

## COMMENTARY

## Global health concerns stirred by emerging viral infections

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Emerging viral infections continue to pose a major threat to global public health. In 1997, a highly pathogenic avian influenza A (H5N1) virus was found to directly spread from poultry to humans unlike previously reported transmission routes of human-to-human and livestock-to-human, stirring a grave concern for a possible influenza pandemic.<sup>1</sup> Several other avian influenza A virus subtypes (H7N9, H9N2, and H7N3) were also associated with human disease, raising an alarm that all subtypes of influenza A virus circulating in domestic and wild birds and livestock can potentially spill over to humans, resulting in pandemics.<sup>2–4</sup> In 1999, a newly emerged paramyxovirus termed Nipah virus was identified as the cause of a severe encephalitis outbreak occurred in Malaysia and Singapore.<sup>5</sup> Soon after, the outbreak of severe acute respiratory syndrome (SARS) happened during 2002 to 2003 in China was caused by a novel coronavirus (CoV) designated SARS-CoV, spreading to 37 countries and resulting in more than 8000 infections and 774 deaths (9.6% mortality rate).<sup>6</sup> More recent years have witnessed the emergence of several other important viral diseases, including a pandemic influenza caused by a swine H1N1 influenza A virus in 2009,<sup>7</sup> the Middle East respiratory syndrome (MERS) caused by a new deadly (>30% mortality) MERS-CoV in 2012,<sup>8</sup> the outbreak of a severe fever with thrombocytopenia syndrome (SFTS) resulted from the infection of a previously unrecognized SFTS bunyavirus in 2010,<sup>9</sup> the Ebola outbreak in West Africa during 2014 to 2016,<sup>10</sup> and the microcephaly crisis associated with Zika virus infection in 2015.<sup>11</sup> Clearly, emerging and re-emerging viral pathogens constantly pose a threat to public health.

The most recent outbreak of viral pneumonia in the city of Wuhan, China, which started in the middle of December, 2019 and now is spreading to many places in China as well as to many other countries and regions around the world, serves as an important reminder of our vulnerability to emerging viral infections. Now tens of thousands of people have been infected with the newly identified CoV termed 2019-nCoV. The airborne and person-to-person spread of the 2019-nCoV have been the major routes of transmissions, as demonstrated by new infections among family members, health care providers, and

communities. In this issue, several papers provide detailed clinical and epidemiological information about this new viral pneumonia outbreak in Wuhan, China.<sup>12–15</sup>

In the last few weeks, rapid progresses have been made in the identification of viral etiology, isolation of infectious virus, development of diagnostic approaches, and antiviral drug discovery and development, thanks to many dedicated scientists in China and also technology and infrastructure investment made by the Chinese government in recent years since SARS outbreak in 2003. The novel 2019-nCoV was identified from patient samples by high-throughput sequencing of the viral RNA genome. More importantly, infectious CoV was also isolated and was found to exhibit morphological characteristics of a typical CoV as determined by electronic microscopy. The availability of viral RNA genome sequence has fostered the development of new tests based on the reverse-transcription polymerase chain reaction (RT-PCR) technology. RT-PCR kits have been developed and are currently being used for diagnosis of the 2019-nCoV infection. In this issue, Zhang et al review the recent advances in the detection of emerging and re-emerging viral infections.<sup>16</sup> A minireview by Chen et al<sup>17</sup> describes the properties of CoV and the underlying molecular mechanism of viral replication and pathogenesis. In another minireview, Li et al provide an overview on the host immune response to CoV infection<sup>18</sup> Interestingly, Ji et al<sup>19</sup> have performed a sequence analysis suggesting that the 2019-nCoV originated from a bat CoV, which was confirmed by others.<sup>20,21</sup> The question arises whether adaptation of the 2019-nCoV in humans enhances viral virulence and/or its spread among populations.

Although rapid achievements were accomplished within such a short period of time, there are still many important and fundamental questions remained to be answered. Further characterization of the isolated virus in cell culture and animal models will provide valuable information as to the underlying molecular mechanism of viral replication and pathogenesis. More significantly, identification of animal reservoir and intermediate hosts for the 2019-nCoV is critical for intervention and prevention of the outbreak. It is of paramount importance to develop sensitive and

reliable diagnostic methods for rapid detection of viral infection, including immunoassay for quantification of virus-specific antibodies. The ultimate control of emerging viral infections requires discovery and development of effective antiviral drugs and vaccines, which may take months or even years. However, it is possible that some of the licensed antiviral drugs for treatment of other viral infections may also have activity against the 2019-nCoV, as previously reported for MERS-CoV.<sup>22</sup> It is worthwhile to evaluate some of the existing antiviral drugs in cell culture using the isolated 2019-nCoV. Any resulting drug inhibiting the 2019-nCoV can be used for the treatment of 2019-nCoV-infected patients. More importantly, isolation and cloning of virus-neutralizing antibodies from recovered patients will immediately impact on the treatment and prevention of 2019-CoV infection.

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## REFERENCES

- Claas EC, Osterhaus AD, van Beek R, et al. Human influenza A H5N1 virus related to a highly pathogenic avian influenza virus. *The Lancet*. 1998;351:472-477.
- Gao R, Cao B, Hu Y, et al. Human infection with a novel avian-origin influenza A (H7N9) virus. *N Engl J Med*. 2013;368:1888-1897.
- Peiris M, Yuen K, Leung C, et al. Human infection with influenza H9N2. *The Lancet*. 1999;354:916-917.
- Tweed SA, Skowronski DM, David ST, et al. Human illness from avian influenza H7N3, British Columbia. *Emerging Infect Dis*. 2004;10:2196-2199.
- Chua KB. Nipah virus: a recently emergent deadly paramyxovirus. *Science*. 2000;288:1432-1435.
- Fouchier RAM, Kuiken T, Schutten M, et al. Aetiology: Koch's postulates fulfilled for SARS virus. *Nature*. 2003;423:240.
- Vijaykrishna D, Poon LLM, Zhu HC, et al. Reassortment of pandemic H1N1/2009 influenza A virus in swine. *Science*. 2010;328:1529.
- Zumla A, Hui DS, Perlman S. Middle East respiratory syndrome. *The Lancet*. 2015;386:995-1007.
- Yu XJ, Liang MF, Zhang SY, et al. Fever with thrombocytopenia associated with a novel bunyavirus in China. *N Engl J Med*. 2011;364:1523-1532. <https://doi.org/10.1056/NEJMoa1010095>
- Baseler L, Chertow DS, Johnson KM, Feldmann H, Morens DM. The pathogenesis of Ebola virus disease. *Annu Rev Pathol: Mech Dis*. 2017;12:387-418.
- Bogoch II, Brady OJ, Kraemer MUG, et al. Anticipating the international spread of Zika virus from Brazil. *The Lancet*. 2016;387:335-336.
- Lu H, Stratton CW, Tang YW. Outbreak of pneumonia of unknown etiology in Wuhan China: the mystery and the miracle. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25678>
- Wang W, Tang JM, Wei FQ. Updated understanding of the outbreak of 2019 novel coronavirus (2019-nCoV) in Wuhan, China. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25689>
- Kofi Ayithey F, Dzuovor C, Kormla Ayithey M, et al. Updates on Wuhan 2019 Novel Coronavirus Epidemic. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25695>
- Li XG, Zai JJ, Wang XM, Li Y. Potential of large 'first generation' human-to-human transmission of 2019-nCoV. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25693>
- Zhang N, Wang L, Deng X, et al. Recent advances in the detection of respiratory virus infection in humans. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25674>
- Chen Y, Liu QY, Guo DY. Emerging coronaviruses: genome structure, replication, and pathogenesis. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25681>
- Li G, Fan YH, Lai YN, et al. Coronavirus infection and immune responses. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25685>
- Ji W, Wang W, Zhao XF, et al. Homologous recombination within the spike glycoprotein of the newly identified coronavirus may boost cross-species transmission to humans. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25682>
- Benvenuto D, Giovanetti M, Ciccozzi A, et al. The 2019-new coronavirus epidemic: evidence for virus evolution. *J Med Virol*. 2020. <https://doi.org/10.1002/jmv.25688>
- Zhou P, Yang X, Wang X, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*. 2020. <https://doi.org/10.1038/s41586-020-2012-7>
- Cong Y, Hart BJ, Gross R, et al. MERS-CoV pathogenesis and antiviral efficacy of licensed drugs in human monocyte-derived antigen-presenting cells. *PLOS One*. 2018;13:e0194868.

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