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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 Nobecovorus 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