

Technical Report 2



Where did COVID-19 come from? Does it matter?

Dharshini Kantharuban¹, Indumini Gunatilake², Chithramali Rodrigo³, Bhumini Karunaratna³, Ishanka Talagala³, Sampatha Goonewardena⁴, Pushpa Jayawardana⁵, Maheeka Seneviwickrama^{4*}

¹ Provincial Director of Health Services office- Eastern Province, Trincomalee, Sri Lanka; ² Postgraduate Institute of Medicine, University of Colombo, Sri Lanka; ³ Ministry of Health, Sri Lanka; ⁴ Department of Community Medicine, Faculty of Medical Sciences, University of Jayewardenepura, Sri Lanka; ⁵ No affiliation

*Correspondence: maheeka@sjp.ac.lk

 <https://orcid.org/0000-0002-4182-284X>

DOI: <http://doi.org/10.4038/jccpsl.v26i5.8358>

Received on 20 May 2020

Accepted on 25 May 2020

Highlights

- Origin of the COVID-19 has created a political turmoil globally.
- Several theories exist regarding the origin of COVID-19.
- Understanding the origin of the COVID-19 is crucial in containment of the current pandemic as well as prevention of the future outbreaks.

Background

Origin of the COVID-19

An increasing number of pneumonia cases have been identified in Wuhan, a large city in Hubei Province, Central China since December 2019. A novel coronavirus, SARS-CoV-2 (initially known as 2019-nCoV) was identified as the pathogen responsible for this outbreak of respiratory illness. Epidemiological investigations identified a link between the first four cases and a large seafood and animal wet market in Wuhan suggesting an animal to human (zoonotic) transmission (1-4). During the early stage of the outbreak (late December 2019), 55% of the cases were linked to the Wuhan wet market (4). Subsequently, a growing number of patients without a recent history of exposure to animal markets were

reported, suggesting the occurrence of human to human transmission (4-5). After January 2020, the epidemiological link to the seafood market became low (4). The COVID-19 epidemic in Wuhan, China passed three stages: the initial stage showing close links to the seafood market; second stage suggestive of community transmission inside Wuhan City and Hubei Province of China; and finally the widespread stage which caused the pandemic (4).

Associations of any undesired event such as 'fingerprinting' and 'politicization' did not spare the worst epidemic of the 21st century, with conspiracy theories spawned and China being blamed (1-3, 5). Accusations were made against China for deliberately releasing the virus as a bioweapon, whereas others stated it to be an accidental viral leakage from a bio-lab in Wuhan (5-7). Proximity of

the two biological labs to the Wuhan seafood market where the first few cases were reported fuelled these conspiracy theories of an 'evil lab' (7). However, no conclusive evidence was consequently found on the Wuhan animal market being the origin of this infection (8).

Several science-based hypotheses are circulating against the conspiracy theories. Scientists claim it could be due to natural selection in an animal host before zoonotic transfer or due to the natural selection in humans following zoonotic transfer (9). There is another possibility of selection during passage: laboratory escape of bat SARS-CoV-2 like coronaviruses which has been ongoing for many years in cell culture and/or in animal models. Considering the documented instances of laboratory escapes of SARS-CoV, the possibility of an unintended laboratory release of SARS-CoV-2 cannot be excluded (9).

Genomic sequencing using broncho-alveolar lavage from a patient working in the Hunan seafood market showed high similarity of nucleotide sequence between bat SARS-related coronavirus and SARS-CoV-2. Similarity of genomic sequence to SARS-CoV was only 79.5% (10). Phylogenetic analysis showed that the virus was clustered with SARS-CoV and bat SARS-CoVs. Sequenced samples from seven patients and bats revealed that the new coronavirus shared 96.2% overall genome sequence similarity with a horseshoe bat coronavirus, *Rhinolophus*. This invention provided further evidence that SARS-CoV-2 most likely originated from bats (10).

Some argue that if an index case is suspected of zoonotic spill over, it should be verified that there is a link, or an exposure history and the animal concerned should have that virus (11). There is lack of evidence to suggest zoonotic transmission had occurred at Wuhan market, as there is no published evidence with animals in the market being tested for SARS-CoV-2 virus. Therefore, the possible animal source of COVID-19 has not yet been confirmed.

Researchers from Cambridge, UK and Germany analysed virus genome samples collected across the world between 24 December 2019 to 4 March 2020

using genetic networking techniques namely 'phylogenetic' methods. The analysis revealed three clusters of closely related distinct 'variants' of SARS-CoV-2, labelled as 'A', 'B' and 'C' (12). Accordingly, type 'A' which was closest to the one found in bat, the "original human virus genome", is not the predominant type in Wuhan. It was not found among Americans living in Wuhan and some Chinese individuals and Americans lived in Wuhan. Muted Type 'A' is the type responsible for the pandemic in America and Australia. Type 'B' was the major cause prevalent among patients from Wuhan and East Asian outbreaks. Type 'C' was the variant responsible for the major devastating outbreak in the European continent. Type 'C' was also found in Singapore, Hong Kong and South Korea but surprisingly not in China (12) (Figure 1).

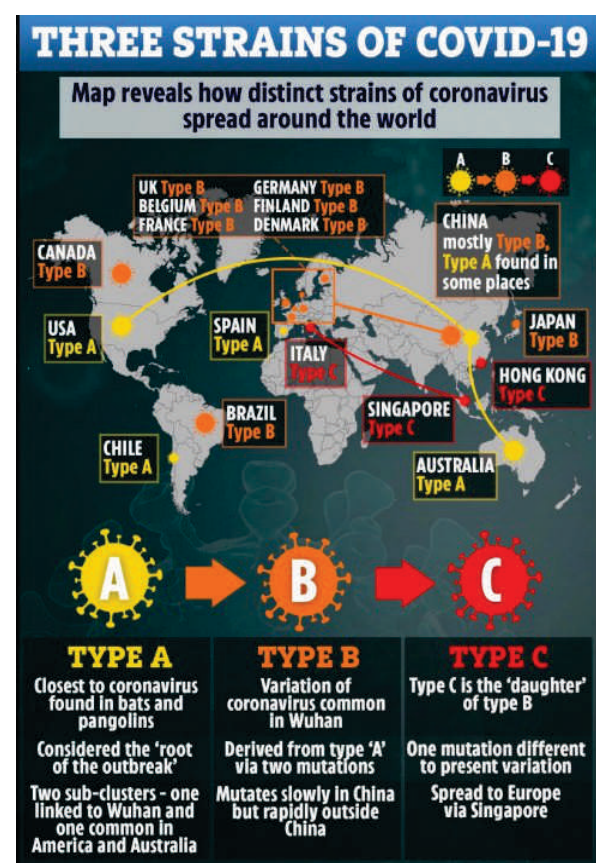


Figure 1: Global spread of distinct types of SARS-CoV-2

Source: Mullin G (2020, April 10). Rapid mutation Coronavirus 'mutated into three distinct strains' as it spread around the world. The US Sun.

Gaps in the existing knowledge

Even though most literature traces back the first COVID-19 case to the Huanan seafood market in Wuhan and suggested animal to human transmission, conspiracy theories are spread across globally. Knowledge on the origin of this novel virus is still under scrutiny.

Public health implications

Identification of the origin of SARS-CoV-2 is of prime importance in many ways. It is important in applying disease preventive and control measures. If the virus had an animal host, control measures should target them. If it is man-made, appropriate measures should be taken to prevent future similar occurrences. Banning of all wet markets by the Chinese government following this outbreak would have caused a major economic blow to the people whose livelihoods related to them (3). If SARS-CoV-2 pre-adapted in another animal species, then there is the risk of future emergence of a new disease (9-11). In contrast, if the adaptive process occurred in humans, then even if repeated zoonotic transfers occur, they are unlikely to take off without the same series of mutations. In addition, identifying the closest viral relatives of SARS-CoV-2 circulating in animals will assist studies of viral function (9-11). Due to the linking of COVID-19 to wet markets, people started avoiding consumption of fish and meat. This could have caused a vicious cycle of lowered immunity due to poor nutrition leading them to be more susceptible to the disease (13). In certain parts of the world and mainly in America, people started calling this novel SARS-CoV-2 virus the “Chinese virus” or “Wuhan virus”. This act by the American leader and their people led to stigmatization and fear among Chinese and South East Asian population. Many Americans and Europeans started avoiding Chinese during the latter part of February and early March 2020 (14-15). The American President directly accused the World Health Organization (WHO) for supporting China and not disclosing the facts and figures about this novel virus as well as the disease fatality. Due to this, there were threats to withdraw provision of funds to WHO in the middle of the pandemic (14-16). Failure

of the current pandemic clearly shows none of the countries were prepared to outrage a massive epidemic not to mention pandemic.

Applicability of the evidence to Sri Lanka

In Sri Lanka, with reporting of a Chinese woman as the country's first case, several incidents of discrimination were reported against foreign nationals, especially Chinese (17-18). Severity of COVID-19 related xenophobia strained the friendship between the two countries to an extent that necessitated diplomatic intervention by the Chinese Ambassador to Sri Lanka (17). A group of Sri Lankan scientists sequenced SARS-CoV-2 genome and revealed the predominant viral type as type A, the main type found in Australia and USA (19). Knowledge on viral transmission is important to apply public health strategies to control the spread and prevention of future epidemics. Avoidance of fish and meat consumption can be overcome, if the correct message reaches the general public.

Recommendations for COVID-19 response in Sri Lanka

Imparting the correct knowledge on the origin of the disease and its mode of transmission will help to avoid spread of misinformation. Health promotion activities play a major role in prevention of outbreaks and epidemics. Carefully designed health education materials in local languages adopted to the country's needs, play a major role in improving health literacy among the target population.

Author Declaration

Author contributions: DK drafted the manuscript. MS revised the manuscript for important intellectual content and other authors helped with literature search. All authors agreed to be accountable for all aspects of the work and approved the final manuscript for submission.

References

1. Rannan Eliya R. *China's no longer the problem*. Daily Mirror, 2 May 2020. Available from: <http://www.dailymirror.lk/opinion/Chinas-no-longer-the-problem/172-184740>.
2. Duarte F. *Who is 'patient zero' in the corona virus outbreak?* BBC Future, 24 February 2020. Available from: <https://www.bbc.com/future/article/20200221-coronavirus-the-harmful-hunt-for-covid-19s-patient-zero>.
3. Woods A. *Shrimp vendor at Wuhan market may be coronavirus 'patient zero'*. The New York Post, 27 March 2020. Available from: <https://nypost.com/2020/03/27/shrimp-vendor-at-wuhan-market-may-be-coronavirus-patient-zero/>.
4. Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, Ren R, Leung KSM, Lau EHY, Wong JY, Xing X, Xiang N, Wu Y, Li C, Chen Q, Li D, Liu T, Zhao J, Liu M, ... Feng J. Early transmission dynamics in Wuhan, China, of novel corona virus-infected pneumonia. *New England Journal of Medicine* 2020; 382(13): 1199-1207. DOI:10.1056/NEJMoa2001316.
5. Epidemiology Unit. *Fact sheet: Corona*. Epidemiology Unit, Ministry of Health. Available from: http://www.epid.gov.lk/web/index.php?option=com_content&view=article&id=146&Itemid=459&lang=en.
6. Cohen J. *Wuhan seafood market may not be source of novel virus spreading globally*. Science, 26 January 2020. DOI: 10.1126/science.abb0611.
7. Kelly M & Cahlan S. *Was the new coronavirus accidentally released from a Wuhan lab? It is doubtful*. Washington Post, 1 May 2020. Available from: <https://www.washingtonpost.com/politics/2020/05/01/was-new-coronavirus-accidentally-released-wuhan-lab-its-doubtful/>.
8. Huifeng H. *Coronavirus did not originate in Wuhan seafood market, Chinese scientists say*. South China Morning Post, 23 February 2020. Available from: <https://www.scmp.com/news/china/science/article/3051981/coronavirus-did-not-originate-wuhan-seafood-market-chinese>.
9. Andersen KG, Rambaut A, Lipkin WI, Holmes EC & Garry RF. The proximal origin of SARS-CoV-2. *Nature Medicine* 2020; 26(4): 450-452. DOI: 10.1038/s41591-020-0820-9.
10. Wu F, Zhao S, Yu B, Chen YM, Wang W, Song ZG, Hu Y, Tao ZW, Tian JH, Pei YY, Yuan ML, Zhang YL, Dai FH, Liu Y, Wang QM, Zheng JJ, Xu L, Holmes EC, Zhang YZ. A new coronavirus associated with human respiratory disease in China. *Nature* 2020; 63(3): 461-462. DOI: 10.1038/s41586-020-2008-3.
11. Nishiura H, Linton NM & Akhmetzhanov AR. Initial cluster of novel coronavirus (2019-nCoV) infections in Wuhan, China is consistent with substantial human-to-human transmission. *Journal of Clinical Medicine* 2020; 9(2): 488-490. DOI: 10.3390/jcm9020488.
12. Forster P, Forster L, Renfrewb C & Forster M. Phylogenetic network analysis of SARS-CoV-2 genomes. *Proceedings of the National Academy of Sciences of the United States of America PNAS*, 28 April 2020; 117(17): 9241-9243. DOI: 10.1073/pnas.2004999117.
13. WHO. *Coronavirus disease (COVID 19) advice for the public: myth busters*. Geneva: World Health Organization, 2020. Available from: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/advice-for-public/myth-busters>.
14. The Guardian. *Trump claims to have evidence coronavirus started in Chinese lab but offers no details*. The Guardian, 30 April 2020. Available from: <https://www.theguardian.com/us-news/2020/apr/30/donald-trump-coronavirus-chinese-lab-claim>.
15. BBC News. *Coronavirus: Trump attacks 'China-centric' WHO over global pandemic*. BBC News, 8 April 2020. Available from: <https://www.bbc.com/news/world-us-canada-52213439>.
16. Handley E & Walsh M. *What happens if the US stops funding the WHO in the middle of the coronavirus pandemic?* ABC News, 16 April 2020. Available from: <https://www.abc.net.au/news/2020-04-16/coronavirus-who-explainer-what-does-trump-funding-decision-mean/12151080>.
17. Husain J. *China unofficially raises concerns over its citizens facing discrimination in Sri Lanka*. News Asia, 1 February 2020. Available from: <https://newsin.asia/china-unofficially-raises->

- concern-over-its-citizens-facing-discrimination-in-sri-lanka/.
18. Daily News. *Discrimination of Chinese nationals over coronavirus outbreak unfair: SLCFA*. Daily News, 6 February 2020. Available from: [https://www.dailynews.lk / 2020/02/06/local/210546/discrimination-chinese-nationals-over-corona virus-outbreak-unfair-slcfa](https://www.dailynews.lk/2020/02/06/local/210546/discrimination-chinese-nationals-over-corona-virus-outbreak-unfair-slcfa).
 19. University of Sri Jayewardenepura. USJ dengue research scientists sequenced SARS-CoV2 (COVID-19) viruses for the first time in Sri Lanka. USJ, 23 April 2020. Available from: [https:/ /www.sjp.ac.lk/medical/usj-dengue-research-scientists-sequenced-sars-cov2-coivd19-viruses-first-time-sri-lanka/](https://www.sjp.ac.lk/medical/usj-dengue-research-scientists-sequenced-sars-cov2-coivd19-viruses-first-time-sri-lanka/).