

Identification of New Variant of SARS CoV-2 Virus of C-36 lineage with L452R Mutation at University Hospital KDU (UHKDU) Sri Lanka

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Multiple variants of SARS-CoV-2 have been documented globally during this pandemic and it is important to identify possible new variants that might spread within a community. In Sri Lanka, B.1.1.7 (UK variant), B.1.428 (European / Middle East variant), B.1.525 (Nigerian variant), B.1.617.2 (Indian variant) and B.1.351 (South African variant) strains have been previously identified. Six members of one family tested positive for SARS CoV-2 by RT-PCR and rapid antigen tests from nasal swab samples between 22nd and 26th of April 2021 at UHKDU. Next Generation Sequencing (NGS) identified three of the members infected with a SARS -CoV-2 variant of pangolin lineage C.36, which contains a L452R mutation, with high infectivity. All six members had mild disease and recovered without any complications even though some had underlying illnesses. The variants B1.427/B1.429 containing the L452R mutation was first detected from California in May 2020 and rapidly increased to >50% between September 2020 to January 2021 in all sequenced cases. This is the first report identifying a new variant of the C.36 lineage containing the L452R mutation from Sri Lanka followed by detection of the same lineage from Vavuniya in June 2021. The emergence of such variants through the accumulation of convergent mutations or from travelers coming into the country needs further evaluation. Constant monitoring of the spread of known variants of concern and the new Sri Lankan variants are required to determine the impact on public health in Sri Lanka.

Keywords: SARS-CoV-2, L452R, variant, Sri Lanka