EDITORIAL

Novel coronavirus 2019, an emerging public health emergency

At the end of December 2019, local health officials in the Chinese city of Wuhan, Hubei province reported a cluster of 27 cases of 'pneumonia of unknown cause'. The clinical symptoms of cases included fever, headache, difficulty breathing and pneumonia, with lung invasive lesions on chest radiography (Wang, Horby, Hayden, & Gao, 2020). In an initial case series of patients admitted to hospital in Wuhan, 6 of 41 (15%) died (Huang et al., 2020). Reported cases were epidemiologically linked to a wholesale seafood and animal market in the city. In January, the first death was reported, and the aetiology was identified as a new coronavirus, '2019-nCoV' (also called 'Wuhan coronavirus'). It has been retrospectively concluded that there was evidence of human-to-human transmission as early as mid-December (Li et al., 2020), and based on modelling studies, it has been estimated that 75,815 individuals (95% credible interval 37,304–130,330) had already been infected in Wuhan as of 25 January (Wu, Leung, & Leung, 2020).

By the end of January, nearly 10,000 confirmed cases and more than 200 deaths had been reported, and 2019-nCoV had spread to at least 19 other countries (https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports/), as well as most parts of China (including major cities such as Beijing, Shanghai and Guangzhou, predicted to have already been seeded by many imported cases; localized epidemics perhaps lagged Wuhan by only 1–2 weeks; Wu et al., 2020). A public health emergency of international concern was declared by the World Health Organization, at the end of January, based on human-to-human spread of the virus and the extensive movement of people within and from China during the intense Chinese New Year travel period. The Emergency Committee (International Health Regulations) has advised that to interrupt virus spread, countries need to detect disease early, isolate and treat cases, trace contacts and promote social distancing measures commensurate with the risk (https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports/).

Isolates of 2019-nCoV to date are morphologically identical to coronaviruses under the electron microscope. Coronaviruses are a large family of viruses which contain several viruses lethal to humans including severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS). The *Coronavirinae* family consists of four genera, *Alphacoronavirus*, *Betacoronavirus*, *Gammacoronavirus* and *Deltacoronavirus* (Chen, Liu, & Guo, 2020). Based on genetic properties, 2019-nCoV belongs to the genus *Betacoronavirus*. In a positive sign of research collaboration, 2019-nCoV sequences are being shared to enable analysis to generate insights into this novel pathogen (https://gisaid.org/CoV2020).

Phylogenic analysis has shown that 2019-nCoV isolates cluster within the group of SARS or SARS-like coronaviruses, but are distinctive from MERS coronaviruses (Chan et al, 2020). They also have a close phylogenic relationship with bat coronaviruses, which might indicate a bat origin of the viruses (Chan et al, 2020). However, intermediate hosts—such as bamboo rat and badger—might be important in the transmission cycle since several early 2019-nCoV cases were vendors in the market where they could have been exposed to wild animals that are sold in this market. Epidemiologic analysis of the first 425 confirmed cases in Wuhan has indicated that most (55%) with onset before January 1 were linked to this market in Wuhan, compared with 8.6% of the subsequent cases (Li et al., 2020).

One research group recently reported 2019-nCoV having recombination between bat coronavirus and an origin-unknown coronavirus in the viral spike (S) glycoprotein, the major viral protein that recognizes cell surface receptors and determines host range (Ji, Wang, Zhao, Zai, & Li, 2020). By analysing the released 2019-nCoV sequences and comparing among different animal species with relative synonymous codon usage (RSCU) analysis, the authors suggested that snake is the most probable wildlife animal reservoir for 2019-nCoV through recombination within spike glycoprotein. Currently, there is no report of 2019-nCoV having been isolated from animal species, but this is a topic of much speculation.

The initial 2019-nCoV infections were apparently transmitted from wild animals to human. With the increased number of human infection cases and extended geographical distribution, human-to-human transmission of 2019-nCoV was confirmed (Chan et al., 2020). Although the viruses were successfully isolated from cells, the exact infection mechanisms remain unclear. The computational remodelling of 2019-nCoV S-protein, the virus protein binding to host receptors, revealed its high tendency to interact with human ACE2 receptor (Xu et al., 2020), which could explain the high efficiency of transmission via respiratory droplets between close contacts.

The numbers of reported 2019-nCoV infections have increased rapidly, and many countries have reported infections for the first time. This indicates the disease has broad geographical, security and political implications. Whilst the control of an infectious respiratory disease relies on established principles of early detection, isolation, hygiene and social distancing, we face many gaps in our knowledge of this new pathogen such as its source, immunity in exposed individuals, the potential for vaccine development and the accuracy of diagnosis. How this pathogen emerged and the drivers of that emergence will be the subject of intense research in the months and years to come. With the examples of SARS and MERS—in which wildlife such as bats have been identified as a reservoir—2019-nCoV is likely

to become another example of an emerging zoonosis. Recent estimates of the basic reproductive number of 2019-nCoV include 2.2 (95% confidence interval, 1.4–3.9) and 2.68 (95% credible interval 2.47–2.86) (Li et al., 2020; Wu et al., 2020). Although these are less than that estimated for SARS (3.0), it highlights the challenge for control given that spread to major, densely populated Chinese cities has already occurred (Li et al., 2020; Wu et al., 2020), and the strain on resources with an estimated epidemic doubling time of 6.4 days (95% credible interval 5.8–7.1) (Wu et al., 2020). It can be assumed that what began as a point source epidemic in Wuhan quickly has become an extended propagating pandemic. Of concern are super-spreading events, which are yet to be identified (Li et al., 2020).

To summarize, what we have learnt about 2019-nCoV to date:

- A novel betacoronavirus (SARS-like coronavirus) likely from a wildlife source (perhaps bats via one or more intermediate species) caused an initial outbreak in the city of Wuhan in early to mid-December 2019;
- This virus was capable of human-to-human transmission, perhaps due to its S-protein affinity for the human ACE2 receptor;
- Human-to-human transmission occurred during mid- to late-December, resulting in widespread dissemination of infected individuals throughout China and also to many other countries;
- Although apparently not highly contagious, reducing the basic reproductive number of 2019-nCoV from 2–3 to < 1, given its wide dissemination, will require vigorous and early disease detection, isolation of infectious individuals and strenuous promotion of social distancing measures;
- The ultimate origin of this novel coronavirus awaits investigation and confirmation.

The emergence of zoonotic pathogens in human populations involves a complex causal web, with both proximal and distant drivers such as urbanization, climate change, global trade and the movement of people, ecosystem destruction and the bushmeat trade. Anticipating emergence is extraordinarily challenging and relies on sustained surveillance, data collection and novel approaches to data analysis. There are numerous reasons to invest in such research, from influenza to Ebola to SARS to 2019-nCoV. *Transboundary and Emerging Diseases* is committed to publishing high-quality research on 2019-nCoV.

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