



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.



Letter to the Editor

Strategies to trace back the origin of COVID-19



Dear editor,

The recent outbreak of coronavirus disease 2019 (COVID-19), caused by the SARS-CoV-2, had raised great concern.¹ Although the virus appears to be less pathogenic than MERS-CoV and SARS-CoV, it shows a better efficacy of human-to-human transmission.^{2–4} WHO raised the global COVID-19 risk to its highest level on Feb 28, 2020. Due to the strict efforts taken by the Chinese Government, there has been considerable descent in newly diagnosed cases in the country. However, the sharp rise in number of new cases outside China signifies that it is still a challenging task to control the virus.

In spite of considerable research advancements on SARS-CoV-2, the origin of the virus is yet ambiguous. Chinese authorities originally announced that the first infection case was reported on December 31, 2019, and many of the initial cases were linked directly to Huanan seafood market in Wuhan, in the Hubei province.⁵ Apart from fish and seafood, the market also sold domestic and wild animals. Thirty-three of the 585 environmental samples collected from the market were found to contain the novel coronavirus, according to China CDC. The hypothesis that the outbreak originated at the market, with its initial transmission from live animals to human beings followed by rapid human-to-human transmission, is suggested to be most likely and convincing.⁶ However, another recent study claimed that the first patient, diagnosed on December 1, 2019, was never exposed to the market.⁷ Thus, origin of the disease still remains a puzzle unresolved. Identification and subsequent elimination of the zoonotic source appears to be the most imperative and demanding task at present to prevent further events of viral spillover at the animal-human interface.⁸ The seafood market was closed on January 1, 2020, and existing animals had been cleaned up, making it very difficult to identify the intermediate hosts. However, tracing the source of the virus might be targeted from the following perspectives:

- (1) Tracing back the viral emergence at the Huanan seafood market. It has been more than two months that the market has been closed and thus, it seems impossible to collect animal samples at present. However, the government can list all merchants in the market and clarify which animals they sold, and pertaining purchase channels of the animals. Thus, sampling the animals from their purchase channels, aimed at detection of viral population in animal samples, promises to be a feasible way of catering the current problem.
- (2) Detection of the SARS-CoV-2-like virus in wild animals. The first case of infection has been suggested not to be related with the market,⁷ assuming the tracing effort should not be limited to the market. The fact that various institutions (such as veterinary units, animal research institutions, wild ani-

mal rescue stations, etc.) have collected a lot of animal samples assures to facilitate rapid detection of the novel virus in the concerned wild animal samples and might provide cues towards the enigma of its origin and intermediate host. Viruses isolated in pangolin and bats^{9,10} have been reported to genetically related to SARS-CoV-2, however, these viruses were unlikely directly linked to the outbreak because they are only 85.5–96.2% overall genome sequence identity with SARS-CoV-2. Larger number of samples would be required for the purpose of detecting and profiling the exact animal source.

- (3) Detection of serum antibody in clinical samples collected before December 2019 in Hubei Province, especially in Wuhan. It appears crucial to specifically identify as who is "patient zero" for the outbreak. Proper identification of "patient zero" might be a valuable know-how to address the complex riddles as how, when and why the virus emerged. It might be possible that the virus has been circulating in the human population before the outbreak in December 2019. Detection and profiling of antibodies against the novel coronavirus, in the sera of human individuals before December 2019, present in Wuhan hospital (the sera kept in the hospital during physical examination or medical treatment, especially fever clinic), might confer scopes to determine as when the event of viral transmission to human population had originally occurred, thus, unraveling its enigmatic origin.

Acknowledgments

This work was supported by the [National Natural Science Foundation of China](#) (Grant No. 31822056), Key Program of the Department of Education of Guangdong Province (2019KZDXM004), the Guangdong Science and Technology Innovation Leading Talent Program (2019TX05N098), and the 111 Project (D20008).

References

1. Wang R, Zhang X, Irwin DM, Shen Y. Emergence of SARS-like coronavirus poses new challenge in China. *J Infect* 2020;**80**:350–71.
2. Chan JF, Yuan S, Kok KH, To KK, Chu H, Yang J, et al. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. *Lancet* 2020;**395**(10223):514–23.
3. Huang R, Xia J, Chen Y, Shan C, Wu C. A family cluster of SARS-CoV-2 infection involving 11 patients in Nanjing, China. *Lancet Infect Dis* 2020. doi:10.1016/S1473-3099(20)30147-X.
4. Lillie PJ, Samson A, Li A, Adams K, Capstick R, Barlow GD, et al. Novel coronavirus disease (Covid-19): the first two patients in the UK with person to person transmission. *J Infect* 2020. doi:10.1038/s41586-020-2012-7.
5. Wang C, Horby PW, Hayden FG, Gao GF. A novel coronavirus outbreak of global health concern. *Lancet* 2020;**395**(10223):470–3.
6. Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020;**395**(10224):565–74.
7. Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet* 2020;**395**(10223):497–506.

8. Zhang Z, Xiao K, Zhang X, Roy A, Shen Y. Emergence of SARS-like coronavirus in china: an update. *J Infect* 2020. doi:[10.1016/j.jinf.2020.03.010](https://doi.org/10.1016/j.jinf.2020.03.010).
9. Zhou P, Yang X-L, Wang X-G, Hu B, Zhang L, Zhang W, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020. doi:[10.1038/s41586-020-2012-7](https://doi.org/10.1038/s41586-020-2012-7).
10. Xiao K, Zhai J, Feng Y, Zhou N, Zhang X, Zou J.-J., et al. Isolation and characterization of 2019-nCoV-like coronavirus from Malayan pangolins. *BioRxiv* doi: [10.1101/2020.02.17.951335](https://doi.org/10.1101/2020.02.17.951335), <https://www.biorxiv.org/content/10.1101/2020.02.17.951335v1>

Xu Zhang
*College of Veterinary Medicine, South China Agricultural University,
Guangzhou 510642, China
Guangdong Laboratory for Lingnan Modern Agriculture, Guangzhou
510642, China*

Xiaoyuan Chen, Zhipeng Zhang
*College of Veterinary Medicine, South China Agricultural University,
Guangzhou 510642, China*

Ayan Roy
*Department of Biotechnology, Lovely Professional University, Punjab,
India*

Yongyi Shen*
*College of Veterinary Medicine, South China Agricultural University,
Guangzhou 510642, China
Guangdong Laboratory for Lingnan Modern Agriculture, Guangzhou
510642, China
Key Laboratory of Zoonosis Prevention and Control of Guangdong
Province, Guangzhou 510642, China*

*Corresponding author at: College of Veterinary Medicine,
South China Agricultural University, Guangzhou 510642, China.
E-mail address: sheny@scau.edu.cn (Y. Shen)

Accepted 21 March 2020