

(96.7%), and S genes (90.4%). The RBD of S protein 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