› PeerJ. 2017 Mar 14;5:e2970. doi: 10.7717/peerj.2970. eCollection 2017.

Occurrence of concurrent infections with multiple serotypes of dengue viruses during 2013–2015 in northern Kerala, India

Manchala Nageswar Reddy [1], Ranjeet Dungdung [1], Lathika Valliyott [1], Rajendra Pilankatta [1]

Affiliations + expand

PMID: 28316881 PMCID: PMC5354076 DOI: 10.7717/peerj.2970

Abstract

Background: Dengue is a global human public health threat, causing severe morbidity and mortality. The occurrence of sequential infection by more than one serotype of dengue virus (DENV) is a major contributing factor for the induction of Dengue Hemorrhagic Fever (DHF) and Dengue Shock Syndrome (DSS), two major medical conditions caused by DENV infection. However, there is no specific drug or vaccine available against dengue infection. There are reports indicating the increased incidence of concurrent infection of dengue in several tropical and subtropical regions. Recently, increasing number of DHF and DSS cases were reported in India indicating potential enhancement of concurrent DENV infections. Therefore, accurate determination of the occurrence of DENV serotype co-infections needs to be conducted in various DENV prone parts of India. In this context, the present study was conducted to analyse the magnitude of concurrent infection in northern Kerala, a southwest state of India, during three consecutive years from 2013 to 2015.

Methods: A total of 120 serum samples were collected from the suspected dengue patients. The serum samples were diagnosed for the presence of dengue NS1 antigen followed by the isolation of dengue genome from NS1 positive samples. The isolated dengue genome was further subjected to RTPCR based molecular serotyping. The phylogenetic tree was constructed based on the sequence of PCR amplified products.

Results: Out of the total number of samples collected, 100 samples were positive for dengue specific antigen (NS1) and 26 of them contained the dengue genome. The RTPCR based molecular serotyping of the dengue genome revealed the presence of all four serotypes with different combinations. However, serotypes 1 and 3 were predominant combinations of concurrent infection. Interestingly, there were two samples with all four serotypes concurrently infected in 2013.

Discussion: All samples containing dengue genome showed the presence of more than one serotype, indicating 100% concurrent infection. However, the combination of serotypes 1 and 3 was predominant. To the best of our knowledge, this is the first report indicating the concurrent infection of dengue in the northern Kerala, India. The phylogenetic analysis of dengue serotype 1 identified in this study shows a close relationship with the strain isolated in Delhi and South Korea during the 2006 and 2015 epidemics respectively. Similarly this study indicates that the phylogeny of dengue serotype 3 of northern Kerala is more closely related to dengue isolate of Rajasthan state, India. The geographical and climatic conditions of Kerala favours the breeding of both the mosquito vectors of dengue (*Aedes albopictus* and *Aedes aegypti*), which may enhance the severity of dengue in the future. Therefore, the study provides an alarming message for the urgent need of an antiviral strategy or other health management systems to curb the spread of dengue infection.

Keywords: Concurrent; CprM; Dengue; Epidemic; Mutation; NS1 antigen; Phylogeny; RNA; RT-PCR; Virus.