

BIO070

Molecular analysis of Dengue Virus Type 1 isolates in Ribeirão Preto in 2011

Adriana Moreira Soares^{1*}; Alberto Anastacio Amarilla¹; Victor Hugo Aquino¹.

¹Departamento de Análises Clínicas, Toxicológicas e Bromatológicas, Faculdade de Ciências Farmacêuticas de Ribeirão Preto, Universidade de São Paulo, São Paulo, Brazil; E-mail: *dri.msoares@gmail.com

Introduction: Dengue is the most important mosquito-borne viral disease worldwide. Dengue virus (DENV) is a member of the genus Flavivirus and family Flaviviridae. DENV include four antigenically related viruses named dengue virus type 1 to 4 (DENV 1-4). Each of the four serotypes is able to cause disease with a full spectrum of clinical manifestation. DENV-1 is composed of five genotypes: genotype I is represented by viruses of Taiwan and Thailand; genotype II is represented by viruses of Thailand; genotype III is represented by strains of Malaysia; genotype IV is represented by viruses of Southeast Asia, South Pacific and Australia and genotype V is represented by viruses of America, Africa and Southeast Asia. Considering that Ribeirão Preto is an endemic city for this disease, it is of great importance to monitor the circulating viruses, which would allow the identification of new serotypes or subtypes that could be related to most severe cases of the disease. Phylogenetic analysis also allows a better assessment of the pattern of migration and evolution of these viruses. **Objective**: The objective of this study was to study the molecular epidemiology of DENV-1 in Ribeirão Preto in 2011. Methods: In this study, four dengue viruses isolated in Ribeirão Preto in 2011 using C6/36 cells were analyzed. The isolations were confirmed by realtime RT-PCR and by indirect immunofluorescence using monoclonal antibody. The partial gene sequence of the nonstructural protein 5 (NS5) was amplified by RT-PCR, purified and sequenced. Sequences were analyzed and aligned with the BioEdit and the MEGA 5.05 software. Based on the alignment, a phylogenetic tree was constructed using the Neighbor-joining method. **Results**: The phylogenetic analysis showed that DENV-1 isolated in Ribeirão Preto correspond to genotype V of DENV-1. Conclusion: They are closely related to other Brazilian DENV-1 isolates.

Keywords: Dengue, Molecular epidemiology, phylogeny.

Financial support: FAPESP