residues for receptor binding” (FIG. 3b). In comparison

with the Guangdong strains, pangolin coronaviruses

reported from Guangxi are less similar to SARS-CoV-2,

with 85.5% genome sequence identity”. The repeated

occurrence of SARS-CoV-2-related coronavirus infec-

tions in pangolins from different smuggling events

suggests that these animals are possible hosts of the

viruses. However, unlike bats, which carry coronaviruses

healthily, the infected pangolins showed clinical signs

and histopathological changes, including interstitial

pneumonia and inflammatory cell infiltration in diverse

organs“. These abnormalities suggest that pangolins are

unlikely to be the reservoir of these coronaviruses but

more likely acquired the viruses after spillover from the

natural hosts.

An intermediate host usually plays an important role

in the outbreak of bat-derived emerging coronaviruses;

for example, palm civets for SARS-CoV and dromedary

camels for MERS-CoV. The virus strains carried by these

two intermediate hosts were almost genetically identi-

cal to the corresponding viruses in humans (more than

99% genome sequence identity)'. Despise an RBD that is

virtually identical to that of SARS-CoV-2, the pangolin

coronaviruses known to date have no more than 92%

genome identity with SARS-CoV-2 (REF). The avail-

able data are insufficient to interpret pangolins as the

intermediate host of SARS-CoV-2. So far, no evidence

has shown that pangolins were directly involved in the

emergence of SARS-CoV-2.