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countries or regions (appendix). With the exception of Australia, Hong Kong, and Italy, the CSSE at Johns Hopkins University has reported newly infected countries ahead of WHO, with Hong Kong and Italy reported within hours of the corresponding WHO situation report.

Given the popularity and impact of the dashboard to date, we plan to continue hosting and managing the tool throughout the entirety of the COVID-19 outbreak and to build out its capabilities to establish a standing tool to monitor and report on future outbreaks. We believe our efforts are crucial to help inform modelling efforts and control measures during the earliest stages of the outbreak.

We declare no competing interests.

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For the **repository of COVID-19 patient data** see https://tinyurl. com/s6qsq5y



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For the Chinese translation see Online for appendix 1

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See Online for appendix 2

Published Online February 19, 2020 https://doi.org/10.1016/ \$1473-3099(20)30119-5 ed within ding of epidemiological information ng WHO is important to understand transmissibility, risk of geographic spread, d impact routes of transmission, and risk factors we plan for infection, and to provide the baseline for epidemiological modelling entirety that can inform planning of response and containment efforts to reduce the burden of disease. Furthermore, itor and detailed information provided in real aks. We time is crucial for deciding where to prioritise surveillance. d control Line list data are rarely available

openly in real time during outbreaks. However, they enable a multiplicity of analyses to be undertaken by different groups, using various models and assumptions, which can help build consensus on robust inference. Parallels exist between this and the open sharing of genomic data.²

The availability of accurate and

robust epidemiological, clinical, and laboratory data early in an epidemic

is important to quide public health

decision-making.1 Consistent recor-

We have built a centralised repository of individual-level information on patients with laboratory-confirmed COVID-19 (in China, confirmed by detection of virus nucleic acid at the City and Provincial Centers for Disease Control and Prevention). including their travel history, location (highest resolution available and corresponding latitude and longitude), symptoms, and reported onset dates, as well as confirmation dates and basic demographics. Information is collated from a variety of sources, including official reports from WHO, Ministries of Health, and Chinese local, provincial, and national health authorities. If additional data are available from reliable online reports. they are included. Data are available openly and are updated on a regular basis (around twice a day).

We hope these data continue to be used to build evidence for planning, modelling, and epidemiological studies to better inform the public, policy makers, and international organisations and funders as to where and how to improve surveillance, response efforts, and delivery of resources, which are crucial factors in containing the COVID-19 epidemic.

The epidemic is unfolding rapidly and reports are outdated quickly, so it will be necessary to build computational infrastructure that can handle the large expected increase in case reports. Data sharing will be vital to evaluate and maintain accurate reporting of cases during this outbreak.³

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A family cluster of SARS-CoV-2 infection involving 11 patients in Nanjing, China

Human infection caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has become a global health concern.^{1,2} Currently, human-to-human transmission of the virus accounts for most infections worldwide.³ We report a family cluster of SARS-CoV-2 infection involving 11 patients in Nanjing, China.

The detailed timeline of exposure for the 11 confirmed patients is presented in the appendix 2. The index patient travelled to Nanjing on Jan 21, 2020, from Xiaogan (about 70 km from Wuhan), and switched trains in Wuhan. After arriving in Nanjing, she stayed with two of her

is spreading rapidly across China, and as of Feb 16, 2020, had been reported in 26 countries globally. sisters (patients 1 and 2) and her mother (patient 3) at their family home. She had a family dinner with her mother, two sisters, and her brother (patient 4) on Jan 21. The index patient had another family dinner with eight relatives on Jan 23. She had been well without any symptoms of infection but started to have a fever and cough on Jan 28. She went to Zhejiang on Jan 24, where she tested positive for SARS-CoV-2 infection on Jan 29. No one in the family cluster had travelled to Wuhan in the previous 2 weeks except for the index patient. Three patients (patients 1-3) who lived together with the index patient and three relatives (patients 4, 6, and 7) who attended the dinner with the index patient on Jan 23 were positive for SARS-CoV-2 infection thereafter. Furthermore, patient 5 who lived with patient 4 and had no direct contact with the index patient was diagnosed with SARS-CoV-2 infection on Jan 30. On Jan 24, two patients (patients 6 and 7) who had been well without any symptoms attended another family dinner with 13 relatives. Three of the relatives (patients 8-10) were diagnosed with SARS-CoV-2 infection within 2 weeks.

Human-to-human transmission can occur among close contacts of SARS-CoV-2.³ However, the family cluster of patients we describe provides evidence that asymptomatic people can be potential sources of SARS-CoV-2 infection.

We obtained written informed consent from the patients and the case study was approved by the institutional ethics board of our hospital (Nanjing Drum Tower Hospital, The Affiliated Hospital of Nanjing University Medical School). We declare no competing interests.

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Outbreak investigation for COVID-19 in northern Vietnam

Two Vietnamese adults returned to their home province of Vinh Phuc in northern Vietnam on Jan 17, 2020, from Wuhan, China, where they had been living since Nov 15, 2019, for a business trip. They presented with mild respiratory symptoms to their local health facilities at 4 days and 8 days, respectively, after arrival in Vinh Phuc. Both individuals were initially placed into respiratory isolation in hospital. Case 1 tested positive for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the causative organism of coronavirus disease 2019 (COVID-19), on Jan 30, 2020, and remained in isolation until recovery. Case 2 was discharged from isolation in hospital after having one negative test result on Jan 28 (11 days after returning from Wuhan). Following discharge, the patient attended a family social function. 2 days later, she was readmitted after a second nasal swab for SARS-CoV-2 taken during her time in hospital was reported as positive.

Screening of 79 individuals who had been in contact with these two patients (namely, family members in the same household and anyone who had been within 2 m of them) was initiated on Jan 31. Six individuals from the same work team, who had also travelled from Wuhan on Jan 17, were isolated, and four of them tested positive for SARS-CoV-2 (cases 3, 4, and 8 in Vinh Phuc, and one case from another province). Five secondary cases were diagnosed within the social network of case 2. These included three household members (cases 6, 7, and 11) and two people who had attended the social function (cases 5 and 9; appendix p 1). Four of these individuals reported mild respiratory symptoms; the remaining patient was asymptomatic (case 7) at the time of diagnosis.

See Online for appendix



On Feb 8, 2020, increased contact investigation was commenced among an additional 343 contacts of the people returning from China and the secondary cases diagnosed in Vinh Phuc, with screening of contacts of any suspected cases, and health workers providing direct medical care. This ongoing investigation includes monitoring of body temperature and suspected symptoms daily. Those with symptoms have been quarantined at health facilities and tested for SARS-CoV-2. This additional cascade screening identified one further case, a boy aged 3 months (case 10) who had brief exposure to case 5 (his grandmother, aged 42 years) on Jan 28. He developed respiratory symptoms 9 days later (cough and rhinorrhoea) and tested positive for SARS-CoV-2 on Feb 11 (appendix pp 2). On Feb 13, when case 11, the father of case 2 and living in the same household, was identified, the resident commune (Son Loi) of case 2 was locked down. Residents were advised to stay in the commune, and body temperature and suspected symptoms in all residents were monitored daily by communebased health workers reinforced by an external team. As of March 2, 18 days after case 11 was detected, no new cases have been identified.

In summary, this outbreak investigation identified six cases of COVID-19 resulting from transmission in Vietnam. One case occurred after secondary spread from a person

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