

Bat cave study sheds new light on origin of SARS virus

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The side face of a Chinese horseshoe bat (*Rhinolophus sinicus*). Credit: Dr. Libiao Zhang from Guangdong Institute of Applied Biological Resource, China

Genetic recombination between viral strains in bats may have produced the direct evolutionary ancestor of the strain that caused a deadly outbreak of severe acute respiratory syndrome (SARS) in humans, according to new research published in *PLOS Pathogens*.

In late 2002, a SARS pandemic broke out in southern China, ultimately killing hundreds of people in dozens of countries by the summer of 2003. Scientists traced the outbreak back to horseshoe bats, hypothesizing that the culprit, SARS coronavirus, originated in these animals and then spread either directly to humans or to animals later purchased by humans at markets.

However, the details of the outbreak's origin remain unclear. SARS [strains](#) found in bats are genetically distinct from the specific SARS strain that caused the outbreak, suggesting that known bat strains did not directly evolve into the outbreak strain.

To address this issue, Ben Hu of the Chinese Academy of Sciences in Wuhan, China, and colleagues spent five years studying SARS viruses found in multiple species of [horseshoe bats](#) living in a single cave in Yunnan Province, China. In the new study, the researchers identified 11 new strains of SARS virus and sequenced their full genomes to uncover their evolutionary relationships.

Genome analysis revealed that the newly identified bat strains, as well as several strains identified in a previous study of the same bat cave, contained all the essential genetic building blocks of the human SARS coronavirus. In some of the strains, for instance, portions of a gene known as the S gene showed high genetic similarity to the same regions found in the SARS coronavirus genome.

Based on their genetic analysis, the researchers hypothesize that [genetic recombination](#) between precursor strains that later evolved into the

newly identified strains may also have given rise to a strain that directly evolved into SARS coronavirus.

Additional lab experiments showed that some of the newly identified bat strains are capable of entering [human](#) cells via the same cellular receptor employed by SARS coronavirus. This suggests that the bat cave contains strains that could potentially be directly transmitted to humans.

Overall, these findings provide new insights into the evolutionary origin of SARS coronavirus. Because of the potential risk of existing bat strains spreading to humans, the researchers propose continued monitoring of the cave they studied, as well as other sites that may pose similar risk.

"Rhinolophus bats in China harbor genetically diverse SARS-related coronaviruses," the authors explain, "which may have given rise to the direct progenitor of SARS coronavirus after recombination."

More information: Hu B, Zeng L-P, Yang X-L, Ge X-Y, Zhang W, Li B, et al. (2017) Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. *PLoS Pathog* 13(11): e1006698.
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