OP 8

COMPREHENSIVE METAGENOMIC PROFILING OF VIRAL AETIOLOGIES IN FEBRILE PATIENTS FROM SRI LANKA

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Introduction and objectives

Sri Lanka carries a significant burden of febrile illness, with dengue a major public health challenge whose endemic nature often masks other viral causes, leading to underdiagnosis. This study used viral metagenomic sequencing to identify vertebrate viruses in blood from febrile patients in Sri Lanka's Northern and Western Provinces.

Methods

Between December 2022 and August 2024, 90 blood samples were collected at the National

Institute of Infectious Diseases and Jaffna Teaching Hospital from patients with clinically suspected dengue presenting within four days of symptom onset and negative for dengue virus by CDC serotype-specific qPCR. Samples underwent virome capture sequencing on the Illumina NextSeq 2000 platform and were analysed using the Rapid Identification of Microbes tool, with consensus sequences generated by MAFFT (v7).

Results

Metagenomic analysis revealed diverse pathogenic, potentially pathogenic, and opportunistic viruses. Pathogenic viruses included *Orthoflavivirus denguei* (39; 43.33%) and a SARS-related coronavirus (1; 1.11%). Potentially pathogenic viruses included *Orthopicobirnavirus hominis* (57; 63.33%), *Gemycircularvirus* sp. (20; 22.22%), and SEN virus (15; 16.67%). Opportunistic viruses included Torque teno virus (28; 31.11%), *Lymphocryptovirus humangamma4* (8; 8.89%), and *Anelloviridae* sp. (18; 20.00%).

Conclusions

These findings underscore the sensitivity of metagenomic sequencing, which detected dengue virus in samples negative by CDC qPCR. The diverse emerging and opportunistic viruses identified demonstrate the complexity of viral aetiologies underlying febrile illness in tropical settings. Frequent detection of opportunistic viruses such as Torque teno virus and *Lymphocryptovirus* suggests a potential contribution to disease severity, emphasising the need for integrated diagnostic strategies in similar settings.