

Recently, 95 full-length genomic sequences of SARS-CoV-2 strains available in the National Center for Biotechnology Information and GISAID databases were subjected to multiple-sequence alignment and phylogenetic analyses for studying variations in the viral genome (260). All the viral strains revealed high homology of 99.99% (99.91% to 100%) at the nucleotide level and 99.99% (99.79% to 100%) at the amino acid level. Overall variation was found to be low in ORF regions, with 13 variation sites recognized in 1a, 1b, 5, 3a, M, 8, and N regions. Mutation rates of 30.53% (29/95) and 29.47% (28/95) were observed at nt 28144 (ORF8) and at 8782 (ORF1a) positions, respectively. Owing to such selective mutations, a few specific regions of SARS-CoV-2 should not be considered for designing primers and probes. The SARS-CoV-2 reference sequence could pave the way to study molecular biology and pathobiology, along with developing diagnostics and appropriate prevention and control strategies for countering SARS-CoV-2 (260).

Nucleic acids of SARS-CoV-2 can be detected from samples (64) such as bronchoalveolar lavage fluid, sputum, nasal swabs, fiber bronchoscope brush biopsy specimens, pharyngeal swabs, feces, blood, and urine, with different levels of diagnostic performance (Table 2) (80, 245, 246). The viral loads