Addendum: A pneumonia outbreak associated with a new coronavirus of probable bat origin

https://doi.org/10.1038/s41586-020-2951-z

Addendum to: *Nature* https://doi.org/10.1038/s41586-020-2012-7

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Here we provide further information about the bat SARS-related coronavirus (SARSr-CoV) strain RaTG13 reported in our Article. Between 1 July and 1 October 2012, we received 13 serum samples collected from 4 patients (one of whom was deceased) who showed severe respiratory disease. These patients had visited a mine cave in Tongguan town, Mojiang County, Yunnan Province, China, to clean bat faeces in order to mine copper before being admitted to the First Affiliated Hospital of Kunming Medical University on 26–27 April 2012. The samples we received were collected by the hospital staff in June, July, August and September 2012. To investigate the cause of the respiratory disease, we tested the samples using PCR methods developed in our laboratory targeting the RNA-dependent RNA polymerases (RdRp) of Ebola virus, Nipah virus and bat SARSr-CoV Rp3, and all of the samples were negative for the presence of these viruses. We also tested the serum samples for the presence of antibodies against the nucleocapsid proteins of these three viruses, and none of the samples gave a positive result. Recently, we retested the samples with our validated enzyme-linked immunosorbent assay (ELISA) against the SARS coronavirus 2 (SARS-CoV-2) nucleocapsid protein—which has greater than 90% amino acid sequence identity with bat SARSr-CoV Rp3—and confirmed that these patients were not infected by SARS-CoV-2.

We suspected that the patients had been infected by an unknown virus. Therefore, we and other groups sampled animals including bats, rats and musk shrews in or around the cave, and found some alphacoronaviruses[1] and paramyxoviruses[2]. Between 2012 and 2015, our group sampled bats once or twice a year in this cave and collected a total of 1,322 samples. From these samples, we detected 293 highly diverse coronaviruses, of which 284 were designated alphacoronaviruses and 9 were designated betacoronaviruses on the basis of partial RdRp sequences. All of the nine betacoronaviruses are SARSr-CoVs, one of which (sample ID4991; renamed RaTG13 in our Article to reflect the bat species, the location and the sampling year) was described in a 2016 publication[1]. The partial RdRp sequence (370 bp) of ID4991 was deposited in GenBank in 2016 under accession number KP876546. All of the identified bat SARSr-CoVs are distantly related to SARS-CoV based on partial RdRp sequences. In 2018, as the next-generation sequencing technology and capability in our laboratory had improved, we performed further sequencing of these bat viruses and obtained almost the full-length genome sequence (without the 5′ and 3′ ends) of RaTG13. In 2020, we compared the sequence of SARS-CoV-2 with our unpublished bat coronavirus sequences and found that it shared a 96.2% identity with RaTG13.

1. Ge, X. Y. et al. Coexistence of multiple coronaviruses in several bat colonies in an abandoned mineshaft. *Virol. Sin*. **31**, 31–40 (2016).
2. Wu, Z. et al. Novel Henipa-like virus, Mojiang paramyxovirus, in rats, China, 2012. *Emerg. Infect. Dis*. **20**, 1064–1066 (2014).