

SplitsTree phylogeny analysis.

In the unrooted phylogenetic tree of different betacoronaviruses based on the S protein, virus sequences from different subgenera grouped into separate clusters. SARS-CoV-2 sequences from Wuhan and other countries exhibited a close relationship and appeared in a single cluster (Fig. 1). The CoVs from the subgenus *Sarbecovirus* appeared jointly in SplitsTree and divided into three subclusters, namely, SARS-CoV-2, bat-SARS-like-CoV (bat-SL-CoV), and SARS-CoV (Fig. 1). In the case of other subgenera, like *Merbecovirus*, all of the sequences grouped in a single cluster, whereas in *Embecovirus*, different species, comprised of canine respiratory CoVs, bovine CoVs, equine CoVs, and human CoV strain (OC43), grouped in a common cluster. Isolates in the subgenera *Nobecovirus* and *Hibecovirus* were found to be placed separately away from other reported SARS-CoVs but shared a bat origin.

CURRENT WORLDWIDE SCENARIO OF SARS-CoV-2

This novel virus, SARS-CoV-2, comes under the subgenus Sarbecovirus of the Orthocoronavirinae subfamily and is entirely different from the viruses