

using the 'Megalalign stoned program, siette the similarity between the novel SARS-CoV-2 isolates was in the range of 99.4% to 100%. Among the other Serbecovirus CoV sequences, the novel SARS-CoV- 2 sequences revealed the highest similarity to bat- SL-CoV, with nucleotide percent identity ranges between 88.12 and 89.65%. Meanwhile, earlier reported SARS-CoVs showed 70.6 to 74.9% similarity to SARS-CoV-2 at the nucleotide level. Further, the nucleotide percent similarity was 55.4%, 45.5% to 47.9%, 46.2% to 46.6%, and 45.0% to 46.3% to the other four subgenera, namely, Hibecovirus, Nobecovirus, Merbecovirus, and Embecovirus, respectively. The percent similarity index of current outbreak isolates indicates a close relationship between SARS-CoV-2 isolates and bat- SL-CoV, indicating a common origin. However, particular pieces of evidence based on _ further complete genomic analysis of current isolates are necessary to draw any conclusions, although it was ascertained that the current novel SARS-CoV-2 isolates belong to the subgenus Sarbecovirus in the diverse range of betacoronaviruses. Their possible ancestor was hypothesized to be from bat CoV strains, wherein bats might have played a crucial role in harboring this class of viruses.