situation in the worldwide population, leading to

disease outbreaks that have not been controlled to

date, although extensive efforts are being put in

place to counter this virus (25). This virus has been

proposed to be designated/named severe acute

respiratory syndrome coronavirus 2 (SARS-CoV-2)

by the International Committee on Taxonomy of

Viruses (ICTV), which determined the virus belongs

to the Severe acute respiratory syndrome-related

coronavirus category and found this virus is related

to SARS-CoVs (26). SARS-CoV-2 is a member of

the order WNidovirales, family Coronaviridae,

subfamily Orthocoronavirinae, which is subdivided

into four genera, viz., Alphacoronavirus,

Betacoronavirus, Gammacoronavirus, and

Deltacoronavirus (3, 27). The genera

Alphacoronavirus and Betacoronavirus originate

from bats, while = Gammacoronavirus and

Deltacoronavirus have evolved from bird and swine

gene pools (24, 28, 29, 275).

Coronaviruses possess an unsegmented, single-

stranded, positive-sense RNA genome of around 30

kb, enclosed by a 5'-cap and 3’-poly(A) tail (30). The

genome of SARS-CoV-2 is 29,891 bp long, with a

G+C content of 38% (31). These viruses are

encircled with an envelope containing — viral