

# WHY PANGOLINS MAY NOT BE THE INTERMEDIATE HOST

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Under scrutiny: There are similarities in genome sequences in pangolin coronavirus and SARS-CoV-2. | Photo Credit: Getty Images

The origin debate on novel coronavirus (SARS-CoV-2) is yet to be settled. Most indications suggest that the virus jumped across the species barrier from bats to humans either directly or through an intermediate host. There is another view that the virus might have escaped or leaked from the Wuhan Institute of Virology lab.

Such lab leaks had indeed happened in the past. In 2004, two researchers in a virology lab in Beijing working on the 2002 SARS virus were independently infected. The virus was transmitted to seven people in all but the outbreak was contained soon enough. A section of scientists and others believe that the SARS-CoV-2 virus might have followed the same course but went on to cause the pandemic.

While irrefutable evidence in support of a natural origin is lacking as scientists have so far not been able to identify bats harbouring viruses very similar to the novel coronavirus to establish that the virus had indeed jumped directly from bats to humans. Nor have they been able to conclusively identify the intermediate host from where the virus jumped to humans and began spreading among people.

While the SARS-CoV-2 virus is quite similar to the RATG13 coronavirus found in horseshoe bats, the genome of the two viruses have only 96% similarity. So the virus, if it had jumped from bats to humans, is yet to be identified in bats. Pangolin has been suggested as a potential intermediate host that could have harboured the coronavirus before it made the giant leap to spread among humans. Many studies have found similarity between the coronavirus in pangolin and SARS-CoV-2 virus in terms of genome sequences. A [study published recently](#) in the journal *iScience* evaluated the biological characteristics of the pangolin coronavirus. The researchers from the Beijing University of Chemical Technology studied the pathogenicity and transmissibility of pangolin coronavirus by infecting Syrian golden hamsters and compared it with hamsters infected with SARS-CoV-2.

They found that the pangolin coronavirus was not only able to effectively infect hamsters but also cause the similar kind of responses in tissues as the novel coronavirus. Though both viruses seem to have the same affinity for the receptors, the pangolin coronavirus was able to efficiently replicate in the respiratory system and brain, much like the SARS-CoV-2. However, the scientists were not able to find infectious pangolin coronavirus in organs other than the respiratory system and brain, which is different from hamsters infected by SARS-CoV-2 virus.

Hamsters infected with pangolin coronavirus did not suffer substantial loss of body, while hamsters infected with SARS-CoV-2 did show a slight reduction in body weight in the first five days of infection and then regained weight.

Alveolar wall thickening of lungs of hamsters infected with pangolin coronavirus was “widespread” whereas the alveolar wall thickening in hamsters infected with SARS-CoV-2 was severe. There were other differences in pathogenesis too. In all, pangolin coronavirus produced moderate disease in hamsters and was less virulent than SARS-CoV-2.

There were differences in the way the viruses replicated — SARS-CoV-2 replicated way higher in the hamsters than the pangolin coronavirus could. Viral shedding by hamsters infected with pangolin coronavirus lasted for three days, while hamsters infected with SARS-CoV-2 shed virus for five days.

The most important difference was in the route of transmission. While pangolin coronavirus did not spread via aerosols but only through contact transmission, SARS-CoV-2 showed an “efficient contact transmissibility and an efficient aerosol transmissibility with a transmission efficiency of 100%”, the authors write. One reason for lack of aerosol transmission in the case of pangolin coronavirus could be because of the less viral aerosols produced by the infected hamsters. The second likely reason could be the larger size of the viral particles exhaled by hamsters infected with pangolin coronavirus. In contrast, SARS-CoV-2-infected hamsters produced significantly higher amounts of viral aerosols, they found. Also, the amount of virus particles exhaled per minute by hamsters infected with SARS-CoV-2 was nearly 2.5 times more than hamsters infected with pangolin coronavirus.

Based on the study, the researchers conclude that the infection characteristics of pangolin coronavirus and SARS-CoV-2 are similar though the pathogenicity and transmissibility are much more in hamsters infected with SARS-CoV-2 virus. Though pangolin coronavirus spread from one hamster to another only through direct contact and not through aerosol, the “public health risk of pangolin coronavirus being potential candidates for global dissemination could not be ignored”, they write. They also caution that “continual monitoring of the mutation and evolution of pangolin coronavirus should be implemented in the future, and the illegal wildlife trade of pangolins should be effectively controlled”.

The study does not conclusively show that pangolins could have been the intermediate host. But the possibility of pangolin coronavirus crossing the species barrier at a future date and infecting humans cannot be ruled out.

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