Splits Tree phyligeny 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 clolse 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 common cluster. Isolates in the subgenera Nobecovorus and Hibecovirus were found to be placed separately away from other reported SARS-CoVs but shared a bat origin.  
CURRENT WORLDWIDE SCENARIO OF F 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