stalk (45). Recently, structural analyses of the S

proteins of COVID-19 have revealed 27 amino acid

substitutions within a 1,273-amino-acid stretch (16).

Six substitutions are located in the RBD (amino

acids 357 to 528), while four substitutions are in the

RBM at the CTD of the S1 domain (16). Of note, no

amino acid change is seen in the RBM, which binds

directly to the angiotensin-converting enzyme-2

(ACE2) receptor in SARS-CoV (16, 46). At present,

the main emphasis is knowing how many differences

would be required to change the host tropism.

Sequence comparison revealed 17 nonsynonymous

changes between the early sequence of SARS-CoV-2

and the later isolates of SARS-CoV. The changes

were found scattered over the genome of the virus,

with nine substitutions in ORFlab, ORF8 (4

substitutions), the spike gene (3 substitutions), and

ORF7a (single substitution) (4). Notably, the same

nonsynonymous changes were found in a familial

cluster, indicating that the viral evolution happened

during person-to-person transmission (4, 47). Such

adaptive evolution events are frequent and constitute

a constantly ongoing process once the virus spreads

among new hosts (47). Even though no functional

changes occur in the virus associated with this

adaptive evolution, close monitoring of the viral