

Study on Origin of Novel Coronavirus

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The SARSCoV2 virus is likely to have diverged from closely related bat viruses called the sarbecovirus, 40-70 years ago, a study published in Nature Microbiology says. The novel coronavirus (SARSCoV2), which has so far infected over 17.6 million people and killed nearly 6.8 million across the world, has been circulating unnoticed in bats for decades. Bats have been the “primary reservoirs” for novel coronavirus.

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In early February, Chinese researchers had found that **SARSCoV2 is most closely related to RaTG13 sarbecovirus, which was isolated from a horseshoe bat in Yunnan province in 2013.** Based on the **nearly 96% genome sequence identity between SARS-CoV2 and RaTG13,** a team led by ZhengLi Shi from the Wuhan Institute of Virology said in a paper published in February in Nature that **an origin in bats is probable for the COVID19 outbreak.** The current study by Prof. Maciej Boni from the Pennsylvania State University in the U.S. and others not only confirms the findings of the Wuhan study but also suggests the probable time when SARSCoV2 diverged from RaTG13.

The authors analysed the evolutionary history of SARSCoV2 using genomic data on sarbecoviruses. They employed three approaches to identify regions in the virus that had not undergone recombination and that could be used to reconstruct its evolution. All approaches suggest that **RaTG13 and SARSCoV2 share a single ancestral lineage** and estimate that SARSCoV2 genetically diverged from related bat sarbecoviruses in 1948, 1969 and 1982, respectively.

Importantly, the study says that **novel coronavirus itself has not arisen from recombination of any sarbecoviruses. The**

ability of the spike protein in the virus to bind to ACE2 human receptors had emerged within bats and is an ancestral trait shared with bat viruses and “not one acquired recently via recombination”. According to it, the results suggest the presence of a “single lineage” circulating in bats with properties that allowed it to infect human cells. This was also the case with the bat sarbecoviruses related to the 2002 SARS lineage.

The Nature Microbiology paper also challenges the notion that pangolins would have served as an intermediate host where the virus would have acquired its ability to infect human cells thus facilitating the jump into humans. They conclude that **it is plausible that pangolins could have been a conduit for transmission to humans, but there is “no evidence that pangolins facilitated adaptation to humans” by being an intermediate host.**

The researchers also caution that the long divergence period raises the possibility of other undocumented virus lineages circulating in horseshoe bats that have the potential to jump from bats to humans. Different and yet unstudied bat sarbecoviruses that have descended from the SARSCoV2/RaTG13 common ancestor forms a clade with properties to infect many different mammals, including humans.