

Abstract

The purpose of the current study was to determine the origin of dengue infection and to study its evolutionary relation. Therefore, 312 suspected patients of dengue hemorrhagic fever admitted in Benazir Bhutto hospital, and Holy Family hospital from Rawalpindi and Islamabad were included in the study. The demographic data was collected on a performa sheet. The screening of patients was done by blood analysis of blood cell count and serological testing. Reverse transcriptase polymerase chain reaction (RT-PCR) was done followed by sequencing and evolutionary relation study. Dengue fever was confirmed in 66% of the patients by RT-PCR while 34.9% were positive for immunoglobulin G (IgG), 35.9% for immunoglobulin M (IgM), and 91% patient were non-structural protein 1 (NS1) positive. The highest positive rate was found in young males aged 17-30 years. Fever, abdominal pain and retroorbital pain were the common symptoms found in 100% of the patients. In blood cell analysis thrombocytopenia was seen in 98.1% of the patients, Leucopenia in 82.3% of the patients, and hemoconcentration in 98.4% of the patients. Molecular characterization showed the predominant serotype was dengue virus type 2 (DENV-2) (92.7%). From the phylogenetics it was concluded that the causative agent of this epidemic was closely related to those that caused outbreaks in India, and Sri Lanka.