

Identifying SARS-CoV-2-related coronaviruses in Malayan pangolins

<https://doi.org/10.1038/s41586-020-2169-0>

Received: 7 February 2020

Accepted: 17 March 2020

Published online: 26 March 2020

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The ongoing outbreak of viral pneumonia in China and across the world is associated with a new coronavirus, SARS-CoV-2¹. This outbreak has been tentatively associated with a seafood market in Wuhan, China, where the sale of wild animals may be the source of zoonotic infection². **Although bats are probable reservoir hosts for SARS-CoV-2, the identity of any intermediate host that may have facilitated transfer to humans is unknown. Here we report the identification of SARS-CoV-2-related coronaviruses in Malayan pangolins (*Manis javanica*)** seized in anti-smuggling operations in southern China. Metagenomic sequencing identified pangolin-associated coronaviruses that belong to two sub-lineages of SARS-CoV-2-related coronaviruses, including one that exhibits strong similarity in the receptor-binding domain to SARS-CoV-2. The discovery of multiple lineages of pangolin coronavirus and their similarity to SARS-CoV-2 suggests that pangolins should be considered as possible hosts in the emergence of new coronaviruses and should be removed from wet markets to prevent zoonotic transmission.

An outbreak of serious pneumonia disease was reported in Wuhan, China, on 30 December 2019. The causative agent was soon identified as a novel coronavirus¹, which was later named SARS-CoV-2. Case numbers grew rapidly from 27 in December 2019 to 3,090,445 globally as of 30 April 2020³, leading to the declaration of a public health emergency, and later a pandemic, by the WHO (World Health Organization). Many of the early cases were linked to the Huanan seafood market in Wuhan city, Hubei province, from where the probable zoonotic source is speculated to originate². Currently, only environmental samples taken from the market have been reported to be positive for SARS-CoV-2 by the Chinese Center for Disease Control and Prevention⁴. However, as similar wet markets were implicated in the SARS outbreak of 2002–2003⁵, it seems likely that wild animals were also involved in the emergence of SARS-CoV-2. Indeed, a number of mammalian species were available for purchase in the Huanan seafood market before the outbreak⁴. Unfortunately, because the market was cleared soon after the outbreak began, determining the source virus in the animal population from the market is challenging. Although a coronavirus that is closely related to SARS-CoV-2, which was sampled from a *Rhinolophus affinis* bat in Yunnan in 2013, has now been identified⁶, similar viruses have not yet been detected in other wildlife species. Here we

identified SARS-CoV-2-related viruses in pangolins smuggled into southern China.

We investigated the virome composition of pangolins (mammalian order Pholidota). These animals are of growing importance and interest because they are one of the most illegally trafficked mammal species: they are used as a food source and their scales are used in traditional Chinese medicine. A number of pangolin species are now regarded as critically endangered on the International Union for Conservation of Nature Red List of Threatened Species. We received frozen tissue samples (lungs, intestine and blood) collected from 18 Malayan pangolins (*Manis javanica*) during August 2017–January 2018. These pangolins were obtained during anti-smuggling operations performed by Guangxi Customs officers. Notably, high-throughput sequencing of the RNA of these samples revealed the presence of coronaviruses in 6 out of 43 samples (2 lung samples, 2 intestinal samples, 1 lung–intestine mixed sample and 1 blood sample from 5 individual pangolins; Extended Data Table 1). With the sequence read data, and by filling gaps with amplicon sequencing, we were able to obtain six complete or near complete genome sequences—denoted GX/P1E, GX/P2V, GX/P3B, GX/P4L, GX/P5E and GX/P5L—that fall into the SARS-CoV-2 lineage (within the genus *Betacoronavirus* of the *Coronaviridae*) in a

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