ASSOCIATION OF DENGUE SEROTYPE VARIANTS WITH DIFFERENT DENGUE CLINICAL FORMS

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Although the four serotypes of the dengue virus may cause hemorrhagic fever (DHF) in dengue primary infection, some serotypes seems to be associated with severe forms of the illness in different geographic area. In this work, 14 isolates of dengue serotype 3 were obtained from patients attended at emergency of private hospitals in Recife during 2003-2004. Four patients had DHF and 10 had classic dengue (CD), albeit five of them had showed low platelets counts. The 5'-end viral genomes were sequenced and the nucleotides and amino acids corresponding sequences were compared with published data and between them to calculate the degree of similarity and generate dendrograms. Capside and membrane sequences showed high degree of similarity therefore, it was not possible to use for clustering. The analysis of the 5'-end of envelope gene generated three clusters: one, with three of four isolates from patient with DHF; other with one isolate from patient with DHF plus two from patients with CD associated with low platelets counts and third one, with seven isolates from patients with CD, being three associated with low platelets count. This preliminary data suggests that the clinical presentation of the illness can be related to the variability of the viral genome.

Keywords : Dengue, DHF, Envelope gene.