

Dengue virus type 1 from field-caught vectors and humans in Brazil: Phylogeny reveals different lineages of the American African genotype in 25 years

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Dengue viruses (DENV) replicate alternately on the mosquito vector (mainly *Aedes aegypti*) and human host. In Brazil, dengue became a major public health problem after DENV-1 introduction in 1986 in Rio de Janeiro and in 2009, this serotype re-emerged causing major epidemics in the country. Since then, a virological and entomological program was established for monitoring DENV in human sera and vectors and it has constituted an important tool for dengue epidemiology and vector-virus-host interactions studies. DENV-1 was identified by virus isolation and RT-PCR during the 1986, 2001 and 2010 entomological surveillances performed in Rio de Janeiro (RJ) and Roraima (RR) and the Real Time qRT-PCR detected 1.6x10⁴ copies/mL of DENV-1 in the macerate of a single *Ae. aegypti* female naturally infected. The phylogeny demonstrated that DENV-1 isolated from both field-caught vector and humans belong to genotype V (Americas/Africa), although the co-circulation of two distinct lineages (lineages II and III) was detected. The use of molecular techniques combined to virus isolation showed to be important approaches for the surveillance and molecular characterization studies of DENV from field-caught vectors. The molecular characterization showed sequence differences lineage-specific, independently in which host the virus was isolated. Moreover, we also determined the viral titer in a single *Ae. aegypti* female naturally infected.

Biography

Marcia de Castro is a PhD researcher on the Transmissores de Hematozoários Laboratory, a reference laboratory for dengue entomological surveillance, for the Brazilian Ministry of Health. Her expertise areas comprises Parasitology, focusing on the entomology and malacology of parasites and vectors, mainly on mosquitoes and dengue viruses surveillance by using molecular biology techniques.

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