Different hematological profiles associated to co-circulating dengue serotypes 1 and 3 in a medium-sized city of São Paulo, Brazil

Andréia M. S. Carmo1,2, Rodrigo B. Suzuki1,3, Aline D. Cabral1, Renata T. Costa1, Gabriela P. Massari1, Michele M. Riquena1, Hélio A. Fracasso1, André Eterovic4, Arlei Marcili5, Mârcia A. Sperança1

1Federal University of ABC, Center for Natural and Human Sciences, São Bernardo do Campo, 09606-070, São Paulo, Brazil; 2Adolfo Lutz Institute, Regional Laboratory Center VIII, Santo André, 09040-160, São Paulo, Brazil; 3Department of Genotyping, Blood Center, Marília Medical School, 17519-030, São Paulo, Brazil; 4Federal University of ABC, Center for Natural and Human Sciences, Santo André, 09210-580, São Paulo, Brazil; 5Department of Preventive Veterinary Medicine and Animal Health, Faculty of Veterinary Medicine, University of São Paulo, 05508-900, São Paulo, Brazil.

Dengue virus, represented by four distinct serotypes, genetically diverse, is the most prevalent arbovirus in the world and is the etiologic agent of asymptomatic to severe hemorrhagic diseases. Spatiotemporal dynamics of Dengue serotypes/genotypes and its association to specific diseases vary among different regions worldwide. In 2007, Dengue cases concentration in urban centers has been changed to increased incidence in small and medium-sized cities in the Brazilian State of São Paulo, as in Marilia, where occurred the first important outbreak. This study aimed to determine the genetic characteristics of DENV circulating serotypes/genotypes during the outbreak of 2007 in Marilia, São Paulo, its phylogenetic reconstruction and association to demographic and hematological patient profiles. From plasma samples of Marilia Dengue serological positive patients, total RNA was extracted and PCR diagnosis was performed by amplification of the junction of the capsid and pre-membrane encoding genes. Molecular typing confirmed co-circulation of Dengue from serotypes 1 and 3 which presented divergent correlation with regard to leucopenia and low platelets counts. With the increase in atypical lymphocytes, leukocytes decreased significantly further in Dengue serotype 3 group and platelets counts were lower in Dengue serotype 1 patients. Phylogenetic reconstitution revealed introduction of Dengue serotype 1 from North region of Brazil and local divergence of Dengue serotype 3 by microevolution. Regional studies of spatiotemporal dynamics of Dengue virus are important for the introduction of vaccines and for disease management and transmission control.

Keywords: dengue; molecular epidemiology; genotype sequence analysis

Support: PRONEX/Dengue, CNPq, Grant number 550106/2010-3 and Federal University of ABC