Transmission of zoonotic viruses from hosts to intermediate hosts and ultimately to humans remains largely unexplored. During the past few decades, bats have been recognized as natural hosts of various zoonotic viruses, such as coronaviruses (CoVs). In this study, the Chinese authors investigated CoVs in bats from nine distinct locations in Yunnan and Guangdong provinces in southern China, to expand the knowledge of the current distribution and evolution of CoVs.

The bat-borne merbecoviruses (HKU4r-CoV and HKU5r-CoV), rhinacoviruses (HKU2r-CoV), and sarbecoviruses (RaTG-13) have been associated with numerous outbreaks in humans. The authors noted that merbecovirus MjHKU4r-CoV, found in pangolins from Guangxi province, exploits the human dipeptidyl peptidase-4 (hDPP4) receptor to induce infection. Also, CoVs recently identified in several pangolin species in Guangdong and Guangxi provinces can utilize human angiotensin-converting enzyme 2 (hACE2) as a receptor for viral entry.



About the study

A total of 729 samples from 20 different bat species belonging to 11 genera and 6 families were collected from nine distinct locations in Yunnan and Guangdong provinces in southern China in 2016 and 2017.

In 58 of 729 samples (8.0%) from nine different bat species, the CoV RNA was detected by reverse transcription polymerase chain reaction. 38 samples belonged to the alpha coronaviruses (αCoVs) genus and 20 to the beta coronaviruses (βCoVs) genus.

The results of the sequence analysis revealed that the full-length genome of the bat TyRo-

CoV-162275 shared the highest identity with the Malayan pangolin HKU4-related coronavirus (MjHKU4r-CoV) from Guangxi Province. The full-length genome of the bat TyRo-CoV-162269 was closely related to HKU33-CoV discovered in a greater bamboo bat from Guizhou Province.

Given that MERS-CoV, bat HKU4-CoV, and pangolin MjHKU4r-CoV utilize hDPP4 as a cell entry receptor, researchers investigated whether bat TyRo-CoV-162275 also utilizes hDPP4 for its entry. The results showed that bat TyRo-CoV-162275, similar to MERS-CoV, may utilize human hDPP4 as its entry receptor, and has a putative furin protease cleavage site in the spike protein. Key residue analysis in the hDPP4 receptor-binding region demonstrated that bat TyRo-CoV-162275 shares ten key sites with pangolin MjHKU4r-CoV.

Conclusion

According to the authors, this is the first report of bat TyRo-CoV-162275 with a furin protease cleavage site.

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