

About the Author

Mr. Lamson is Assistant Director of Special Projects in the Laboratory of Viral Diseases, Wadsworth Center, New York State Department of Health. His research focuses on molecular epidemiology and sequence analysis of adenoviruses and enteroviruses with next-generation whole-genome and di-deoxy Sanger sequencing.

References

1. Scott MK, Chommanard C, Lu X, Appelgate D, Grenz L, Schneider E, et al. Human adenovirus associated with severe respiratory infection, Oregon, USA, 2013–2014. *Emerg Infect Dis.* 2016;22:1044–51. <https://doi.org/10.3201/eid2206.151898>
2. Kajon AE, Ison MG. Severe infections with human adenovirus 7d in 2 adults in family, Illinois, USA, 2014. *Emerg Infect Dis.* 2016;22:730–3. <https://doi.org/10.3201/eid2204.151403>
3. Zhao S, Wan C, Ke C, Seto J, Dehghan S, Zou L, et al. Re-emergent human adenovirus genome type 7d caused an acute respiratory disease outbreak in southern China after a twenty-one year absence. *Sci Rep.* 2014;4:7365. <https://doi.org/10.1038/srep07365>
4. Killerby ME, Rozwadowski F, Lu X, Caulcrick-Grimes M, McHugh L, Haldeman AM, et al. Respiratory illness associated with emergent human adenovirus genome type 7d, New Jersey, 2016–2017. *Open Forum Infect Dis.* 2019;6:ofz017. <https://doi.org/10.1093/ofid/ofz017>
5. Bautista-Gogel J, Madsen CM, Lu X, Sakthivel SK, Froh I, Kamau E, et al. Outbreak of respiratory illness associated with human adenovirus type 7 among persons attending Officer Candidates School, Quantico, Virginia, 2017. *J Infect Dis.* 2019. <https://doi.org/10.1093/infdis/jiz060>
6. Lamson DM, Kajon A, Shudt M, Girouard G, St George K. Detection and genetic characterization of adenovirus type 14 strain in students with influenza-like illness, New York, USA, 2014–2015. *Emerg Infect Dis.* 2017;23:1194–7. <https://doi.org/10.3201/eid2307.161730>
7. Okada M, Ogawa T, Kubonoya H, Yoshizumi H, Shinozaki K. Detection and sequence-based typing of human adenoviruses using sensitive universal primer sets for the hexon gene. *Arch Virol.* 2007;152:1–9. <https://doi.org/10.1007/s00705-006-0842-8>
8. Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. *Mol Biol Evol.* 2013;30:2725–9. <https://doi.org/10.1093/molbev/mst197>
9. Shean RC, Makhous N, Stoddard GD, Lin MJ, Greninger AL. VAPiD: a lightweight cross-platform viral annotation pipeline and identification tool to facilitate virus genome submissions to NCBI GenBank. *BMC Bioinformatics.* 2019;20:48. <https://doi.org/10.1186/s12859-019-2606-y>
10. Kajon AE, Lamson DM, Bair CR, Lu X, Landry ML, Menegus M, et al. Adenovirus type 4 respiratory infections among civilian adults, northeastern United States, 2011–2015. *Emerg Infect Dis.* 2018;24:201–9. <https://doi.org/10.3201/eid2402.171407>

Address for correspondence: Daryl M. Lamson, Wadsworth Center – Viral Diseases, 120 New Scotland Ave, Albany, NY 12201-0509, USA; email: daryl.lamson@health.ny.gov

Risk for Transportation of Coronavirus Disease from Wuhan to Other Cities in China

Zhanwei Du,¹ Lin Wang,¹ Simon Cauchemez, Xiaoke Xu, Xianwen Wang, Benjamin J. Cowling, Lauren Ancel Meyers

Author affiliations: University of Texas at Austin, Austin, Texas, USA (Z. Du, L.A. Meyers); Institut Pasteur, Paris, France (L. Wang, S. Cauchemez); Dalian Minzu University, Dalian, China (X. Xu); Dalian University of Technology, Dalian (X. Wang); The University of Hong Kong, Hong Kong (B.J. Cowling); Santa Fe Institute, Santa Fe, New Mexico, USA (L.A. Meyers)

DOI: <https://doi.org/10.3201/eid2605.200146>

On January 23, 2020, China quarantined Wuhan to contain coronavirus disease (COVID-19). We estimated the probability of transportation of COVID-19 from Wuhan to 369 other cities in China before the quarantine. Expected COVID-19 risk is >50% in 130 (95% CI 89–190) cities and >99% in the 4 largest metropolitan areas.

In December 2019, a novel coronavirus, since named severe acute respiratory syndrome coronavirus 2, emerged in Wuhan, China (1), causing a respiratory illness that the World Health Organization has named coronavirus disease (COVID-19). On January 30, 2020, the World Health Organization declared the outbreak a public health emergency of international concern (2). By January 31, 2020, a total of 192 fatalities and 3,215 laboratory-confirmed cases had been reported in Wuhan; 8,576 additional cases were spread across >300 cities in mainland China, and 127 exported cases were reported in 23 countries spanning Asia, Europe, Oceania, and North America. The rapid global expansion, rising fatalities, unknown animal reservoir, and evidence of person-to-person transmission potential (3,4) initially resembled the 2003 SARS epidemic and raised concerns about global spread.

On January 22, 2020, China announced a travel quarantine of Wuhan and by January 30 expanded the radius to include 16 cities, encompassing a population of 45 million. At the time of the quarantine, China was already 2 weeks into the 40-day Spring Festival, during which residents and visitors make several billion trips throughout China to celebrate

¹These first authors contributed equally to this article.

the Lunar New Year (5). Considering the timing of exported COVID-2019 cases reported outside of China, we estimate that only 8.95% (95% credibility interval [CrI] 2.22%–28.72%) of persons infected in Wuhan by January 12 might have had COVID-19 confirmed by January 22. By limiting our estimate to infections occurring ≥ 10 days before the quarantine, we account for an ≈ 5 –6-day incubation period and 4–5 days between symptom onset and case detection (Appendix, <https://wwwnc.cdc.gov/EID/article/26/5/20-0146-App1.pdf>) (2–4,6). The low detection rate coupled with an average lag of 10 days between infection and detection (7) suggest that newly

infected persons who traveled out of Wuhan just before the quarantine might have remained infectious and undetected in dozens of cities in China for days to weeks. Moreover, these silent importations already might have seeded sustained outbreaks that were not immediately apparent.

We estimated the probability of transportation of infectious COVID cases from Wuhan to cities throughout China before January 23 by using a simple model of exponential growth coupled with a stochastic model of human mobility among 369 cities in China (Appendix). Given that $\approx 98\%$ of all trips taken during this period were made by train or car,

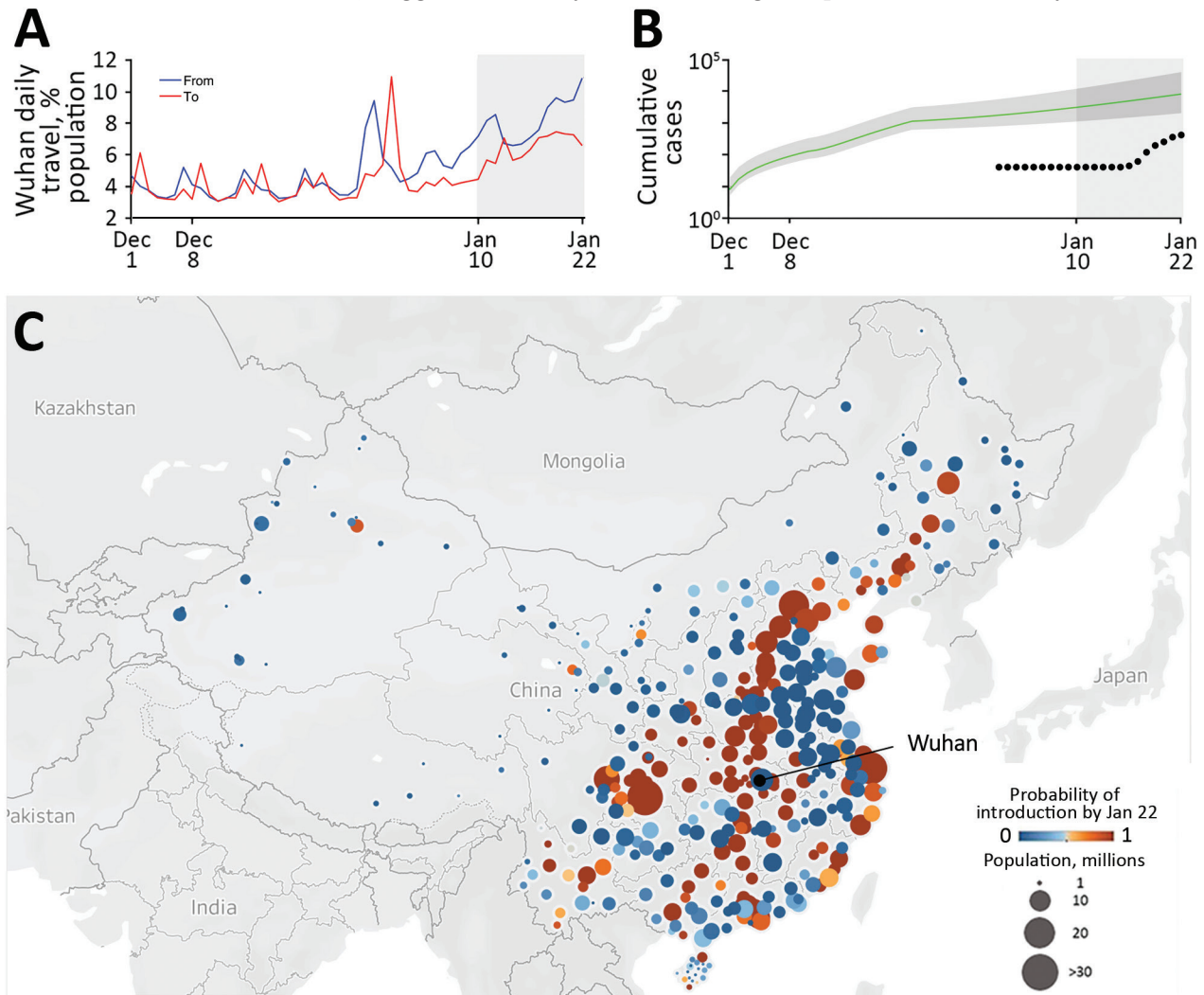


Figure. Risks for transportation of coronavirus disease (COVID-19) from Wuhan, China, before a quarantine was imposed on January 23, 2020. A) Daily travel volume to and from Wuhan, given as a percentage of the Wuhan population. Gray shading indicates the start of Spring Festival season on January 10, 2020, a peak travel period in China. B) Estimated and reported daily prevalence of COVID-19 in Wuhan. The green line and shading indicate model estimates of cumulative cases since December 1, 2019, with 95% credible interval bounds, assuming an epidemic doubling time of 7.31 days (95% credible interval 6.26–9.66 days). Black dots indicate cumulative confirmed case counts during January 1–22, 2020 (10). Gray shading at right indicates the start of Spring Festival season. C) Probability that ≥ 1 COVID-19 case infected in Wuhan traveled to cities in China by January 22, 2020. The 131 cities with a risk threshold $>50\%$ are indicated in shades of orange; 239 cities below that threshold are indicated in shades of blue. Map generated by using Mapbox (<https://www.mapbox.com>).

our analysis of air, rail, and road travel data yields more granular risk estimates than possible with air passenger data alone (8).

By fitting our epidemiologic model to data on the first 19 cases reported outside of China, we estimate an epidemic doubling time of 7.31 days (95% CrI 6.26–9.66 days) and a cumulative total of 12,400 (95% CrI 3,112–58,465) infections in Wuhan by January 22 (Appendix). Both estimates are consistent with a similar epidemiologic analysis of the first 425 cases confirmed in Wuhan (4). Assuming these rates of early epidemic growth, we estimate that 130 cities in China have a $\geq 50\%$ chance of having a COVID case imported from Wuhan in the 3 weeks preceding the quarantine (Figure). By January 26, a total of 107 of these 130 high-risk cities had reported cases. However, 23 had not, including 5 cities with importation probabilities $>99\%$ and populations >2 million: Bazhong, Fushun, Laibin, Ziyang, and Chuxiong.

Under our lower bound estimate of 6.26 days for the doubling time, 190/369 cities lie above the 50% threshold for importation. Our risk assessment identified several cities throughout China likely to be harboring yet undetected cases of COVID-19 a week after the quarantine, suggesting that early 2020 ground and rail travel seeded cases far beyond the Wuhan region under quarantine.

Our conclusions are based on several key assumptions. To design our mobility model, we used data from Tencent (<https://heat.qq.com>), a major social media company that hosts applications including WeChat (≈ 1.13 billion active users in 2019) and QQ (≈ 808 million active users in 2019) (Statista, <https://www.statista.com>); consequently, our model might be demographically biased by the Tencent user base. Further, considerable uncertainty regarding the lag between infection and case detection remains. Our assumption of a 10-day lag is based on early estimates for the incubation period of COVID-19 (4) and prior estimates of the lag between symptom onset and detection for SARS (9). We expect that estimates for the doubling time and incidence of COVID-19 will improve as reconstructed linelists and more granular epidemiologic data become available (Appendix). However, our key qualitative insights likely are robust to these uncertainties, including extensive prequarantine exportations throughout China and far greater case counts in Wuhan than those reported before the quarantine.

Acknowledgments

We thank Henrik Salje, Dongsheng Luo, Bo Xu, Cécile Tran Kiem, Dong Xun, and Lanfang Hu for helpful discussions.

Code for estimating epidemiological parameters and probabilities of case introductions, as well as aggregate mobility data, are available from GitHub (https://github.com/linwangidd/2019nCoV_EID). Aggregate data also are available (Appendix Table 3). Additional code and data requests should be addressed to L.A.M. (laurenmeyers@austin.utexas.edu).

We acknowledge the financial support from National Institutes of Health (grant no. U01 GM087719), the Investissement d'Avenir program, the Laboratoire d'Excellence Integrative Biology of Emerging Infectious Diseases program (grant no. ANR-10-LABX-62-IBEID), European Union V.E.O project, the Open Fund of Key Laboratory of Urban Land Resources Monitoring and Simulation, Ministry of Land and Resources (grant no. KF-2019-04-034), and the National Natural Science Foundation of China (grant no. 61773091).

About the Author

Dr. Du is a postdoctoral researcher in the Department of Integrative Biology at the University of Texas at Austin. He develops mathematical models to elucidate the transmission dynamics, surveillance, and control of infectious diseases.

References

1. Wuhan Municipal Health Commission. Wuhan Municipal Health Commission briefing on the pneumonia epidemic situation 31 Dec 2019 [in Chinese]. 2020 [cited 2020 Jan 11]. <http://wjw.wuhan.gov.cn/front/web/showDetail/2019123108989>
2. World Health Organization. Statement on the second meeting of the International Health Regulations (2005) Emergency Committee regarding the outbreak of novel coronavirus (2019-nCoV). Geneva: the Organization; 2020 [cited 2020 Feb 5]. [https://www.who.int/news-room/detail/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-\(2005\)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-\(2019-ncov\)](https://www.who.int/news-room/detail/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-ncov))
3. Imai N, Dorigatti I, Cori A, Donnelly C, Riley S, Ferguson NM. MRC Centre for Global Infectious Disease Analysis. News 2019-nCoV. Report 2: estimating the potential total number of novel coronavirus cases in Wuhan City, China. London: Imperial College London; 2020 [cited 2020 Feb 5]. <https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/2019-nCoV-outbreak-report-22-01-2020.pdf>
4. Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, et al. Early transmission dynamics in Wuhan, China, of novel coronavirus-infected pneumonia. *N Engl J Med*. 2020 Jan 29 [Epub ahead of print]. <https://doi.org/10.1056/NEJMoa2001316>
5. Enserink M. War stories. *Science*. 2013;339:1264–8. <https://doi.org/10.1126/science.339.6125.1264>
6. World Health Organization. Disease outbreak news: novel coronavirus – Thailand (ex-China). 2020 Jan 14 [cited 2020

- Jan 27]. <https://www.who.int/csr/don/14-january-2020-novel-coronavirus-thailand-ex-china/en>
7. Wilder-Smith A, Telesman MD, Heng BH, Earnest A, Ling AE, Leo YS. Asymptomatic SARS coronavirus infection among healthcare workers, Singapore. *Emerg Infect Dis.* 2005;11:1142–5. <https://doi.org/10.3201/eid1107.041165>
 8. MOBS Lab. 2019 nCOV [cited 2020 Jan 26]. <https://www.mobs-lab.org/2019ncov.html>
 9. Chan JF-W, Yuan S, Kok K-H, To KK-W, Chu H, Yang J, 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 Jan 24 [Epub ahead of print]. [https://doi.org/10.1016/S0140-6736\(20\)30154-9](https://doi.org/10.1016/S0140-6736(20)30154-9)
 10. Wuhan Municipal Health Commission. Bulletin on pneumonitis associated with new coronavirus infection [In Chinese] [cited 2020 Jan 29]. <http://wjw.wuhan.gov.cn/front/web/list2nd/no/710>

Address for correspondence: Lauren Ancel Meyers, Department of Integrative Biology, The University of Texas at Austin, 2415 Speedway, Stop C0930, Austin, TX 78712, USA. email: laurenmeyers@austin.utexas.edu

Potential Presymptomatic Transmission of SARS-CoV-2, Zhejiang Province, China, 2020

Zhen-Dong Tong,¹ An Tang,¹ Ke-Feng Li,¹ Peng Li,¹ Hong-Ling Wang, Jing-Ping Yi, Yong-Li Zhang, Jian-Bo Yan

Author affiliation: Zhoushan Center for Disease Control and Prevention, Zhoushan, China

DOI: <https://doi.org/10.3201/eid2605.200198>

We report a 2-family cluster of persons infected with severe acute respiratory syndrome coronavirus 2 in the city of Zhoushan, Zhejiang Province, China, during January 2020. The infections resulted from contact with an infected but potentially presymptomatic traveler from the city of Wuhan in Hubei Province.

In January 2020, we investigated a 2-family cluster of persons infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the city of

¹These first authors contributed equally to this article.

Zhoushan in Zhejiang Province, China. We attributed the infections to contact with an infected but potentially presymptomatic traveler from the city of Wuhan in Hubei Province. Our epidemiologic investigation was reviewed and approved by the Ethics Committee of the Zhoushan Centers for Disease Control and Prevention (CDC).

The initial 2 cases of SARS-CoV-2 infection (coronavirus disease [COVID-19]) in Zhoushan were diagnosed in 2 teachers (persons A and D) from the same department at a college that had sponsored an academic conference on January 5, 2020. A 45-year-old teacher from Wuhan (person W) arrived on January 5 for the conference and joined persons A and D on January 6 for dinner, where they ate from common serving plates. After returning to Wuhan on January 7, person W experienced the onset of fever, cough, sore throat, and malaise on January 8. He visited a local hospital where, according to the patient's self-report, he was confirmed to have COVID-19 by a local office of the Chinese CDC. For person A and D, the only known potential exposures for SARS-CoV-2 were their dinner and conference attendance with person W (Figure).

On January 10, person A (a 29-year-old man) experienced the onset of fever, cough, and skin tingling and went to a local hospital for treatment. Laboratory tests at the hospital indicated leukopenia, and a real-time reverse transcription PCR (rRT-PCR) test for influenza A and B viruses was negative. The patient was given an antipyretic and some traditional medicines commonly used in China. After 3 days, his fever subsided, but his cough persisted. On January 15, the patient went to a different hospital, where routine blood test results were unremarkable but a chest radiograph revealed bilateral invasive lesions. He was prescribed amoxicillin and levofloxacin for 3 days. Because his cough did not improve, he was hospitalized for further evaluation. When the treating physician learned that the patient had had contact with a visitor from Wuhan before symptom onset, a throat swab specimen was sent for rRT-PCR testing for SARS-CoV-2 (1). On January 19, SARS-CoV-2 infection was confirmed at the laboratory of the Zhoushan CDC.

Person A lived with his 28-year-old wife (person B) and his 21-year-old sister (person C). The 2 women were confined at home for 14 days starting on the day of person A's hospital admission. Because of their 10 days of contact with person A after his fever onset, their respiratory specimens were collected on January 20 by Zhoushan CDC staff for