

(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