

The comprehensive sequence analysis of the SARS-CoV-2 RNA genome identified that the CoV from Wuhan is a recombinant virus of the bat coronavirus and another coronavirus of unknown origin. The recombination was found to have happened within the viral spike glycoprotein, which recognizes the cell surface receptor. Further analysis of the genome based on codon usage identified the snake as the most probable animal reservoir of SARS-CoV-2 (143). Contrary to these findings, another genome analysis proposed that the genome of SARS-CoV-2 is 96% identical to bat coronavirus, reflecting its origin from bats (63). The involvement of bat-derived materials in causing the current outbreak cannot be ruled out. High risk is involved in the production of bat-derived materials for TCM practices involving the handling of wild bats. The use of bats for TCM practices will remain a severe risk for the occurrence of zoonotic coronavirus epidemics in the future (139).

Furthermore, the pangolins are an endangered species of animals that harbor a wide variety of viruses, including coronaviruses (144). The coronavirus isolated from Malayan pangolins (*Manis javanica*) showed a very high amino acid identity with COVID-19 at E (100%), N (98.2%), N (96.7%), and S genes (90.4%). The RBD of S protein