in CoV isolated from pangolin was almost identical

(one amino acid difference) to that of SARS-CoV-2.

A comparison of the genomes \_ suggests

recombination between pangolin-CoV-like viruses

with the bat-CoV-RaTG13-like virus. All this

suggests the potential of pangolins to act as the

intermediate host of SARS-CoV-2 (145).

Human-wildlife interactions, which are

increasing in the context of climate change (142), are

further considered high risk and responsible for the

emergence of SARS-CoV. COVID-19 is also

suspected of having a similar mode of origin. Hence,

to prevent the occurrence of another zoonotic

spillover (1), exhaustive coordinated efforts are

needed to identify the high-risk pathogens harbored

by wild animal populations, conducting surveillance

among the people who are susceptible to zoonotic

spillover events (12), and to improve the biosecurity

measures associated with the wildlife trade (146).

The serological surveillance studies conducted in

people living in proximity to bat caves had earlier

identified the serological confirmation of SARS-

related CoVs in humans. People living at the

wildlife-human interface, mainly in rural China, are

regularly exposed to SARS-related CoVs (147).

These findings will not have any significance until a