Journal of Infection 80 (2020) e28–e29

Contents lists available at ScienceDirect

Journal of Infection

journal homepage: www.elsevier.com/locate/jinf

Letter to the Editor

Emergence of SARS-like coronavirus in China: An update

Dear Editor,

Recently, the emergence of the novel coronavirus (SARS-CoV-2) that causes coronavirus disease 2019 (COVID-19) in Wuhan, China, has raised great concern all over the world and poses serious threat to global public health, as reported earlier in this journal [1,2]. Before 2019, only six CoVs were reported to infect human beings: 1) HCoV-229E, HCoV-OC43, HCoV-NL63 and HKU1, associated with mild upper respiratory diseases; 2) SARS-CoV, causing an outbreak in 2002, and MERS-CoV, causing an outbreak in 2012, associated with infective manifestations in the lower respiratory tract and severe respiratory syndrome. COVID-19 outbreak in late December 2019 is the third coronavirus-related epidemic. The epidemic is currently in its full swing with the infected human beings accelerating. In the present report, we have comprehensively summarized the spread, prevention, control and research progress pertaining to the alarming epidemic.

The SARS-CoV-2 was first detected in Wuhan, central China. With the migration of population, it is spreading rapidly from Wuhan to all provinces of China. The number of confirmed cases has been sharply rising since January 2020. At present, 98,192 infected cases have been diagnosed (WHO, Coronavirus disease 2019 Situation Report 46, March 6). It is extremely concerning to note that the number of human infections has already surpassed the infection frequency of SARS till date (Table 1). In addition to China, this virus has also been detected in 88 other countries. WHO raised the global COVID-19 risk to its highest level on Feb 28, 2020 (WHO, Coronavirus disease 2019 Situation Report 39). The SARS-CoV-2 has been more contagious but less deadly than SARS-CoV so far (Table 1).

Table 1
Pathogenicity of the three coronavirus.

Virus	Year identified	Cases of human infections	Number of deaths	Fatality rate (%)
SARS-CoV	2002	8096	744	9.19%
MERS-CoV	2012	2494	858	34.40%
SARS-CoV-2	2019	98,192	3380	3.44%

SARS-CoV-2 infection generally exhibits milder symptoms as compared to SARS and MERS related infections. Furthermore, incubation period of SARS-CoV-2 infection (usually 1–14 days) is longer than SARS infection (usually 1–7 days). Considering such facts, it is evident that the patients infected with SARS-CoV-2 do not receive early diagnosis and health care, thus, unknowingly spread the virus through contacts. The spread of infection, thus, remains unnoticed and unattended initially. Human-to-human transmission of the virus has already been confirmed [3,4]. In addition, millions of people in China have already travelled over the course of the Spring Festival [1]. These multiple factors have lead to a rapid spread of the virus and resulted in a large number of infected cases. The decision to shut down Wuhan and its 12 neighboring cities, extend Lunar New Year holiday and postpone the start of the new semester at schools et al., promises to greatly slow the spread of the intimidating virus.

SARS-CoV-2 infection has displayed clinical symptoms that greatly resemble SARS-CoV infection [5]. Most patients with confirmed infection of COVID-19 have been reported to exhibit mild-to-severe respiratory illness (symptoms include fever, cough, shortness of breath et al.,), while 2% of the cases have also showed symptoms of gastrointestinal disorders, including diarrhea [6]. Therefore, in addition to air transmission and contact transmission, we should also pay attention to the fecal and sewage pollution. A lesson has been learned is Amoy Gardens in Hong Kong, where an index patient used toilet with defective sewage system (the U shaped water trap connected to most of the floor drains were probably dry and might not have been functioning properly), lead to a count of 321 SARS infection cases [7].

Both SARS-CoV and MERS-CoV are believed to originate in bats, and these infections have been transmitted directly to humans from market civets and dromedary camels, respectively [8]. The SARS-CoV-2 has been reported to display an identity of 86.9–88.0% at the nucleotide sequence level with bat SARS-like CoV genomes [9,10]. Although bats have been suggested to be the reservoir of this virus, the question that how widespread is the virus in its reservoir, still remains obscure and unanswered. Furthermore, considering the fact that the disease emerged in Wuhan, central China, in the winters when the bats hibernate in the low temperatures, the event of a direct viral transmission to humans from bats appears impossible. In addition, it is still ambiguous whether the outbreak has resulted from a single spillover event (like the SARS) or from a series of repeated crossing over of the virus across species barriers (like MERS). Alarmingly, if the virus repeated spillover from its reservoir, disease control would be a challenging task. Extensive research needs to be carried out to identify and unravel the virus's zoonotic origin to prevent further events of viral spillover at the animal-human interface.

Acknowledgments

This work was supported by the National Natural Science Foundation of China (Grant No. 31822056), Fund for the key program Research Group of the Department of Education of Guangdong Province (2019KZDXM004), the Guangdong Science and Technology Innovation Leading Talent Program (2019TX05N098), and the 111 Project (D20008).

https://doi.org/10.1016/j.jinf.2020.03.010

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Accepted 10 March 2020