OP 10

GENOMIC INSIGHTS INTO DENGUE VIRUS CIRCULATION IN NORTHERN SRI LANKA

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Introduction and Objectives
Dengue is a major public health challenge in Sri Lanka. However, molecular surveillance data from Northern Sri Lanka remain limited. Owing to its proximity to South India, Jaffna may play an important role in regional dengue virus (DENV) transmission. This study aimed to characterise circulating DENV strains in Jaffna and investigate regional transmission patterns.

Methods
Acute-phase blood samples were collected from 216 clinically suspected dengue patients attending Teaching Hospital Jaffna during January–February 2024. Viral RNA was extracted and screened using serotype-specific qPCR. VirCap sequencing was performed on selected samples, and sequence data were analysed using Rapid Identification of Microbes (RIM) workflows. Phylogenetic and mutational analyses used globally representative DENV-3 genome datasets.

Results
DENV infection was confirmed in 49/216 (22.7%) patients. DENV-3, 29/49 (59.2%), was the predominant serotype, followed by DENV-2, 20/49 (40.8%). Seven Jaffna DENV-3 genomes were successfully sequenced. Phylogenetic analysis showed that Jaffna and Colombo viruses belonged to Genotype III lineage B.3, with complete intermixing and no geographic separation. Sri Lankan B.3 sequences clustered most closely with 2022 Indian sequences, suggesting regional viral connectivity. Conserved envelope substitutions (E_V158I, E_I380T, E_A219T, E_E404A) were shared across B.3 viruses, while NS1_K341R and NS1_L217F were present in Sri Lankan but absent from Indian B.3 sequences.

Conclusions
These findings provide a short-term snapshot of DENV circulation in Northern Sri Lanka and support Jaffna's potential value as a sentinel site for regional dengue surveillance. Longer-term genomic monitoring is needed to support outbreak preparedness and cross-border dengue control.