

The data described here, presenting the first complete genome sequence of a DENV-4 strain isolated in Brazil, will contribute to further studies focusing on the molecular evolution of emerging DENV strains.

Nucleotide sequence accession number. The complete genome sequence of DENV-4 strain Br264RR/10 is available in GenBank under accession number [JN983813](https://www.ncbi.nlm.nih.gov/nuccore/JN983813).

ACKNOWLEDGMENTS

This work was supported by grants from POM-Fiocruz and PRONEX Rede Dengue (CNPq 550120/2010-6). V.C.S. and G.A.V.S. received fellowship support from the Fundação de Amparo à Pesquisa do Estado do Amazonas (FAPEAM) and the PPSUS program, and T.S. had a CNPq fellowship.

We are grateful to Lee Crainey of the London School of Hygiene & Tropical Medicine and Fernando Abad-Franch of the Instituto Leônidas e Maria Deane for help editing the manuscript.

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Received 4 November 2011 Accepted 7 November 2011

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doi:10.1128/JVI.06731-11

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