

## OP 6

### Co-infections with multiple dengue virus serotypes in patients from 3 different Provinces of Sri Lanka

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#### Introduction

The circulation of multiple dengue viral (DENV) serotypes in a same locale has caused co-infections with mixed serotypes in individuals due to subsequent or simultaneous infections.

#### Objective

The objective of the present investigation was to study the clinical presentations together with reverse transcription PCR (RT-PCR) and serology of co-infections to identify pattern of disease severity in co-infected patients from 3 different Provinces of Sri Lanka.

#### Design, setting and methods

Clinically diagnosed dengue fever (DF)/ dengue haemorrhagic fever (DHF) patients from Teaching Hospitals, Jaffna and Kandy and General Hospitals, Gampaha and Negambo with fever days less than 5 were included in the study. Clinical and hematological data were also assessed. DENV capsid gene detection was performed followed by DENV sero-typing by a series of RT-PCR. Anti-DENV IgM/IgG detection was performed using ELISA.

#### Results

Of the 1249 patients, RT-PCR was positive in 329 from 2009 to 2012. Of the 329 RT-PCR positive patients, 34/329 (10.33%) had co-infections with two or more DENV serotypes. All 4 DENV serotypes were found to be co-circulating during the study period and DENV-1 was the predominant type circulated in all 3 Provinces. Highest number of co-infection (17/34) occurred with DENV-1 and DENV-2. Of the 34 co-infected patients, 24 had DF and the rest had DHF. Sixteen primary and 28 secondary infections were identified in the study cohort. Of the 16 primary infections, 12 were DF and 4 were DHF. Of the 28 secondary infections, 22 were DF and 6 were DHF. No significant difference was noted between the total white blood cell count and platelet counts in mono- and co-infections.

#### Conclusions

In this population DENV-1 was the dominant serotype followed by DENV-2. Presence of DENV co-infections in all 3 Provinces indicates the hyperendemicity of DENV in the country. The absence of significant association of disease severity between the mono- and co-infections points out the progression of the disease into severe forms driven by non-viral factors. The presence of DENV co-infections may lead to recombination of genetic components contributing to the emergence of new DENV strains that might be more virulent and aggressive in causing severe dengue.

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