FA057

PROFILE OF NUCLEOTIDE SUBSTITUTION FOR PATHOGENICITY DIAGNOSIS OF DENGUE VIRUS (DENV)

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Introduction: Dengue (DENV) is a disease which is potentially fatal and whose fast dissemination drew the attention of Brazilian public authorities in the 90th decade. The simultaneous presence of two or more dengue serotypes in the same area raises the risk of disease complication such as hemorrhagic fever (DHF) because of immunity system abuse. It is, therefore, essential to understand how the viral polymorphism may influence pathogenicity. Large sequence repository is now available in electronic database and we investigated the nucleotide substitution rate throughout the whole 11 kb viral sequence. **Objective:** Design diagnostic tools using PCR to investigate the pathogenicity dynamic of Dengue in the region of Bahia. **Materials and Methods:** We retrieve 2700 homologous DNA sequences from GenBank by homology search (BLASTN) with DENV-1. The homologous regions were aligned with the whole sequence of DENV-1 with CLUSTAL in order to identify the viral regions that are most documented. The relative nucleotide substitution rate per base was measured using a Perl script and plotted along the DENV-1 DNA sequence. **Results:** We found that nucleotide substitution in the region of 3700-4000 bp was significantly higher than in other regions, especially than the regions of 0-200 and 10600-10700 bp. **Conclusion:** Because of their higher substitution rate, we assume region of 3700-4000 bp to be suitable for pathogenicity investigation because of their higher rate of evolution. More conserved regions such as 0-200 and 10600-10700 bp will be used for serotypes identification. PCR primers are being designed around these regions for this purpose.