

Molecular Characterization and Phylogenetic Relationship of SARS-CoV-2 Strains Infecting a NAVY Cohort during the First Wave of the COVID-19 in Sri Lanka

HS Jayasinghearachchi^{1#}, DS Govindapala², WMID Nakkawita², PH Premaratne², CL Goonasekara², DGP Kawyangana³ KWT Chathuranga³, US Kulasekara³ and AD De Silva^{2#}

¹*Instititue for Combinatorial Advance Research and Education, General Sir John Kotelawala Defence University*

²*Faculty of Medicine, General Sir John Kotelawala Defence University*

³*BML 2, Faculty of Medicine, General Sir John Kotelawala Defence University*

^{1#}jayasinghearachchihs@kdu.ac.lk, ^{2#}dharshan_fom@kdu.ac.lk

This study was based on the first 26 asymptomatic and minimally symptomatic patients from a NAVY cluster of 936, who were diagnosed with COVID-19 by real time-PCR (RT-PCR) during the first wave in Sri Lanka. The aim of this study is to determine genomic variations, mutations, and phylogenetic relationships of SARS CoV-2 strains identified from this group to those circulated locally and globally during the first wave. Ten SARS CoV-2 positive samples with high viral load (CT \leq 22) were subjected to whole-genome sequencing. Comparative genome analysis, real-time mutation tracking, and phylogenetic analysis were performed. Nine SARS CoV-2 strains belonged to Pangolin B.1.3 lineage while strain 141 belonged to lineage B.1. All the ten genomes contained linkage of missense variants nsp3:Q57H, nsp2:T85I, nsp12:P323L concurrently with dominant spike D614G mutation. This is the first study to report on the SARS CoV-2 strains with these amino acid changes circulating in Sri Lanka during April 2020. Based on the phylogenetic analysis, all ten SARS-CoV-2 strains formed a distinct clade within the main clade strains reported from the USA lineage B.1.3 and the parent lineage B.1 in the USA during early March-2020 and strains isolated in Sri Lanka during July-2020. High genetic similarity among genomes indicates the single source of transmission within the study population. Detection of strains with the linkage of missense variants nsp3:Q57H, nsp2:T85I, nsp12:P323L concurrently with dominant S:D614G mutation, phylogenetic clustering suggests different routes of transmission of SARS CoV-2 which might be linked to the importation of strains from the USA probably through travellers.

Keywords: SARS COV-2, molecular characterization, phylogenetic analysis, Navy cohort, first wave in Sri Lanka