

Circulating Dengue Strains During the Covid 19 Pandemic in the Western Province of Sri Lanka

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Dengue has been considered endemic to Sri Lanka since 1989 with regular dengue epidemics. We sought to identify the dengue strains and the circulating serotypes from July 2019 to December 2021. 299 consenting patients presenting with febrile illness were recruited from the medical wards at Colombo North Teaching Hospital (CNTH), National Institute for Infectious Diseases (NIID), and University Hospital- Kotelawala Defence University (UH-KDU) of the western province. All samples were tested by Reverse transcriptase-polymerase chain reactions (RT-PCR) and/or real-time-PCR tests to determine dengue positivity and serotype. Sequencing (NGS) was carried out on samples with adequate viral load ($Ct \leq 22$) followed by phylogenetic analysis using the Geneious software. The testing showed that 51% were positive for the dengue virus. The serotyping showed that 12% of the positives were DENV-1, 45% DENV-2, 40% DENV-3, and 3% DENV-4 respectively. Phylogenetic analysis of sequenced samples showed two genotypically distinct variants of the DENV-3 as well as DENV-1. One DENV-3 variant was similar to those reported in 2017/18 in Sri Lanka while the other was similar to the one reported in India, in 2016/18. One DENV-1 variant was similar to the 2018 strain found in Sri Lanka while the other was similar to the variant reported in China in 2014/16. Phylogenetic analysis of DENV-2 sequences showed one cluster of a similar genotype reported in 2017/18. DENV4 is yet to be sequenced. Our data suggest that during the study period multiple strains have been circulating in the western province even though no serious epidemic was reported.

Keywords: dengue, serotypes, phylogenetic, DENV-1, DENV-2, DENV-3