Data sharing and outbreaks: best practice exemplified

The current outbreak of the 2019 novel coronavirus (2019-nCoV) is yet another example of the importance of infections at the animal–human interface, and the concerns that arise from the emergence of a newly identified organism as it spreads through human populations and across national and international borders.

At the beginning of an outbreak such as this, readily available information is important to begin the assessment necessary to understand the risks and begin outbreak containment activities. This information includes initial reports from the outbreak site and from laboratories supporting the initial investigation, and information obtained from previous outbreaks with similar organisms.

But what is not known is of equal importance. Information is required that will help refine the risk assessment as the outbreak continues and ensure that patients are managed in the best possible way. This information includes routes of transmission and transmissibility, the natural history of infection in humans, the populations at risk, the successful clinical practices that are being used to manage patients, the laboratory information needed to diagnose patients, and the genetic sequence information used to assess viral stability. Much of this information is emerging in real time, challenging our understandings and nonetheless refining our responses.

The two Articles that have been published in *The Lancet* provide some of this information: the study by Jasper Fuk-Woo Chan and colleagues[1] of a family cluster of six people who returned to their homes in Shenzhen, Guangdong province, a coastal area of south China bordering Hong Kong, with infection after having travelled to Wuhan, Hubei province, China; and the study by Chaolin Huang and colleagues[2] of 41 people confirmed to have infection and admitted to hospital in Wuhan, where the outbreak is thought to have begun. These early but important Articles include contact information and estimates of incubation periods, the ages of those who are infected and their clinical manifestations, laboratory and radiological information, and information about the contacts that led to their infection.

The picture these two manuscripts paint is of a disease with a 3–6 day incubation period and insidious onset with fever, cough, and myalgia—with or without diarrhoea or shortness of breath, or both. Laboratory findings include leucopenia, and radiological findings of bilateral ground-glass opacities.[1,2] Some patients have mild disease, but older patients (aged >60 years) progress to severe acute respiratory distress syndrome, and a need for intubation and intensive care. And some infections terminate in death, but a case-fatality rate cannot be determined.

These Articles also confirm that many patients had contact with the market that is the suspected point source of infection,[2] while others did not but did have had contact with patients in their family cluster or elsewhere.[1] Although these reports confirm person-to-person transmission, the means of transmission and the transmissibility cannot be hypothesised from the information published.

Rapid peer review and publication online permits the authors to claim credit, important for their academic standing, while at the same time provides peer-reviewed information urgently needed to continue to refine the risk assessment. Such rapidly shared scientific information can be used to provide real-time guidance for epidemiologists working to contain the outbreak, clinicians managing patients, and modellers helping to understand potential future directions and the possible effectiveness of various interventions.

The information in these Articles are pieces of the jigsaw puzzle that are being fit together by WHO as it continues to collect official reports and informal information from its virtual groups of national clinicians, epidemiologists, and virologists working at outbreak sites and brought together from around the world. When pieced together, these emerging data will permit regular refinement of the risk assessment, and real-time guidance to countries for patient management and outbreak control, including the best case definition for use in surveillance around outbreak sites and elsewhere.

Early official information from the Chinese Government about the outbreak in Wuhan suggested that the source of the outbreak was being confirmed, that patients were being isolated, that tracing of contacts of known patients were being identified and observed for fever, and that no health workers had been infected.[3] The cause of the outbreak was

rapidly identified by genetic sequencing as a novel coronavirus. Risk assessment at that time was guarded but suggested that the outbreak was more like that caused by the Middle East respiratory syndrome (MERS) coronavirus than the severe acute respiratory syndrome (SARS) coronavirus.

However, this information was from what now appears to be first-generation cases from a point source, but at the time it seems that a second generation, and perhaps a third generation, of cases was already reported in the incubation period, and this generation appears to have included health workers.

Health worker infections are an ominous finding in any emerging infection. Front-line health workers can be initially at risk and infected when they examine and treat patients who present with a respiratory infection; if handwashing or other infection prevention and control measures are not in place, these health workers are at great risk of infection and become the inadvertent carriers to patients who are in hospital for other diseases and treatments, family members, and the community.

Early in the SARS coronavirus outbreak, frontline health workers became infected, which amplified transmission to patients in hospitals where outbreaks were occurring.[4] Early evidence from the initial MERS outbreaks suggested that health workers were likewise being infected, but that their infections were less severe than those of patients in hospitals who became infected and had comorbidities such as diabetes or chronic respiratory disease.[5]

Today, the epidemiology of both SARS and MERS viruses is mostly understood, and the same will be true for the current outbreak of 2019-nCoV if data continue to be freely shared and used to provide real-time guidance. These Articles and others being rapidly disseminated and shared will have a major role in assuring that this global collaboration occurs.

David L Heymann
david.heymann@lshtm.ac.uk

Infectious Disease Epidemiology, London School of Hygiene & Tropical Medicine, London WC1E 7HT, UK

1   Chan JF-W, Yuan S, Kok, K-H, 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; published online Jan 24. https://doi.org/10.1016/S0140-6736(20)30154-9.

2   Huang C, Wang Y, Li X, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet* 2020; published online Jan 24. https://doi.org/10.1016/S0140-6736(20)30183-5.

3   Outbreak of SARS-like pneumonia being investigated in China. The Japan Times, Dec 31, 3019. https://www.japantimes.co.jp/news/2019/12/31/asia-pacific/science-health-asia-pacific/outbreak-sars-like-pneumonia-investigated-china/#.XijKzsj7TD4 (accessed Jan 23, 2020).

4   Heymann DL, Rodier G. SARS: lessons from a new disease. In: Knobler S, Mahmoud A, Lemon S, et al, eds. Learning from SARS: preparing for the nest disease outbreak: workshop summary. Washington, DC, USA: National Academic Press, 2004.

5   Petersen E, Hui DS, Perlman S, Zumla A. Middle East respiratory syndrome—advancing the public health and research agenda on MERS-lessons from the South Korea outbreak. *Int J Infect Dis* 2015; **36:** 54–55.