## MOLECULAR EPIDEMIOLOGY OF DENGUE VIRUSES IN NORTHERN BRAZIL

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Currently, dengue is the most important arboviral disease that affects humans. Dengue virus (DENV) is transmitted to humans by the Aedes aegypti mosquitoes. The spectrum of dengue infections range from asymptomatic to severe disease. Two major clinical pictures are described, dengue fever (DF) and dengue hemorrhagic fevers (DHF)/dengue shock syndrome (DHF/DSS). Epidemiological information associated to phylogenetic studies has indicated that some DENV strains are more virulent than other. DENV comprises four distinct serotypes (DENV-1,2,3, and 4), and according to the World Health Organization, at least 2.5 billion people live in over 100 countries where dengue viruses have been transmitted. Up to 50 million infections occur annually with 500 000 cases of dengue haemorrhagic fever and 25,000 deaths mainly among children. Phylogenetic and molecular analyses have demonstrated a considerable genetic variability among DENV serotypes, which leads to the recognition of different genotypes within each serotype, namely: for DEV-1 and DENV-2, four genotypes have been described, while for serotypes 3 and 4, four and two genotypes have been assigned, respectively. In Brazil, currently three (DENV-1, 2 and 3) dengue serotypes have been found co-circulating all over the country, and the DENV-3 is responsible for the majority of the cases in Brazil since it introduction in 2000. However, in 2008 the serotype 2 has been associated with severe dengue (DHF/DSS) cases in Northern and Northeast Brazil. This work will provide a better understanding regarding the molecular epidemiology and evolutionary aspects of the three dengue serotypes associated with dengue disease and its distinct clinical manifestations in northern Brazil.

Key words: dengue virus, molecular epidemiology, evolution