Co-infections with multiple dengue virus serotypes in patients from 3 different Provinces of Sri Lanka, a dengue hyper endemic country

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Background: The circulation of multiple dengue viral (DENV) serotypes in a same locale has caused people to get infected with mixed DENV serotypes in subsequent or simultaneous infections. The objective was to study the clinical presentations together with reverse transcriptase PCR (RT-PCR) and serology of co-infections to identify pattern of disease severity among co-infections in patients from 3 different provinces of Sri Lanka.

Methods & Materials: 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. Clinical and haematological data were assessed. DENV capsid gene detection was performed by RT-PCR followed by DENV sero-typing. DENV IgM/IgG detection were performed using ELISA.

Results: Out of the 1249 RT-PCR performed on patients during 2009-2012, 329 were RT-PCR positive and of which 34/329 (10.33%) patients had DENV co-infections with two or more serotypes. In these three Provinces all 4 DENV serotypes were found to be co-circulating during 2009-2012 and DENV-1 was the predominant serotype circulated in all 3 provinces. Highest number of co-infection (17/34) was DENV-1 with DENV-2. Of 34 co-infected patients, 24 were diagnosed as DF and the rest were DHF (n=10). There were 16 primary and 18 secondary DENV infections. Out of the primary DENV infections 12/16 were DF and the rest 4/16 were DHF. In the secondary DENV infections 22/28 were DF and 6/28 were DHF. No significant difference was noted between the total white blood cell count and platelet counts in monotypic and co-infections with multiple DENV serotypes.

Conclusion: In this population DENV-1 was the dominant DENV serotype followed by DENV-2. Presence of DENV co-infections in all 3 provinces indicates the hyperendemicity of DENV throughout the country. The absence of significant association of disease severity between the monotypic and co-infections with multiple DENV serotypes point out the progression of the disease into severe forms driven by factors other than viral factors. The presence of DENV co-infections may also 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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