

CoV-2 is considered a new γ -Betacoronavirus belonging to the subgenus Sarbecovirus (3). A few other critical zoonotic viruses (MERS-related CoV and SARS-related CoV) belong to the same genus. However, SARS-CoV-2 was identified as a distinct virus based on the percent identity with other Betacoronavirus; conserved open reading frame 1a/b (ORF 1a/b) is below 90% identity (3). An overall 80% nucleotide identity was observed between SARS-CoV-2 and the original SARS-CoV, along with 89% identity with ZC45 and ZXC21 SARS-related CoVs of bats (2, 31, 36). In addition, 82% identity has been observed between SARS-CoV-2 and human SARS-CoV Tor2 and human SARS-CoV BJO1 2003 (31). A sequence identity of only 51.8% was observed between MERS-related CoV and the recently emerged SARS-CoV-2 (37). Phylogenetic analysis of the structural genes also revealed that SARS-CoV-2 is closer to bat SARS-related CoV. Therefore, SARS-CoV-2 might have originated from bats, while other amplifier hosts might have played a role in disease transmission to humans (31). Of note, the other two zoonotic CoVs (MERS-related CoV and SARS-related CoV) also originated from bats (38, 39). Nevertheless, for SARS and MERS, civet