

Swine acute diarrhea syndrome coronavirus (SADS-CoV) was first identified in suckling piglets having severe enteritis and belongs to the genus Alphacoronavirus (106). The outbreak was associated with considerable scale mortality of piglets (24,693 deaths) across four farms in China (134). The virus isolated from the piglets was almost identical to and had 95% genomic similarity with horseshoe bat (*Rhinolophus* species) coronavirus HKU2, suggesting a bat origin of the pig virus (106, 134, 135). It is also imperative to note that the SADS-CoV outbreak started in Guangdong province, near the location of the SARS pandemic origin (134). Before this outbreak, pigs were not known to be infected with bat-origin coronaviruses. This indicates that the bat-origin coronavirus jumped to pig by breaking the species barrier. The next step of this jump might not end well, since pigs are considered the mixing vessel for influenza A viruses due to their ability to be infected by both human and avian influenza A viruses (136).

Similarly, they may act as the mixing vessel for coronaviruses, since they are in frequent contact with both humans and multiple wildlife species. Additionally, pigs are also found to be susceptible to human with SARS-CoV and MERS-CoV, making this scenario a nightmare (109, 137).