

Molecular epidemiology of dengue / dengue haemorrhagic fever in the northern part of Sri Lanka

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Introduction and objective

There was limited access to the northern part of Sri Lanka due to the war until mid 2009. This is the first study to describe the molecular epidemiology of circulating DENV serotypes and their association to DHF in the North using RT-PCR and next generation sequencing (NGS) of DENV-1.

Design, setting and methods

A total of 765 patients from the Teaching Hospital, Jaffna from 2009 to 2012 with clinically suspected DF/DHF were investigated. Identification and typing of DENV were carried out using a combination of RT-PCR and a single-tube multiplex PCR. Primers by Lanciotti et al were used to detect the C and PrM genes of the DENV and one of the DENV-1, cDNA samples was subjected to NGS. Phylogenetic trees were constructed for DENV-1 full genome using previously reported method.

Results

Of the 765 patients, 205 were positive for DENV by RT-PCR. Of these 205 patients, 64 were from 2009/2010 and the rest were from 2011/2012 outbreak. DENV-1, DENV-2, DENV-3 and DENV-4 were found in 12 (18.7%), 19 (29.6%), 25 (39%) and 1 (1.5%) patients, respectively in 2009/2010 with 7 patients having (10.9%) co-infection with DENV-2 and DENV-3. In contrast, in the 2011/2012 outbreak, DENV-1 was the dominant serotype (55.3%) and DENV-4 was not detected in any patients. In 2009/2010 outbreak, 86% of the DHF was caused by DENV-3

and DENV-2. However, in 2011/2012, more than one third of the DHF cases were by DENV-1. When one of the DENV-1 samples was subjected to NGS, high quality, consensus sequence of DENV-1 was identified and the whole genome sequence has been deposited in the NCBI Gen Bank (Acc No: KP398852). Our phylogeographic data showed that Sri Lankan DENV-1 isolate form a monophyletic group indicating a common ancestry.

Conclusions

The present study showed a shift in the transmission of DENV serotypes. Our phylogeographic analysis indicates that 2011/2012 DF/DHF outbreak in the North most likely originated from a minor variant of a DENV-1 strain that has been circulating in Sri Lanka.