

Sequencing of SARS-CoV2 virus strains in Sri Lanka

With the emergence of several new variants, which are associated with rapid spread, infection in younger individuals, more severe disease and evasion of vaccine induced immunity, sequencing the SARS-CoV2 viruses in Sri Lanka is crucial. While the new variants which have the mutations H69-, N501, are associated with over 50% transmissibility, the viruses that carry the mutation E484K are able to evade vaccine associated immunity. Therefore, in order to understand the transmission dynamics, implications in vaccine efficacy and possible potential of causing re-infections in those who have already had COVID-19, Sri Lanka is sequencing its SARS-CoV2 strains on a regular basis.

The sequencing of the SARS-CoV2 viruses is carried out by the Department of Immunology and Molecular Medicine of the University of Sri Jayewardenepura since March 2020. Sequencing carried out by the team of scientists from this Department have shown that while there were multiple viruses of different lineages circulating in March to May 2020, the current circulating SARS-CoV2 virus is of the B.1.411 which is an exclusively Sri Lankan lineage. Through their sequencing activities they have identified individuals who came to Sri Lanka been infected with the variants carrying the above mutations (B.1.1.7 and B.1.258), they were not identified from within the community. The Department of Immunology and Molecular Medicine of the University of Sri Jayewardenepura will continue to sequence the SARS-CoV2 viruses in Sri Lanka from different districts and quarantine centres to monitor any new introductions or de novo emergence of concerning mutations. These activities are funded by the WHO.