# SARS-CoV-2 Variants in the Central Province of Sri Lanka: Detection and Surveillance with an Economical and Scalable Molecular Protocol

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Emergence of SARS-CoV-2 variants sharing common mutations, like N501Y, E484K and L452R, is a threat to public health. Increasing number of infected cases and cost and resource-intensive nature of sequencing assays necessitate a real time monitoring strategy to complement whole genome sequencing. The objective of the study was to detect mutations (N501Y, E484K and L452R) associated with variants of concern (VOC) and variants of interest (VOI) using single nucleotide polymorphism real-time RT-PCR (SNP-rtRT-PCR). SARS-CoV-2 samples (n = 325) positive by real-time RT-PCR (Ct < 30) for COVID-19 diagnosis were randomly selected from November 2020 to 2021 from selected areas of the Central Province of Sri Lanka. An in-house SNP-rtRT-PCR targeting N501Y, E484K and L452Rwas conducted using a maximum of 30 samples per month. For November 2020, March 2021 and October 2021, the samples tested were 25, 12 and 6, respectively due to less number of positive samples based on our inclusion criteria. From November 2020 to March 2021, no SNPs were detected in the samples tested. N501Y was detected in the samples from April (29/30), May (30/30) and June (30/30) 2021. One sample with both, N501Y and E484K, mutations were identified in April 2021. From July to November 2021, L452R was the predominantly identified mutation in the samples tested. Based on the SNP surveillance, the mutations associated with VOCs and VOIs have been circulating in the study areas of the Central Province of Sri Lanka since April 2021. L452R mutation has been predominantly present from July 2021.

**Keywords:** Single nucleotide polymorphism, SARS-CoV-2 variants, Central Province, Sri Lanka

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